

GenCore version 4.5  
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OM protein - protein search, using sw model  
Run on: June 28, 2001, 16:14:34 ; Search time 362.28 Seconds  
(without alignments)  
18.575 Million cell updates/sec

Title: US-09-724-406-10  
Perfect score: 587  
Sequence: 1 DIVLTQSPASLAVSLGQRAT.....COQSNEDPTWFGGKLEIK 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
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15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
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18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577	98.3	111	15	AA195123
2	577	98.3	111	15	AA195123
3	570	97.1	113	22	AA195123
4	567	96.6	222	18	AA195123
5	567	96.6	238	19	AA195123
6	567	96.6	238	21	AA195123
7	567	96.6	238	21	AA195123
8	566	96.4	132	15	AA195123
	566	96.4	132	20	AA195123
	561	95.6	111	21	AA195123

12	561	95.6	111	21	AA195123
13	561	95.6	111	21	AA195123
14	561	95.6	305	21	AA195123
15	561	95.6	305	21	AA195123
16	561	95.6	305	21	AA195123
17	561	95.6	305	21	AA195123
18	557	94.9	111	10	AA195123
19	557	94.9	131	10	AA195123
20	550	93.7	131	14	AA195123
21	548	92.4	112	22	AA195123
22	540	92.0	131	11	AA195123
23	536	91.3	106	14	AA195123
24	536	91.3	106	21	AA195123
25	528	89.9	120	15	AA195123
26	526	89.6	111	14	AA195123
27	526	89.6	111	21	AA195123
28	524	89.3	246	18	AA195123
29	524	89.3	246	18	AA195123
30	524	89.3	288	19	AA195123
31	524	89.3	288	19	AA195123
32	524	89.3	531	21	AA195123
33	524	89.3	531	21	AA195123
34	524	89.3	531	21	AA195123
35	522	88.9	554	21	AA195123
36	522	88.9	103	21	AA195123
37	520	88.6	111	20	AA195123
38	520	88.6	111	20	AA195123
39	519	88.4	238	19	AA195123
40	519	88.4	238	19	AA195123
41	519	88.4	238	21	AA195123
42	517	88.1	281	19	AA195123
43	517	88.1	281	19	AA195123
44	508	86.5	238	19	AA195123
45	508	86.5	238	21	AA195123

ALIGNMENTS

RESULT 1  
ID AAR55123 standard; Protein; 111 AA.  
XX AC AAR55123;  
XX DT 27-JAN-1995 (first entry)  
XX DE Mouse anti-HIV mu5.5 light chain variable region.  
XX KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;  
XX OS human immunodeficiency virus; variable region; VH chain; murine.  
XX PH Mus musculus.  
XX FT Key  
XX FT Region Location/Qualifiers  
XX FT Region 1..23  
XX FT Region 24..38 /label= FR1  
XX FT Region 39..53 /label= CDR1  
XX FT Region 54..60 /label= FR2  
XX FT Region 61..92 /label= CDR2  
XX FT Region 93..101 /label= FR3  
XX FT Region 102..111 /label= CDR3  
XX FT Region /label= FR4  
XX PN JP06125783-A.  
XX PD 10-MAY-1994.

Murine derived pro  
Murine derived pro  
Antibody 4H5 L cha  
Antibody 4H5 L cha  
Murine derived pro  
Murine derived pro  
Immunoglobulin L c  
Amino acids sequen  
Anti-CD4 antibody  
Anti-SAF-1 monoclo  
Anti-Leu 3a light  
MAE15 light chain.  
Light chain amino  
Sequence of the mo  
MAE11 light chain.  
Light chain amino  
Anti-CD19 antibody  
Modified single ch  
Mouse OKT3 variant  
Mouse bispecific a  
Amino acid sequen  
Fv-antibody constr  
Antibody 4H5 L cha  
Murine derived pro  
Mus musculus anti-  
Variable light cha  
Humanised anti-Fas  
Humanised anti-Fas  
Human SCFVCD19 pro  
Chimeric CD19/cTCR  
Anti-Fas humanised  
Humanised anti-Fas

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Fri Jun 29 08:04:16 2001

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XX PF 28-DEC-1991; 91JP-0359808.
XX PR 28-DEC-1991; 91JP-0359808.
XX PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
XX DR WPI: 1994-187942/23.
XX DR N-PSDB; AAQ65554.
XX PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
XX PT and recombinant antibody consisting of the H- and L-chains,
XX PT useful in AIDS therapy
XX PS Example 3; Fig 4; 22pp; Japanese.
XX CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
XX CC The heavy and light chain variable regions from these antibodies
XX CC were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were
XX CC introduced into human framework regions to construct chimeric
XX CC antibodies (AAR55124-R55127).
XX SQ Sequence 111 AA;

Query Match 98.3%; Score 577; DB 15; Length 111;
Best Local Similarity 97.3%; Pred. No. 1e-40; Indels 0; Gaps 0;
Matches 108; Conservative 2; Mismatches 1;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSYDFDGSYMNWYQKPGQPPKVLIIYAASNLES 60
Db 1 divltqspaslavslgqratisckasqsydfdgdsymnwyyqkpgppkvllyaaasnlies 60
QY 61 GIPARFSGSGGDTFTLNHPVEEDAAATYCCQSNEDPWTf99ggtkleik 111
Db 61 giparfsgsggdtftlnhpveeedaatyccqsnedpwtf99ggtkleik 111

RESULT 2
AAR60302
ID AAR60302 standard; Protein; 111 AA.
XX AC AAR60302;
XX DT 09-MAR-1995 (first entry)
XX DE Anti HIV antibody light chain variable region.
XX KW Antibody; heavy chain; light chain; human immunodeficiency virus;
XX KW HIV; acquired immune deficiency syndrome; AIDS; treatment;
XX KW prophylaxis; Mus musculus; Homo sapiens.
XX OS Mus musculus.
XX FH Location/Qualifiers
XX FT 1..23 /label= Framework region 1.
XX FT 24..38 /label= CDR1.
XX FT 39..53 /label= Framework region 2.
XX FT 54..60 /label= CDR2.
XX FT 61..92 /label= Framework region 3.
XX FT 93..101 /label= CDR3.
XX FT 102..111 /label= Framework region 4.
XX PN W09415969-A.
XX PD 21-JUL-1994.

XX PF 14-JAN-1993; 93WO-JP00039.
XX PR 14-JAN-1993; 93AU-0032671.
XX PR 14-JAN-1993; 93WO-JP00039.
XX PA (KAGA) CHEMA SERO THERAPEUTIC RES INST.
XX PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
XX PI Tokiyoshi S;
XX DR WPI: 1994-249145/30.
XX DR N-PSDB; AAQ70372.
XX PT Recombinant chimeric anti HIV antibody - useful for the treatment
XX PT and prevention of HIV
XX PS Claim 15; Figure 4; 51pp; Japanese.
XX CC The recombinant antibody light chain has neutralising activity
XX CC against HIV. Chimeric antibodies comprising both mouse and human
XX CC sequences are useful in the treatment/prevention of AIDS caused by
XX CC HIV.
XX SQ Sequence 111 AA;

Query Match 98.3%; Score 577; DB 15; Length 111;
Best Local Similarity 97.3%; Pred. No. 1e-40; Indels 0; Gaps 0;
Matches 108; Conservative 2; Mismatches 1;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSYDFDGSYMNWYQKPGQPPKVLIIYAASNLES 60
Db 1 divltqspaslavslgqratisckasqsydfdgdsymnwyyqkpgppkvllyaaasnlies 60
QY 61 GIPARFSGSGGDTFTLNHPVEEDAAATYCCQSNEDPWTf99ggtkleik 111
Db 61 giparfsgsggdtftlnhpveeedaatyccqsnedpwtf99ggtkleik 111

RESULT 3
AAB71895
ID AAB71895 standard; Protein; 113 AA.
XX AC AAB71895;
XX DT 09-MAY-2001 (first entry)
XX DE Monoclonal antibody ST40 light chain.
XX KW Antibody; ST40; molecular mimetic; CD4; human immunodeficiency virus;
XX KW HIV; infection.
XX OS Unidentified.
XX PN W0200109191-A1.
XX PD 08-FEB-2001.
XX FF 02-AUG-2000; 2000WO-GB02972.
XX PR 02-AUG-1999; 99EP-0401968.
XX PA (SYNT-) SYNT:EM SA.
XX PI Casset F, Granier C, Kaczorek M, Lahana R, Rees A, Roux F;
XX DR WPI: 2001-168699/17.
XX CC Designing molecular mimetics to mimic a parent molecule activity,
XX CC useful e.g. therapeutically and diagnostically, uses computational
XX CC screening to identify active chemical groups by accessibility within
XX CC the parent molecule

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Fri Jun 29 08:04:16 2001

FT 74..80  
FT /label= CDR\_L2  
FT /note= "claim 9"  
FT 113..121  
FT /label= CDR\_L3  
FT /note= "claim 9"  
XX AU9859701-A.  
XX  
XX 08-OCT-1998.  
XX  
XX 30-MAR-1998; 98AU-0059701.  
XX  
XX 08-OCT-1997; 97JP-0276064.  
XX  
XX 01-APR-1997; 97JP-0082953.  
XX  
XX 25-JUN-1997; 97JP-0169088.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX Atio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;  
XX  
XX WPI; 1998-543440/47.  
XX  
XX N-PSDB; AA70130.  
XX  
XX New antibodies and proteins bind conserved epitope of Fas antigen -  
XX used to evaluate drugs in animal models and to treat Fas-associated  
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
XX myocarditis, hepatitis and AIDS  
XX  
XX Reference Example 4; Page 189-190; 292pp; English.  
XX  
XX This is the amino acid of the light chain of murine anti-human Fas  
XX monoclonal antibody HFE7A. cDNA (see AA70130) encoding the light  
XX chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)  
XX RNA by RT-PCR (see AA70127-28). The invention provides humanised  
XX HFE7A antibodies (see AA70131-37) produced by CDR grafting. These  
XX antibodies are capable of inducing apoptosis in abnormal cells  
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
XX cells. They are used to evaluate, in animal models, treatments of  
XX diseases that involve Fas/Fas ligand interactions, and also to treat  
XX such diseases, including autoimmune disease (e.g. systemic lupus  
XX erythematosus, Hashimoto's disease, graft versus host disease,  
XX Sjogren syndrome, pernicious anaemia, Addison's disease,  
XX scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid  
XX arthritis, autoimmune haemolytic anaemia, sterility, myasthenia  
XX gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura  
XX and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
XX myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
XX anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
XX  
XX Sequence 238 AA;  
XX  
XX Query Match 96.6%; Score 567; DB 19; Length 238;  
XX Best Local Similarity 97.3%; Pred. No. 1.4e-39;  
XX Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGPKVLIYAASNLES 60  
XX 21 divltqspaslavslgqratisckasqsvdgdsgymnwqkpgppklliyaasnles 80  
XX  
XX 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQNEDPMTFGGKLEIK 111  
XX 81 giparfsgsgstdfnlhnpveeedaatyycqsgnedprtfgggtkleik 131  
XX  
XX RESULT 6  
XX AAB14748  
XX ID AAB14748 standard; Protein: 238 AA.  
XX  
XX AC AAB14748;  
XX

DT 24-NOV-2000 (first entry)  
XX Mouse anti-Fas antibody HFE7A light chain.  
XX  
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
XX murine; complementarity determining region; CDR; human Fas;  
XX Fas ligand; apoptosis modulator; programmed cell death;  
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
XX hepatitis; AIDS; graft rejection; light chain.  
XX  
XX Mus musculus.  
XX  
XX JP2000169393-A.  
XX  
XX 20-JUN-2000.  
XX  
XX 30-SEP-1999; 99JP-0278301.  
XX  
XX 30-SEP-1998; 98JP-0276883.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX WPI; 2000-485645/43.  
XX  
XX N-PSDB; AA72109.  
XX  
XX Preventive or treating agent for the diseases caused by an abnormality  
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
XX anti-Fas antibody -  
XX  
XX Example 4; Page 70; 139pp; Japanese.  
XX  
XX The invention relates to compositions for the prevention or treatment  
XX of diseases caused by an abnormality in the Fas/Fas ligand system  
XX containing an anti-Fas antibody as the active component. The anti-Fas  
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
XX or a humanised version of HFE7A containing identical CDRs  
XX (complementarity determining regions) to antibody HFE7A. Via its  
XX interaction with Fas, the antibody of the invention acts as a modulator  
XX of apoptosis. The composition of the invention may therefore be used in  
XX the treatment or prevention of conditions such as autoimmune diseases,  
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
XX and organ graft rejection. The present sequence represents the  
XX light chain of the murine anti-human Fas monoclonal antibody HFE7A,  
XX which is produced by hybridoma HFE7A (FERM-BP-5828).  
XX  
XX Sequence 238 AA;  
XX  
XX Query Match 96.6%; Score 567; DB 21; Length 238;  
XX Best Local Similarity 97.3%; Pred. No. 1.4e-39;  
XX Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGPKVLIYAASNLES 60  
XX 21 divltqspaslavslgqratisckasqsvdgdsgymnwqkpgppklliyaasnles 80  
XX  
XX 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQNEDPMTFGGKLEIK 111  
XX 81 giparfsgsgstdfnlhnpveeedaatyycqsgnedprtfgggtkleik 131  
XX  
XX RESULT 7  
XX AAW90898  
XX ID AAW90898 standard; Protein: 238 AA.  
XX  
XX AC AAW90898;  
XX  
XX 08-AUG-2000 (first entry)  
XX  
XX Murine anti-Fas antibody HFE7A light chain protein.  
XX  
XX

Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; sterility; myasthenia gravis; Goodpasture syndrome; Crohn's disease; scleroderma; sterility; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Mus musculus.

EP990663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Serizawa N, Haryama H, Nakahara K, Tamaki I, Takahashi T;

WPI; 2000-258930/23.

N-PSDB; AAA11547.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Example reference 4; Page 104; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a murine anti-Fas monoclonal antibody HFE7A light chain described in the method of the invention.

Sequence 238 AA;

Query Match 96.6%; Score 567; DB 21; Length 238;

Best Local Similarity 97.3%; Pred. No. 1.4e-39;

Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60  
|||||

Db 21 divltqspaslavslgqratisckasqsvdygdsymnwqqpgqpkvliyaasnes 80  
QY 61 GIPARFSGSGCTFTLNHPVEEEDAAATYYCQSNEDPWTFGGTTKLEIK 111  
|||||  
Db 81 giparfsgsgtftlnhpveeedaattyyccsqsnedprtfgggtkleik 131  
|||||

RESULT 8

AAR70189

ID AAR70189 standard; Protein; 132 AA.

XX AAR70189;

XX AAR70189;

DT 20-SEP-1995 (first entry)

XX Mouse Mab 3B3 light chain.

DE Mouse Mab 3B3 light chain.

XX Chimeric antibody; humanized antibody; antibody engineering;

KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy.

KW Mus sp.

OS Mus sp.

XX Key

FT Location/Qualifiers

FT 1..20

FT /label= Sig\_peptide

FT 44..58

FT /label= CDR

FT /note= "complementarity determining region"

FT 74..80

FT /label= CDR

FT /note= "complementarity determining region"

FT 113..121

FT /label= CDR

FT /note= "complementarity determining region"

FT 113..121

FT /label= CDR

FT /note= "complementarity determining region"

FT 113..121

FT /label= CDR

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FT /note= "complementarity determining region"

FT 113..121

FT /label= CDR

FT /note= "complementarity determining region"

FT 113..121

FT /label= CDR

FT /note= "complementarity determining region"

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Db 21 divltqspaslavslgqratisckasqsvdygdsgymnyqkpgppklliyaasnles 80
QY 61 GIPARFSGSGTDFTLNHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
Db 81 giparfsgsgtdftlnhpveeadaatyyccgsnedpptfgggkcleik 131

RESULT 9
AAY23767
ID AAY23767 standard; Protein: 132 AA.
XX
AC
XX
XX
DT 13-SEP-1999 (first entry)
XX
DE Light chain variable region of murine IL-4 antibody 3B9.
XX
XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
KW rheumatoid arthritis; host-versus-graft disease; renal disease;
KW allergy.
XX
XX Mus sp.
XX
XX US5928904-A.
XX
XX 27-JUL-1999.
XX
XX 07-JUN-1995; 95US-0483632.
XX
XX 07-JUN-1995; 95US-0483632.
XX
XX 07-SEP-1993; 93US-0117366.
XX
XX 14-OCT-1993; 93US-0136783.
XX
XX 07-SEP-1994; 94WO-US10308.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Gross MS, Holmes SD, Sylvester DR;
XX
XX WPI: 1999-429500/36.
XX
XX N-PSDB; AAX65884.
XX
XX New DNA molecules encoding recombinant antibodies useful for
XX treating IL4-mediated conditions
XX
XX Example 3; Fig 1; 50pp; English.
XX
XX The present sequence represents the light chain variable region of
XX murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
XX in the production chimeric and humanised IL-4 monoclonal antibodies.
XX The antibodies of the invention are used in therapeutic and
XX pharmaceutical compositions for treating IL-4 mediated and
XX immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
XX conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
XX rheumatoid arthritis, host-versus-graft disease and renal disease.
XX They are also useful in the diagnosis of an allergy or condition
XX associated with excess IL-4 production through the measurement e.g. by
XX ELISA of circulating endogenous IL-4 levels in humans.
XX
XX Sequence 132 AA;
QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGQPPKLLIYAASNLES 60
Db 21 divltqspaslavslgqratisckasqsvdygdsgymnyqkpgppklliyaasnles 80

Query Match 96.4%; Score 566; DB 20; Length 132;
Best Local Similarity 97.3%; Pred. No. 9.6e-40;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 61 GIPARFSGSGTDFTLNHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
Db 81 giparfsgsgtdftlnhpveeadaatyyccgsnedpptfgggkcleik 131

RESULT 11

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QY 61 GIPARFSGSGTDFTLNHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
Db 81 giparfsgsgtdftlnhpveeadaatyyccgsnedpptfgggkcleik 131

RESULT 10
AAY18120
ID AAY18120 standard; Protein: 132 AA.
XX
AC
XX
XX 11-AUG-1999 (first entry)
XX
DE Light chain sequence for murine 3B9 antibody.
XX
XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
KW autoimmune disease; graft versus host disease.
XX
XX Mus sp.
XX
XX US9914110-A.
XX
XX 22-JUN-1999.
XX
XX 07-JUN-1995; 95US-0483636.
XX
XX 07-JUN-1995; 95US-0483636.
XX
XX 07-SEP-1993; 93US-0117366.
XX
XX 14-OCT-1993; 93US-0136783.
XX
XX 07-SEP-1994; 94WO-US10308.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Gross MS, Holmes SD, Sylvester DR;
XX
XX WPI: 1999-370482/31.
XX
XX N-PSDB; AAX79519.
XX
XX Recombinant IL4 antibodies
XX
XX Claim 24; Fig 1; 50pp; English.
XX
XX This sequence represents the light chain of the murine 3B9
XX antibody of the invention. The antibody is a chimeric or
XX humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
XX immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
XX the treatment of allergic disorders such as allergic rhinitis,
XX conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
XX The antibodies are also useful for regulating B and T cell proliferation
XX and as such are useful in the treatment of autoimmune diseases and graft
XX versus host disease.
XX
XX Sequence 132 AA;
QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGQPPKLLIYAASNLES 60
Db 21 divltqspaslavslgqratisckasqsvdygdsgymnyqkpgppklliyaasnles 80

Query Match 96.4%; Score 566; DB 20; Length 132;
Best Local Similarity 97.3%; Pred. No. 9.6e-40;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 61 GIPARFSGSGTDFTLNHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
Db 81 giparfsgsgtdftlnhpveeadaatyyccgsnedpptfgggkcleik 131

RESULT 11

```

AAV59267  
ID AAV59267 standard; protein; 111 AA.

AC AAV59267;  
DT 17-APR-2000 (first entry)  
DE Antibody 4H5 L chain fragment.  
KW CD4 antigen; anti-human; antibody; 4H5; drug.  
XX Mus sp.  
OS JP11332563-A.  
PN 07-DEC-1999.

PD 26-MAY-1998; 98JP-0163034.  
PF 26-MAY-1998; 98JP-0163034.  
PR (ASAH ) ASAHI KASEI KOGYO KK.  
XX WPI: 2000-091351/08.  
XX N-PSDB; AAZ58690.

XX An antibody and the nucleic acid coding the antibody -  
XX Disclosure; Page 22-23; 25pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The  
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC application for drugs. It is highly safe in human dose. The present  
CC sequence represents a L chain fragment of the antibody 4H5.

XX Sequence 111 AA;

Query Match 95.6%; Score 561; DB 21; Length 111;  
Best Local Similarity 96.4%; Pred. No. 2.1e-39;  
Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGDSDYNNWYQQKPGPPKVLIIYAASNLES 60  
Db 1 divltqspaslavslgqratisckasqsvdygdsgymwyqqkpgppklliyaaasnl 60  
QY 61 GIPARFSGSGGTDFTLNIHPVEEEDAATYVCOQSNEDPWTFGGKLEIK 111  
Db 61 giparfsgsggtdfnlnhpveeedaatyycqssedpptfgggtkleik 111

RESULT 12  
AAV51144  
ID AAV51144 standard; Protein; 111 AA.  
AC AAV51144;  
XX 31-MAR-2000 (first entry)  
DT Murine derived protein fragment #6.

DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; murine.

OS Mus sp.  
XX WO9961629-A1.  
PN 02-DEC-1999.  
XX 24-MAY-1999; 99WO-JP02711.

PR 25-MAY-1998; 98JP-0159957.  
PR 26-MAY-1998; 98JP-0163023.  
XX (ASAH ) ASAHI KASEI KOGYO KK.  
PA (ASAH ) ASAHI MEDICAL CO LTD.  
XX Ono M, Soka T, Morimoto I, Miyamura K;  
PI WPI: 2000-086720/07.

XX Devices containing antibodies recognising CD4 or CD34 and their use for  
PT the separation of CD4 or CD34 positive cells -  
PT Disclosure; Page 95; 111pp; Japanese.

XX This invention describes a novel device (I) for separating cluster  
CC differentiation (CD)-positive cells using a recombinant (chimeric or  
CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
CC for the separation of CD4 or CD34 positive cells, which is useful for  
CC the collection of hematopoietic undifferentiated cells, elimination of  
CC lymphocytes from cells to be used in bone marrow transplantation, the  
CC detection of leukemic cells and the production of medicinal  
CC compositions for the treatment of HIV infection and autoimmune diseases.  
CC This sequence represents a murine derived protein fragment which is used  
CC to illustrate the method of the invention.

XX Sequence 111 AA;

Query Match 95.6%; Score 561; DB 21; Length 111;  
Best Local Similarity 96.4%; Pred. No. 2.1e-39;  
Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGDSDYNNWYQQKPGPPKVLIIYAASNLES 60  
Db 1 divltqspaslavslgqratisckasqsvdygdsgymwyqqkpgppklliyaaasnl 60  
QY 61 GIPARESGSGGTDFTLNIHPVEEEDAATYVCOQSNEDPWTFGGKLEIK 111  
Db 61 giparfsgsggtdfnlnhpveeedaatyycqssedpptfgggtkleik 111

RESULT 13  
AAV51146  
ID AAV51146 standard; Protein; 111 AA.  
XX AAV51146;  
XX 31-MAR-2000 (first entry)  
DT Murine derived protein fragment #8.

DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; murine.

OS Mus sp.  
XX WO9961629-A1.  
PN 02-DEC-1999.  
XX 24-MAY-1999; 99WO-JP02711.  
PR 25-MAY-1998; 98JP-0159957.  
PR 26-MAY-1998; 98JP-0163023.

XX (ASAH ) ASAHI KASEI KOGYO KK.  
PA (ASAH ) ASAHI MEDICAL CO LTD.  
PI Ono M, Soka T, Morimoto I, Miyamura K;  
XX WPI: 2000-086720/07.

DR N-PSDB; AAZ44232.  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 PT  
 XX PS Disclosure; Page 97-98; 11pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 XX Sequence 111 AA;

Query Match 95.6%; Score 561; DB 21; Length 111;  
 Best Local Similarity 96.4%; Pred. No. 2.1e-39;  
 Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGDSDYNNWYQKPGQPPKVLIIYAASNL 60  
 DB 1 divltqspaslavslgqratisckasqsvdydgdsymnwyyqkpgppklliyaasnl 60  
 QY 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQSNEDEPWFEGGKLEIK 111  
 DB 61 giparfsgsgstdfnlhnpveeedaattyccqssedpptfgggkkleik 111

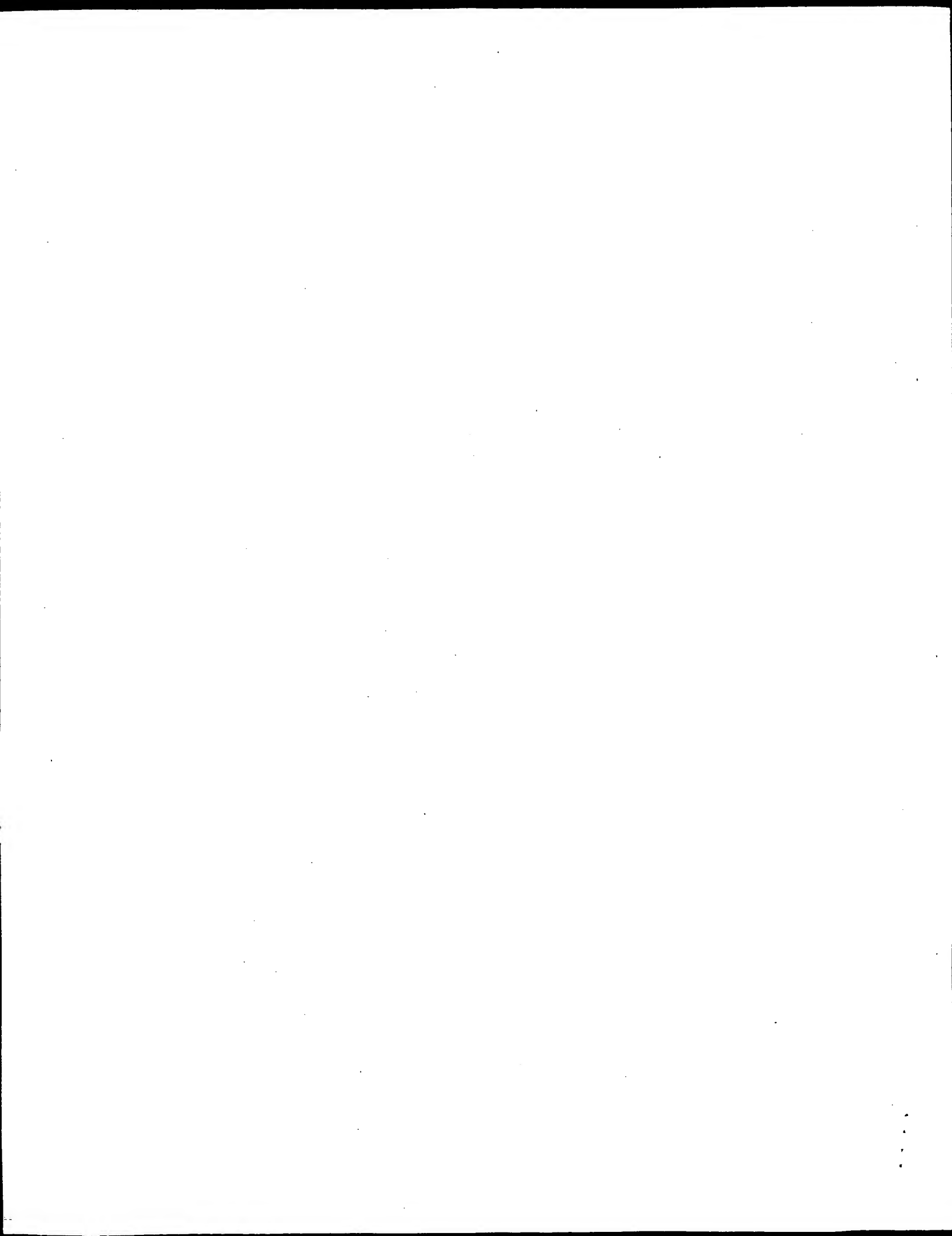
RESULT 14  
 AAY59264  
 ID AAY59264 standard; protein; 305 AA.  
 AC AAY59264;  
 XX  
 DT 17-APR-2000 (first entry)  
 DE Antibody 4H5 H chain sequence.  
 DE  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 XX WPI: 2000-091351/08.  
 DR N-PSDB; AAZ58663.  
 XX  
 XX An antibody and the nucleic acid coding the antibody -  
 PT  
 XX  
 XX Disclosure; Page 16-17; 25pp; Japanese.  
 PS  
 CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the H chain sequence of the antibody 4H5.  
 XX  
 XX Sequence 305 AA;

Query Match 95.6%; Score 561; DB 21; Length 305;  
 Best Local Similarity 96.4%; Pred. No. 5.7e-39;  
 Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGDSDYNNWYQKPGQPPKVLIIYAASNL 60  
 DB 23 divltqspaslavslgqratisckasqsvdydgdsymnwyyqkpgppklliyaasnl 82  
 QY 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQSNEDEPWFEGGKLEIK 111  
 DB 83 giparfsgsgstdfnlhnpveeedaattyccqssedpptfgggkkleik 133  
 RESULT 15  
 AAY59265  
 ID AAY59265 standard; protein; 305 AA.  
 XX  
 AC AAY59265;  
 XX  
 DT 17-APR-2000 (first entry)  
 DE Antibody 4H5 L chain sequence.  
 DE  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 XX WPI: 2000-091351/08.  
 DR N-PSDB; AAZ58664.  
 XX  
 XX An antibody and the nucleic acid coding the antibody -  
 PT  
 XX  
 XX Disclosure; Page 17-18; 25pp; Japanese.

The invention provides an antibody having affinity to CD4 antigen. The  
 anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 application for drugs. It is highly safe in human dose. The present  
 sequence represents the L chain sequence of the antibody 4H5.  
 XX  
 XX Sequence 305 AA;  
 QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGDSDYNNWYQKPGQPPKVLIIYAASNL 60  
 DB 156 divltqspaslavslgqratisckasqsvdydgdsymnwyyqkpgppklliyaasnl 215  
 QY 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQSNEDEPWFEGGKLEIK 111  
 DB 216 giparfsgsgstdfnlhnpveeedaattyccqssedpptfgggkkleik 266

Search completed: June 28, 2001, 16:14:35  
 Job time: 1323 sec









F;23-92/Disulfide bonds: #status predicted

Query Match 97.3%; Score 571; DB 1; Length 111;  
 Best Local Similarity 96.4%; Pred. No. 5.8e-43;  
 Matches 107; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60  
 |||||  
 Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60  
 |||||

Qy 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGSGTKLEIK 111  
 |||||  
 Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGSGTKLEIK 111  
 |||||

RESULT 3  
 KVM543  
 Ig kappa chain V region (PC7043) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
 C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: A01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 R:Mo, J.A.; Bona, C.A.; Holmdahl, R.  
 Eur. J. Immunol. 23, 2503-2510, 1993  
 A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec  
 A:Reference number: S42176; MUID:94009207  
 A:Accession: S42187  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:CROSS-references: EMBL:225444; NID:9407832; PIDN:CAA80931.1; PID:9407833  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42194  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MO>  
 A:CROSS-references: EMBL:225458; NID:9407844; PIDN:CAA80945.1; PID:9407845  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42190  
 A:Molecule type: DNA  
 A:Residues: 13-99 <MO>  
 A:CROSS-references: EMBL:225450; NID:9407838; PIDN:CAA80937.1; PID:9407839  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42189  
 A:Molecule type: DNA  
 A:Residues: 15-99 <MO>  
 A:CROSS-references: EMBL:225448; NID:9407836; PIDN:CAA80935.1; PID:9407837  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42188  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MO>  
 A:CROSS-references: EMBL:225446; NID:9407834; PIDN:CAA80933.1; PID:9407835  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42191  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:CROSS-references: EMBL:225452; NID:9407840; PIDN:CAA80939.1; PID:9407841  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42192  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:CROSS-references: EMBL:225454; NID:9407842; PIDN:CAA80941.1; PID:9407843  
 A:Note: V-kappa-21E; anti-collagen  
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa  
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 96.3%; Score 565; DB 1; Length 111;  
 Best Local Similarity 96.4%; Pred. No. 1.9e-42;  
 Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60  
 |||||  
 Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60  
 |||||

Qy 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGSGTKLEIK 111  
 |||||  
 Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGSGTKLEIK 111  
 |||||

RESULT 4  
 KVM583  
 Ig kappa chain V region (PC7183) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: B01937; A01937  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: B01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k  
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;16-94/Domain: immunoglobulin homology <IMM>  
 F;23-92/Disulfide bonds: #status predicted

Query Match 95.4%; Score 560; DB 1; Length 111;  
 Best Local Similarity 95.5%; Pred. No. 5.2e-42;  
 Matches 106; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60  
 |||||  
 Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60  
 |||||

Qy 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGSGTKLEIK 111  
 |||||  
 Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGSGTKLEIK 111  
 |||||

RESULT 5  
 KVM510  
 Ig kappa chain V region (PC7210) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: D01937; A01937  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: D01937  
 A:Molecule type: protein  
 A:Residues: 1-110 <WEI>  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k  
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;16-94/Domain: immunoglobulin homology <IMM>  
 F;23-92/Disulfide bonds: #status predicted

Query Match 93.8%; Score 550.5; DB 1; Length 110;  
 Best Local Similarity 94.6%; Pred. No. 3.5e-41;

Matches 105; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSLDYDGSYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 QY 61 GIPARFSGSGGTDTFTLNHPVEEEDAATYYCQSNEDPWTFFGGTKLEIK 111  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 61 GIPARFSGSGGTDTFTLNHPVEEEDAATYYCHQS-EDPWTFFGSGTKLEIK 110  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....

RESULT 6

SI9971  
 Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: SI9971  
 R:Weissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.  
 submitted to the EMBL Data Library, March 1992  
 A:Description: Structural characterization of CD4 mAb.  
 A:Reference number: SI9963  
 A:Accession: SI9971  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <WEI>  
 A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289  
 A:Experimental source: clone M-T310  
 A:Accession: SI9973  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <WEI>  
 A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293  
 A:Experimental source: M-T404  
 A:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 93.7%; Score 550; DB 2; Length 112;  
 Best Local Similarity 93.7%; Pred. No. 3.9e-41;  
 Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSLDYDGSYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 QY 61 GIPARFSGSGGTDTFTLNHPVEEEDAATYYCQSNEDPWTFFGGTKLEIK 111  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 61 GIPARFSGSGGTDTFTLNHPVEEEDAATYYCQSSDEPPTFFGGTKLEIK 111  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....

RESULT 7

SI9976  
 Ig kappa chain precursor V region (M-T310) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000  
 C:Accession: PH1226  
 R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flegler, D.; Lenz  
 Gene 121, 271-278, 1992  
 A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on  
 A:Reference number: PH1224; MUID:93077041  
 A:Accession: PH1226  
 A:Molecule type: mRNA  
 A:Residues: 1-131 <WEI>  
 A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766  
 A:Note: this mouse sequence was hybridized and fused with a human constant region gene  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-131/Product: Ig light chain V region #status predicted <MAT>  
 F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 93.7%; Score 550; DB 2; Length 131;  
 Best Local Similarity 93.7%; Pred. No. 4.5e-41;

Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 21 DIVLTQSPASLAVSLGORATISCKASQSLDYDGSYNNWYQKQPPKVLIIYAASNLES 80  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 QY 61 GIPARFSGSGGTDTFTLNHPVEEEDAATYYCQSNEDPWTFFGGTKLEIK 111  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 81 GIPARFSGSGGTDTFTLNHPVEEEDAATYYCQSSDEPPTFFGGTKLEIK 131  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....

RESULT 8

KVMSCL  
 Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 31-Mar-2000  
 C:Accession: A01936  
 R:McKean, D.J.; Bell, M.; Potter, M.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
 A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related  
 A:Reference number: A93822; MUID:79012520  
 A:Accession: A01936  
 A:Molecule type: protein  
 A:Residues: 1-111 <MCK>  
 C:Comment: This chain was isolated from a myeloma protein.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 93.4%; Score 548; DB 1; Length 111;  
 Best Local Similarity 93.7%; Pred. No. 5.7e-41;  
 Matches 104; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDTGTGSEYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 QY 61 GIPARFSGSGGTDTFTLNHPVEEEDAATYYCQSNEDPWTFFGGTKLEIK 111  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 61 GIPARFSGSGGTDTFTLNHPVEEEDAATYYCQSNEDPWTFFGGTKLEIK 111  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....

RESULT 9

SI9976  
 Ig kappa chain V region (M-T413) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: SI9976  
 R:Weissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.  
 submitted to the EMBL Data Library, March 1992  
 A:Description: Structural characterization of CD4 mAb.  
 A:Reference number: SI9963  
 A:Accession: SI9976  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <WEI>  
 A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 542; DB 2; Length 112;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-40;  
 Matches 102; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSLDYDGSYNNWYQKQPPKVLIIYAASNLES 60  
 |||||.....:|||||.....:|||||.....:|||||.....:|||||.....

```

QY      61  GIPARFSSGSGTDTLNIHPVEEDAATYYCQSNEDPWTFGGCKLEIK 111
        |||||
        61  GIPARFSSGSGTDTLNIHPVEEXAATYYCQSNEDPWTFGGCKLEIK 111
        |||||
Db      61  GIPARFSSGSGTDTLNIHPVEEXAATYYCQSNEDPWTFGGCKLEIK 111
        |||||

RESULT 12

```

A:Reference number: A90412; MUID:78235887

A:Contents: M63

A:Accession: B90412

A:Molecule type: protein

A:Residues: 1-35 <BUR>

R:McKean, D.; Potter, M.; Hood, L.

Biochemistry 12, 760-771, 1973

A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains

A:Reference number: A90374; MUID:73140225

A:Contents: M63

A:Accession: B90374

A:Molecule type: protein

A:Residues: 21-46,'Q',48-53,'B',55-57,'Z',59-86,'F',88-131 <MCK>

A:Note: This sequence has since been revised in reference A93822

R:McKean, D.J.; Bell, M.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related

A:Reference number: A93822; MUID:79012520

A:Contents: M63; AB22

A:Accession: B93822

A:Molecule type: protein

A:Residues: 1-53,69-107 <MC2>

A:Accession: C93822

A:Molecule type: protein

A:Residues: 21-119,'Y',121-131 <MC3>

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152

A:Contents: PC9245; PC4050

A:Accession: C93204

A:Molecule type: protein

A:Residues: 21-119,'Y',121-131 <WEI>

A:Accession: D93204

A:Molecule type: protein

A:Residues: 21-119,'L',121-123,'A',125-129,'L',131 <WE2>

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A:Reference number: PH0571; MUID:92381444

A:Accession: PH1078

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 21-122 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73

C:Comment: The M63 precursor sequence is shown.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status experimental <SIG>

F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>

F:36-114/Domain: immunoglobulin homology <IMM>

F:43-112/Disulfide bonds: #status predicted

Query Match 85.3%; Score 501; DB 1; Length 131;

Best Local Similarity 84.7%; Pred. No. 8.1e-37;

Matches 94; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNYQKPGQPPKVLIIYAASNL 60

Db 21 NVLTQSPASLAVSLGORATISCKASQSVDSYGNFPMHYQKPGQPPKLLIYASNL 80

QY 61 GIPARFSGSGSDFTLTINHPVEEADAATYYCOQSNEDPWTFGGKLEIK 111

Db 81 GVPARFSGSGSDFTLTIDPVEADDAATYYCOQNNEDPWTFGGKLEIK 131

RESULT 15

KVMS37

Ig kappa chain V regions (PC3741, T111) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 21-Jan-2000

C:Accession: A93204; A93822; A01934

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152

A:Contents: PC3741

A:Accession: A93204

A:Molecule type: protein

A:Residues: 1-111 <WEI>

R:McKean, D.J.; Bell, M.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related

A:Reference number: A93822; MUID:79012520

A:Contents: T111

A:Accession: A93822

A:Molecule type: protein

A:Residues: 1-111 <MCK>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 85.0%; Score 499; DB 1; Length 111;

Best Local Similarity 85.6%; Pred. No. 1e-36;

Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNYQKPGQPPKVLIIYAASNL 60

Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDSYGNFPMHYQKPGQPPKLLIYASNL 60

QY 61 GIPARFSGSGSDFTLTINHPVEEADAATYYCOQSNEDPWTFGGKLEIK 111

Db 61 GIPARFSGSGSDFTLTINHPVEADDAATYYCOQSNEDPWTFGGKLEIK 111

Search completed: June 28, 2001, 15:58:43

Job time: 371 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:20 ; Search time 411.58 Seconds  
(without alignments)  
35.682 Million cell updates/sec

Title: US-09-724-406-10  
Perfect score: 587  
Sequence: 1 DIVLQSPASLAVSLGORAT.....COQSNEDPWFGGGKLEIK 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_16.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organellar.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertebrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	457	77.9	103	11 Q9JL80	Q9JL80 mus musculus
2	393	67.0	108	4 Q9UL77	Q9UL77 homo sapien
3	377.5	64.3	109	4 Q9UL78	Q9UL78 homo sapien
4	374	63.7	108	4 Q9UL70	Q9UL70 homo sapien
5	366	62.4	114	4 Q9UL90	Q9UL90 homo sapien
6	361	61.5	108	4 Q9UL79	Q9UL79 homo sapien
7	360.5	61.4	107	4 Q9UL81	Q9UL81 homo sapien
8	357	60.8	108	4 Q9UL83	Q9UL83 homo sapien
9	353.5	60.2	109	4 Q9UL85	Q9UL85 homo sapien
10	349	59.5	214	11 Q9JLA5	Q9JLA5 mus musculus
11	340.5	58.0	104	11 Q9JL82	Q9JL82 mus musculus
12	339.5	57.8	109	4 Q9UL86	Q9UL86 mus musculus
13	335	57.1	107	11 Q9ER29	Q9ER29 mus musculus
14	333.5	56.8	106	5 Q9UA10	Q9UA10 schistosoma
15	329	56.0	97	11 Q9JL76	Q9JL76 mus musculus
16	325	55.4	107	11 Q9JL84	Q9JL84 mus musculus
17	323	55.0	298	11 Q9QYF0	Q9QYF0 mus musculus
18	320	54.5	99	11 Q9JL74	Q9JL74 mus musculus
19	319	54.3	101	11 Q9JL78	Q9JL78 mus musculus

20	293	49.9	109	6 Q9NOW5	Q9NOW5 oryctolagus
21	235.5	40.1	107	4 Q9NSD6	Q9NSD6 homo sapien
22	233	39.7	107	4 Q9UL82	Q9UL82 homo sapien
23	204	34.8	130	4 Q9NF29	Q9NF29 homo sapien
24	172.5	29.4	109	11 Q9ET13	Q9ET13 mus musculus
25	150	25.6	135	4 Q9H524	Q9H524 homo sapien
26	133	22.7	123	11 Q61243	Q61243 mus musculus
27	129	22.0	93	4 Q9UL76	Q9UL76 homo sapien
28	115.5	19.7	337	13 Q9IB02	Q9IB02 spheeroides
29	107	18.2	142	13 Q9HQ2	Q9HQ2 ginglymosto
30	106.5	18.1	122	4 Q9G603	Q9G603 homo sapien
31	106.5	18.1	122	4 Q9G604	Q9G604 homo sapien
32	106.5	18.1	137	4 Q9UDR1	Q9UDR1 homo sapien
33	106	18.1	136	13 Q9YHR9	Q9YHR9 ginglymosto
34	105	17.9	100	6 Q77624	Q77624 bos taurus
35	105	17.9	136	13 Q9YHP4	Q9YHP4 ginglymosto
36	103.5	17.6	334	13 Q9IB05	Q9IB05 spheeroides
37	103	17.5	118	4 Q9UL91	Q9UL91 homo sapien
38	102.5	17.5	228	11 Q70153	Q70153 rattus norv
39	101.5	17.3	509	11 Q08907	Q08907 mus musculus
40	101	17.2	288	4 Q00517	Q00517 mus musculus
41	100	17.0	136	13 Q9YHP2	Q9YHP2 ginglymosto
42	100	17.0	145	4 Q9H022	Q9H022 homo sapien
43	100	17.0	504	4 Q9UIJ6	Q9UIJ6 homo sapien
44	99.5	17.0	503	4 P78324	P78324 homo sapien
45	99	16.9	137	13 Q9YHQ0	Q9YHQ0 ginglymosto

## ALIGNMENTS

RESULT 1

Q9JL80 ID Q9JL80 PRELIMINARY; PRT; 103 AA.

AC Q9JL80;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF206026; AAF69324.1; -  
DR InterPro; IPR003006; -  
DR InterPro; IPR003596; -  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 103  
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 77.9%; Score 457; DB 11; Length 103;  
Best Local Similarity 81.6%; Pred. No. 1.2e-42;  
Matches 84; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 9 ASLAVSLGRATISCKASQVDFDGDSDYNNVYQKPGOPPKVLIYAASNEESGTPAREFG 68

Db 1 ASLAVSLGRATISCKASQVDFDGDSDYNNVYQKPGOPPKVLIYAASNEESGTPAREFG 60

QY 69 SSGSGDTFTLNHPVEEDAAATYCOQSNEDPWFGGGKLEIK 111

Db 61 SSGSGDTFTLNHPVEEDAAATYCOQSNEDPWFGGGKLEIK 103

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RESULT 2
Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 67.0%; Score 393; DB 4; Length 108;
Best Local Similarity 65.8%; Pred. No. 1.3e-35;
Matches 73; Conservative 17; Mismatches 17; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLASVGLGORATISCKASQSVDFDGDSDYMNWYQKPKVLIYAASNL 60
DB 1 DIQMTQSPSLASVGDRTVITCRASQSI----SSLYNYYQKPKGKAPNLLIYAAS 56
QY 61 GIPARFSGSGGDTFTLNTHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111
DB 57 GVPFRSGSGGDTFTLTISLQPEDVATYYCQSYSTSWTFEGTKVEIK 107

RESULT 3
Q9UL78
ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035036; AAD56272.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 63.7%; Score 374; DB 4; Length 108;
Best Local Similarity 64.0%; Pred. No. 1.5e-33;
Matches 71; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLASVGLGORATISCKASQSVDFDGDSDYMNWYQKPKVLIYAASNL 60
DB 1 DIQMTQSPSLASVGDRTVITCRASQGI----SNLYAWYQKPKGKVPKSLIYAAS 56
QY 61 GIPARFSGSGGDTFTLNTHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111
DB 57 GVPFRSGSGGDTFTLTISLQPEDVATYYCQKYNAPRTFGPGTKLEIK 107

RESULT 5
Q9UL80
ID Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

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DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 64.3%; Score 377.5; DB 4; Length 109;
Best Local Similarity 65.8%; Pred. No. 6.4e-34;
Matches 73; Conservative 14; Mismatches 21; Indels 3; Gaps 1;

QY 1 DIVLTQSPASLASVGLGORATISCKASQSVDFDGDSDYMNWYQKPKVLIYAASNL 60
DB 1 EIVLTQSPFTLSLSPGERATLSCRASQSV---SSSLAWYQQKPKGQAPRLIYGA 57
QY 61 GIPARFSGSGGDTFTLNTHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111
DB 58 GIPDRFSGSGGDTFTLTISRLEPEDCAVYYCQYGGSSPLTFGGTKVEIK 108

RESULT 4
Q9UL70
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 63.7%; Score 374; DB 4; Length 108;
Best Local Similarity 64.0%; Pred. No. 1.5e-33;
Matches 71; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLASVGLGORATISCKASQSVDFDGDSDYMNWYQKPKVLIYAASNL 60
DB 1 DIQMTQSPSLASVGDRTVITCRASQGI----SNLYAWYQKPKGKVPKSLIYAAS 56
QY 61 GIPARFSGSGGDTFTLNTHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111
DB 57 GVPFRSGSGGDTFTLTISLQPEDVATYYCQKYNAPRTFGPGTKLEIK 107

RESULT 5
Q9UL80
ID Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

```



OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL; AF035034; AAD56270.1; -.  
 DR InterPro; IPR003006; -.  
 DR InterPro; IPR003596; -.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;  
 Query Match 62.4%; Score 366; DB 4; Length 114;  
 Best Local Similarity 62.8%; Pred. No. 1.2e-32;  
 Matches 71; Conservative 15; Mismatches 25; Indels 2; Gaps 2;  
 QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKPGPKVLIYAASNL 59  
 Db 1 DVVMTQSPSLPVTLPQASISCRSSQSPVSDGNTYLNWFQORPGQSPRLIYKVSNRD 60  
 QY 60 SGIPARFSGSGGTDFTLNHPVEEDAATYYCQSQSNE-DPWTFGGGKLEIK 111  
 Db 61 SGVPDRFSGSGGTDFTLTIASRVEDGVYICMGQTHWPPWTFGGGKVEIK 113  
 RESULT 6  
 QYUL79 PRELIMINARY; PRT; 108 AA.  
 ID QYUL79;  
 AC QYUL79;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL; AF035035; AAD56271.1; -.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; -.  
 DR InterPro; IPR003596; -.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;  
 Query Match 61.5%; Score 361; DB 4; Length 108;  
 Best Local Similarity 63.18; Pred. No. 4e-32;  
 Matches 70; Conservative 15; Mismatches 22; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKPGPKVLIYAASNL 60  
 Db 1 DIVMTQSPSLPVTLPQASISCRSSQSPVSDGNTYLNWFQORPGQSPRLIYKVSNRD 56  
 QY 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSQSNE-DPWTFGGGKLEIK 111  
 Db 57 GVPDRFSGSGGTDFTLTIASRVEDGVYICMGQTHWPPWTFGGGKVEIK 107  
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 QYUL81 PRELIMINARY; PRT; 107 AA.  
 ID QYUL81;  
 AC QYUL81;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL; AF035033; AAD56269.1; -.  
 DR HSP; P80362; IWL.  
 DR InterPro; IPR003006; -.  
 DR InterPro; IPR003596; -.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;  
 Query Match 61.4%; Score 360.5; DB 4; Length 107;  
 Best Local Similarity 62.2%; Pred. No. 4.5e-32;  
 Matches 69; Conservative 20; Mismatches 17; Indels 5; Gaps 2;  
 QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKPGPKVLIYAASNL 60  
 Db 1 DIQMTQSPSLPVTLPQASISCRSSQSPVSDGNTYLNWFQORPGQSPRLIYKVSNRD 56  
 QY 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSQSNE-DPWTFGGGKLEIK 111  
 Db 57 GVPDRFSGSGGTDFTLTIASRVEDGVYICMGQTHWPPWTFGGGKVEIK 106  
 RESULT 8  
 QYUL83 PRELIMINARY; PRT; 108 AA.  
 ID QYUL83;  
 AC QYUL83;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 60.8%; Score 357; DB 4; Length 108;
Best Local Similarity 63.1%; Pred. No. 1.1e-31;
Matches 70; Conservative 17; Mismatches 20; Indels 4; Gaps 1;

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:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVMTQSPATLSVSPGERATLSCWASQST-----SSNLAWYQKPGQAPRLIIYCASTRAT 56

QY 61 GIPARFSGSGGTDFTLNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 GIPARFSGSGGTDFTLNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 107

RESULT 9
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035029; AAD56265.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 60.2%; Score 353.5; DB 4; Length 109;
Best Local Similarity 63.4%; Pred. NO. 2.7e-31;
Matches 71; Conservative 16; Mismatches 20; Indels 5; Gaps 2;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYNNWYQKPGPPKVLIIYAASNLES 60
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Db 1 EIVMTQSPATLSVSPGERATLSCWASQST-----SSNLAWYQKPGQAPRLIIYCASTRAT 56

QY 61 GIPARFSGSGGTDFTLNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
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Db 57 GIPARFSGSGGTDFTLNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 108

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RESULT 10
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01789; IWCP.
DR InterPro; IPR003006; -.
DR InterPro; IPR003600; -.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR SMART; SM00410; IG_like; 1.
DR NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 59.5%; Score 349; DB 11; Length 214;
Best Local Similarity 59.5%; Pred. No. 1.9e-30;
Matches 66; Conservative 18; Mismatches 23; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYNNWYQKPGPPKVLIIYAASNLES 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQLTQSPSPMYASLGERVTITCKASQDI-----NSYLSWFOQKPGKPKTLIYRANRLVD 56

QY 61 GIPARFSGSGGTDFTLNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 GIPARFSGSGGTDFTLNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 107

RESULT 11
Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Walkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-D-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206024; AAF69322.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
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Query Match          58.0%; Score 340.5; DB 11; Length 104;
Best Local Similarity 64.1%; Pred. No. 6.7e-30;
Matches 66; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

Qy 10 SLAVSLGORATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNIESGIPARFSG 68
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Qy 69 SGSGDTFTLNHPVEEDAATYCCQSNEDPWTFFGGTGKLEIK 111
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Db 62 SGSGDTFTLISRVEAEDLGVFCQTHPYTFGGTGKLEIK 104

RESULT 12
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035028; AAD5264.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 109
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SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match          57.8%; Score 339.5; DB 4; Length 109;
Best Local Similarity 60.4%; Pred. No. 9.1e-30;
Matches 67; Conservative 16; Mismatches 25; Indels 3; Gaps 1;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDPDGSYNNWYQKPGQPKVLIYAASNLES 60
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Qy 61 GIPARFSGSGSGTFTLNHPVEEDAATYCCQSNEDPWTFFGGTGKLEIK 111
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Db 58 GIPDRFSGSGSGTFTLTISRLEPDAFYVYCCQYSGSIPTFFGPGTKVDIK 108

RESULT 13
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AC Q9ER29;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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Query Match          57.1%; Score 335; DB 11; Length 107;
Best Local Similarity 59.8%; Pred. No. 2.8e-29;
Matches 64; Conservative 17; Mismatches 24; Indels 2; Gaps 1;

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Qy 62 IPARFSGSGSGTFTLNHPVEEDAATYCCQSNEDPWTFFGGTGK 108
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Db 61 VPDRFSGSGSGTFTLTISVQVTDLADYFCQGHYRTPTFFGSGTKL 107

RESULT 14
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AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF207620; AAF19434.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR003008; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF000047; Ig; 1.
DR ProDom; PD000600; -; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 106
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SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match          56.8%; Score 333.5; DB 5; Length 106;
Best Local Similarity 58.7%; Pred. No. 4e-29;
Matches 64; Conservative 16; Mismatches 24; Indels 5; Gaps 1;
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Job time: 948 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:13 ; Search time 138.34 Seconds  
(without alignments)  
16.163 Million cell updates/sec

Title: US-09-724-406-10  
Perfect score: 587  
Sequence: 1 DIVLTQSPASLAVSLQRAT.....CQSNEDPWTFGGKLEIK 111

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Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	566	96.4	132	2	US-08-483-636-2
4	566	96.4	132	2	US-08-483-632-2
5	536	91.3	106	3	US-08-466-151-6
6	528	89.9	120	1	US-08-111-080-24
7	528	89.9	120	1	US-08-211-980-24
8	528	89.9	120	5	PCT-US93-07967-24
9	526	89.6	111	3	US-08-466-151-2
10	520	88.6	111	2	US-08-887-352B-5
11	520	88.6	111	4	US-09-109-207C-5
12	500	85.2	131	1	US-08-137-117D-25
13	500	85.2	131	2	US-08-436-717-25
14	498	84.8	131	2	US-08-483-636-58
15	498	84.8	131	2	US-08-483-632-58
16	492	83.8	131	2	US-08-483-636-14
17	492	83.8	131	2	US-07-634-278-54
18	490	83.5	111	1	US-07-634-278-54
19	490	83.5	111	1	US-08-477-728-54
20	490	83.5	111	1	US-08-474-040-54
21	490	83.5	111	1	US-08-487-200-54
22	490	83.5	111	4	US-08-484-537-54
23	490	83.5	131	1	US-07-634-278-67
24	490	83.5	131	1	US-08-477-728-67
25	490	83.5	131	1	US-08-474-040-67
26	490	83.5	131	1	US-08-487-200-67
27	490	83.5	131	4	US-08-484-537-67

28 484 82.5 131 2 US-08-521-751A-10 Sequence 10, Appl  
29 484 82.5 239 2 US-08-553-497A-18 Sequence 18, Appl  
30 481 81.9 131 4 US-08-579-378A-18 Sequence 18, Appl  
31 481 81.9 218 5 PCT-US96-13152-2 Sequence 2, Appl  
32 480 81.8 131 3 US-08-836-561-25 Sequence 25, Appl  
33 479 81.6 131 1 US-08-137-117D-33 Sequence 33, Appl  
34 479 81.6 131 2 US-08-436-717-33 Sequence 33, Appl  
35 479 81.6 218 5 PCT-US94-14106-57 Sequence 57, Appl  
36 478 81.4 111 1 US-08-275-053-11 Sequence 11, Appl  
37 478 81.4 112 3 US-09-065-059-13 Sequence 11, Appl  
38 478 81.4 121 1 US-08-111-080-22 Sequence 22, Appl  
39 478 81.4 121 1 US-08-211-980-22 Sequence 22, Appl  
40 478 81.4 121 5 PCT-US93-07967-22 Sequence 22, Appl  
41 477.5 81.3 110 1 US-08-017-570-2 Sequence 2, Appl  
42 477.5 81.3 110 1 US-08-471-426-2 Sequence 2, Appl  
43 477.5 81.3 110 5 PCT-US94-01709-2 Sequence 2, Appl  
44 477 81.3 111 1 US-08-491-845-16 Sequence 16, Appl  
45 477 81.3 115 4 US-08-513-968-51 Sequence 51, Appl

## ALIGNMENTS

RESULT 1  
US-08-491-845-8  
; Sequence 8, Application US/08491845  
; Patent No. 5773247  
; GENERAL INFORMATION:  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: SETOSAKI, Kouichi  
; APPLICANT: OSATOMI, Kiyoshi  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/491,845  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP93/00039  
; FILING DATE: 14-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: MAEDA-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-491-845-8

Query Match 97.4%; Score 572; DB 1; Length 111;

US-08-483-632-2

Sequence 2, Application US/08483632  
Patent No. 5928904  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TREATMENT OF IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-632-2

Query Match 96.4%; Score 566; DB 2; Length 132;  
Best Local Similarity 97.3%; Pred. No. 8.8e-54;  
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYNNWYQKPGQPKVLIYAASNLES 60  
Db 21 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYNNWYQKPGQPKVLIYAASNLES 80  
QY 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSQSNEPDTFTFGGKLEIK 111  
Db 81 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSQSNEPDTFTFGGKLEIK 131  
RESULT 5  
US-08-466-151-6  
Sequence 6, Application US/08466151  
Patent No. 6037453  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 06-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/879495  
FILING DATE: 07-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P2C1D1  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-466-151-6

Query Match 91.3%; Score 536; DB 3; Length 106;  
Best Local Similarity 95.3%; Pred. No. 1.1e-50;  
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYNNWYQKPGQPKVLIYAASNLES 60  
Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYNNWYQKPGQPKVLIYAASNLES 60  
QY 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSQSNEPDTFTFGGK 106  
Db 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSQSNEPDTFTFGGK 106  
RESULT 6  
US-08-111-080-24  
Sequence 24, Application 08/111080  
Patent No. 5558865  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: 30run  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA

```

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-111-080-24

Query Match      89.9%; Score 528; DB 1; Length 120;
Best Local Similarity 91.8%; Pred. No. 9.5e-50;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY    1 DIVLTQSPASLAVSLGORATISCKASQSDVDFGDSVMNMYQKPGPKVLIIYAASNLES 60
Ddb   1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSVMNMYQKPGPKLLIYAASNYES 60

QY    61 GPIPARFGSGSGTDTFLNIHPVEEDAATYYCQSNEDPWFEGGGTKLEI 110
Ddb   61 GPIPARFYGGSGTDFTNTIHPEVEDAATYYCQSIDDPSTFGGGTKLEI 110

RESULT 7
US-08-211-980-24
; Sequence 24, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980
; FILING DATE:

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TELEFAX: (312) 474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US93-07967-24

Query Match 89.9%; Score 528; DB 5; Length 120;  
 Best Local Similarity 91.8%; Pred. No. 9.5e-50;  
 Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNWYQKPGQPKVLIYAASNLES 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNWYQKPGQPKVLIYAASNLES 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 GIPARFSGSGGTDFTLNIHPVEEEDAATYCCQSNEDPWTFGGKLEI 110  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 GIPARFSGSGGTDFTLNIHPVEEEDAATYCCQSNEDPWTFGGKLEI 110  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9  
 US-08-466-151-2  
 ; Sequence 2, Application US/08466151  
 ; Patent No. 6037453  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Immunoglobulin Variants  
 ; NUMBER OF SEQUENCES: 65  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/466,151  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/466163  
 ; FILING DATE: 06-Jun-1995  
 ; APPLICATION NUMBER: 08/405617  
 ; FILING DATE: 15-MAR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/185899  
 ; FILING DATE: 26-JAN-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/879495  
 ; FILING DATE: 07-MAY-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/744768  
 ; FILING DATE: 14-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Svoboda, Craig G.  
 ; REGISTRATION NUMBER: 39,044  
 ; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-1489  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 111 amino acids

TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-466-151-2

Query Match 89.8%; Score 526; DB 3; Length 111;  
 Best Local Similarity 91.0%; Pred. No. 1.4e-49;  
 Matches 101; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNWYQKPGQPKVLIYAASNLES 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNWYQKPGQPKVLIYAASNLES 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 GIPARFSGSGGTDFTLNIHPVEEEDAATYCCQSNEDPWTFGGKLEI 111  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 EIPARFSGSGGTDFTLNIHPVEEEDAATYCCQSHEDPYTFGAGTKLEIK 111  
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RESULT 10  
 US-08-887-352B-5  
 ; Sequence 5, Application US/08887352B  
 ; Patent No. 5994511  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
 ; TITLE OF INVENTION: Improving Polypeptides  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/887,352B  
 ; FILING DATE: 03-Jul-1997  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Svoboda, Craig G.  
 ; REGISTRATION NUMBER: 39,044  
 ; REFERENCE/DOCKET NUMBER: P1123  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-1489  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 111 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; US-08-887-352B-5

Query Match 88.6%; Score 520; DB 2; Length 111;  
 Best Local Similarity 90.1%; Pred. No. 6.2e-49;  
 Matches 100; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNWYQKPGQPKVLIYAASNLES 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 DIQLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNWYQKPGQPKVLIYAASNLES 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 GIPARFSGSGGTDFTLNIHPVEEEDAATYCCQSNEDPWTFGGKLEI 111  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 EIPARFSGSGGTDFTLNIHPVEEEDAATYCCQSHEDPYTFGAGTKLEIK 111  
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 RESULT 11  
 US-09-109-207C-5

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; Sequence 5, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109, 207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-109-207C-5

Query Match      88.6%; Score 520; DB 4; Length 111;
Best Local Similarity 90.1%; Pred. No. 6.2e-49;
Matches 100; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMWYQKPGQPKVLIYAASNL 60
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Db 1 DIQLTQSPASLAVSLGQRATISCKASQSVDFDGSYMWYQKPGQPKVLIYAASYL 60
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 61 GIPARESGSGTDFTLNHPVEEEDAATYYCQSNEDPMTFEGGKLEIK 111
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Db 61 EIPARESGSGTDFTLNHPVEEEDAATFYCQSHEDPYTFGAGTKLEIK 111
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RESULT 12
US-08-137-117D-25
; Sequence 25, Application US/08137117D
; Patent No. 5795365
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-25

Query Match      85.2%; Score 500; DB 1; Length 131;
Best Local Similarity 85.6%; Pred. No. 1.1e-46;
Matches 95; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMWYQKPGQPKVLIYAASNL 60
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 21 DIVLTQSPASLAVSLGQRATISCKASQSVSTSGSYMHWYQKPGQTPKLLIYLASNL 80
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 61 GIPARESGSGTDFTLNHPVEEEDAATYYCQSNEDPMTFEGGKLEIK 111
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 81 GVPARESGSGTDFTLNHPVEEEDAATYYCQHSRENPTYTFEGGKLEIK 131
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 13
US-08-436-717-25
; Sequence 25, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
```



Qy 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGDSDSYNNWYQQKPGQPPKVLIIYAASNLES 60  
Db 20 DIVMTQSPDLSLAVSLGERATINCKASQSVDFDGDSDSYNNWYQQKPGQPPKVLIIYAASNLES 79  
Qy 61 GIPARFSGSGGTDFTLNIHPVEEEDAAATYYCQGSNEDPWTFGGGTKLEIK 111  
Db 80 GVPDRFSGSGGTDFTLTISSLQAEDVAVYYCQGSNEDPPTFGGGTKVEIK 130

Search completed: June 28, 2001, 16:01:13  
Job time: 521 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:35 ; Search time 105.36 Seconds  
(without alignments)  
36.089 Million cell updates/sec

Title: us-09-724-406-10

Perfect score: 587

Sequence: 1 DIVLTQSPASLAVSLGQRAT.....COQSNEDPWTFGGKLEIK 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	574	97.8	111	1	KV3Q_MOUSE
2	571	97.3	111	1	KV3Q_MOUSE
3	565	96.3	111	1	KV3M_MOUSE
4	560	95.4	111	1	KV3N_MOUSE
5	550.5	93.8	110	1	KV3P_MOUSE
6	548	93.4	111	1	KV3L_MOUSE
7	502	85.5	111	1	KV3R_MOUSE
8	501	85.3	131	1	KV3I_MOUSE
9	499	85.0	111	1	KV3H_MOUSE
10	495	84.3	111	1	KV3S_MOUSE
11	494	84.2	111	1	KV3T_MOUSE
12	493	84.0	111	1	KV3C_MOUSE
13	492	83.8	111	1	KV3J_MOUSE
14	490	83.5	111	1	KV3A_MOUSE
15	480	81.8	111	1	KV3K_MOUSE
16	476	81.1	111	1	KV3U_MOUSE
17	472.5	80.5	112	1	KV3B_MOUSE
18	471	80.2	111	1	KV3D_MOUSE
19	469	79.9	132	1	KV3F_MOUSE
20	468	79.7	112	1	KV3G_MOUSE
21	454	77.3	108	1	KV3V_MOUSE
22	442	75.3	111	1	KV3E_MOUSE
23	406	69.2	134	1	KV4C_HUMAN
24	398	67.8	114	1	KV4A_HUMAN
25	391.5	66.7	133	1	KV4B_HUMAN
26	386	65.8	108	1	KV5P_MOUSE
27	375.5	64.0	133	1	KV2F_HUMAN
28	374.5	63.8	129	1	KV3M_HUMAN
29	374	63.7	129	1	KV1W_HUMAN
30	372	63.4	108	1	KV1B_HUMAN
31	372	63.4	108	1	KV1E_HUMAN
32	371.5	63.3	129	1	KV3H_HUMAN
33	371	63.2	108	1	KV1H_HUMAN

34	371	63.2	108	1	KV1M_HUMAN	P01605	homo sapien
35	371	63.2	108	1	KV1V_HUMAN	P80362	homo sapien
36	365.5	62.3	129	1	KV3L_HUMAN	P18135	homo sapien
37	363	61.8	108	1	KV1K_HUMAN	P01603	homo sapien
38	363	61.8	108	1	KV1N_HUMAN	P01606	homo sapien
39	362.5	61.8	113	1	KV2G_MOUSE	P01631	mus musculus
40	362	61.7	108	1	KV1P_HUMAN	P01608	homo sapien
41	361.5	61.6	107	1	KV6A_MOUSE	P01675	mus musculus
42	361.5	61.6	109	1	KV3B_HUMAN	P01620	homo sapien
43	361.5	61.6	109	1	KV3D_HUMAN	P01622	homo sapien
44	358	61.0	108	1	KV1O_HUMAN	P01607	homo sapien
45	358	61.0	108	1	KV1R_HUMAN	P01610	homo sapien

## ALIGNMENTS

RESULT 1							
ID	KV3Q_MOUSE	STANDARD;	PRT;	111	AA.		
AC	P01669;						
DT	21-JUL-1986 (Rel. 01, Created)						
DT	21-JUL-1986 (Rel. 01, Last sequence update)						
DT	15-JUL-1999 (Rel. 38, Last annotation update)						
DE	IG KAPPA CHAIN V-III REGION PC 7769.						
OS	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_TaxID=10090;						
RN	[1]						
RP	SEQUENCE.						
RX	MEDLINE=79073152; PubMed=103003;						
RA	Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;						
RT	"Rearrangement of genetic information may produce immunoglobulin						
RT	diversity."						
RL	Nature 276:785-790 (1978).						
DR	PIR; E01937; KVM569.						
DR	InterPro: IPR003006;						
DR	Pfam: PF00047; Ig; 1.						
KW	Immunoglobulin V region.						
FT	DOMAIN 1						
FT	DOMAIN 2						
FT	DOMAIN 3						
FT	DOMAIN 4						
FT	DISULFID						
FT	NON_TER						
SQ	SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;						
Query Match 97.8%; Score 574; DB 1; Length 111;							
Best Local Similarity 97.3%; Pred. No. 2.3e-51;							
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;							
QY	1	DIVLTQSPASLAVSLGQRATISCKASQSVDPDGSYNNYQKRPQPKVLIYAASNL	60				
Db	1	DIVLTQSPASLAVSLGQRATISCKASQSVDPDGSYNNYQKRPQPKVLIYAASNL	60				
QY	61	GIPARFSGSGGTDFTLNHPVEEDAATYYCOQSNEDPWTFGGKLEIK 111					
Db	61	GIPARFSGSGGTDFTLNHPVEEDAATYYCOQSNEDPWTFGGKLEIK 111					
RESULT 2							
ID	KV3O_MOUSE	STANDARD;	PRT;	111	AA.		
AC	P01667;						
DT	21-JUL-1986 (Rel. 01, Created)						
DT	21-JUL-1986 (Rel. 01, Last sequence update)						
DT	15-JUL-1999 (Rel. 38, Last annotation update)						
DE	IG KAPPA CHAIN V-III REGION PC 6308.						

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity";  
 RL Nature 276:785-790(1978).  
 DR PIR; C01937; KVM508.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 97.3%; Score 571; DB 1; Length 111;  
 Best Local Similarity 96.4%; Pred. No. 4.7e-51;  
 Matches 107; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60  
 Qy 61 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111  
 Db 61 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111

RESULT 3  
 KV3M\_MOUSE  
 ID KV3M\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01665;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 7043.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity";  
 RL Nature 276:785-790(1978).  
 DR PIR; A01937; KVM543.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 96.3%; Score 565; DB 1; Length 111;  
 Best Local Similarity 96.4%; Pred. No. 1.9e-50;  
 Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60  
 Qy 61 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111  
 Db 61 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111

RESULT 4  
 KV3N\_MOUSE  
 ID KV3N\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01666;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 7183.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity";  
 RL Nature 276:785-790(1978).  
 DR PIR; B01937; KVM583.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 95.4%; Score 560; DB 1; Length 111;  
 Best Local Similarity 95.5%; Pred. No. 6.1e-50;  
 Matches 106; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60  
 Qy 61 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111  
 Db 61 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111

RESULT 5  
 KV3P\_MOUSE  
 ID KV3P\_MOUSE STANDARD; PRT; 110 AA.  
 AC P01668;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 7210.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity.";  
 RL Nature 276:785-790(1978).  
 DR PIR: D01937; KWS10.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 100  
 FT DOMAIN 101 110  
 FT DISULFID 23 92  
 FT NON\_TER 110 110  
 SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 93.8%; Score 550.5; DB 1; Length 110;  
 Best Local Similarity 94.6%; Pred. No. 5.5e-49;  
 Matches 105; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKPGQPPKVLIIYAASNL 60  
 DB 1 DIVLTQSPASLAVSLGORATISCKASQSLDYDGSYNNWYQKPGQPPKVLIIYAASNL 60  
 QY 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGTTKLEIK 111  
 DB 61 GIPARFSGSGTDTLNIHPVEEDAATYCHOS-EDPWTFGGTTKLEIK 110

RESULT 6  
 KV3L\_MOUSE  
 ID KV3L\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01664;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION CBPC 101.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE.

RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 related mouse kappa variable regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR: A01936; KWSCL.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.

FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 93.4%; Score 548; DB 1; Length 111;  
 Best Local Similarity 93.7%; Pred. No. 9.9e-49;  
 Matches 104; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKPGQPPKVLIIYAASNL 60  
 DB 1 DIVLTQSPASLAVSLGORATISCKASQVDYTGESYNNWYQKPGQPPKVLIIYAASNL 60  
 QY 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGTTKLEIK 111  
 DB 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGTTKLEIK 111

RESULT 7  
 KV3R\_MOUSE  
 ID KV3R\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01670;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 6684.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity.";  
 RL Nature 276:785-790(1978).  
 DR PIR: A01938; KWS84.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 85.5%; Score 502; DB 1; Length 111;  
 Best Local Similarity 87.4%; Pred. No. 4.3e-44;  
 Matches 97; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKPGQPPKVLIIYAASNL 60  
 DB 1 DIVLTQSPASLAVSLGORATISCKASQSVTSGSYNNWYQKPGQPPKVLIIYAASNL 60  
 QY 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGTTKLEIK 111  
 DB 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGTTKLEIK 111

RESULT 8  
 KV3L\_MOUSE  
 ID KV3L\_MOUSE STANDARD; PRT; 131 AA.  
 AC P01661;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM5M6.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 85.38; Score 501; DB 1; Length 131;
Best Local Similarity 84.78; Pred. No. 6.6e-44;
Matches 94; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDFGDSYMNWYQKPGQPKVLIYAASNL 60
DB 21 NVLTQSPASLAVSLGQRATISCKASQSDVDFGDSYMNWYQKPGQPKVLIYAASNL 80
QY 61 GIPARFSGSGSDFTLTNIHPVEEEDAAATYCCQSNEDPWTFGGKLEIK 111
DB 81 GVPARFSGSGSRDFTLTIDPVEADDAATYCCQNNEDPWTFGGKLEIK 131

RESULT 9
KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01938; KVM575.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 85.08; Score 499; DB 1; Length 111;
Best Local Similarity 85.6%; Pred. No. 8.7e-44;
Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDFGDSYMNWYQKPGQPKVLIYAASNL 60
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDFGDSYMNWYQKPGQPKVLIYAASNL 60
QY 61 GIPARFSGSGSDFTLTNIHPVEEEDAAATYCCQSNEDPWTFGGKLEIK 111
DB 61 GIPARFSGSGSRDFTLTIDPVEADDAATYCCQNNEDPWTFGGKLEIK 111

RESULT 10
KV3S_MOUSE STANDARD; PRT; 111 AA.
ID KV3S_MOUSE
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01938; KVM575.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

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RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC 1- MISCELLANEOUS; THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM537.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 85.08; Score 499; DB 1; Length 111;
Best Local Similarity 85.6%; Pred. No. 8.7e-44;
Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDFGDSYMNWYQKPGQPKVLIYAASNL 60
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDFGDSYMNWYQKPGQPKVLIYAASNL 60
QY 61 GIPARFSGSGSDFTLTNIHPVEEEDAAATYCCQSNEDPWTFGGKLEIK 111
DB 61 GIPARFSGSGSRDFTLTIDPVEADDAATYCCQNNEDPWTFGGKLEIK 111

RESULT 10
KV3S_MOUSE STANDARD; PRT; 111 AA.
ID KV3S_MOUSE
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01938; KVM575.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

```





```
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 83.8%; Score 492; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 4.4e-43;
Matches 93; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60
Db 1 NIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60

QY 61 GIPARFSGSGGTDTFLNIHPVEEDAAATYCCQSNEDPWTFFGGTKLEIK 111
Db 61 GVPARFSGSGRTDFTLTIDPVEADDAATYCCQNNEDPYTFGGTKLEIK 111

RESULT 14
KV3A_MOUSE STANDARD; PRT; 111 AA.
AC P01654;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 2880/PC 1229.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01930; KVM580.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

Query Match 83.5%; Score 490; DB 1; Length 111;
Best Local Similarity 82.9%; Pred. No. 7.1e-43;
Matches 92; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60

QY 61 GIPARFSGSGGTDTFLNIHPVEEDAAATYCCQSNEDPWTFFGGTKLEIK 111
Db 61 GVPARFSGSGRTDFTLTIDPVEADDAATYCCQNNEDPYTFGGTKLEIK 111

RESULT 15
KV3K_MOUSE STANDARD; PRT; 111 AA.
AC P01663;
```

```
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01935; KVM5M6.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;
```

```
Query Match 81.8%; Score 480; DB 1; Length 111;
Best Local Similarity 82.0%; Pred. No. 7.2e-42;
Matches 91; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60
Db 1 NIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60

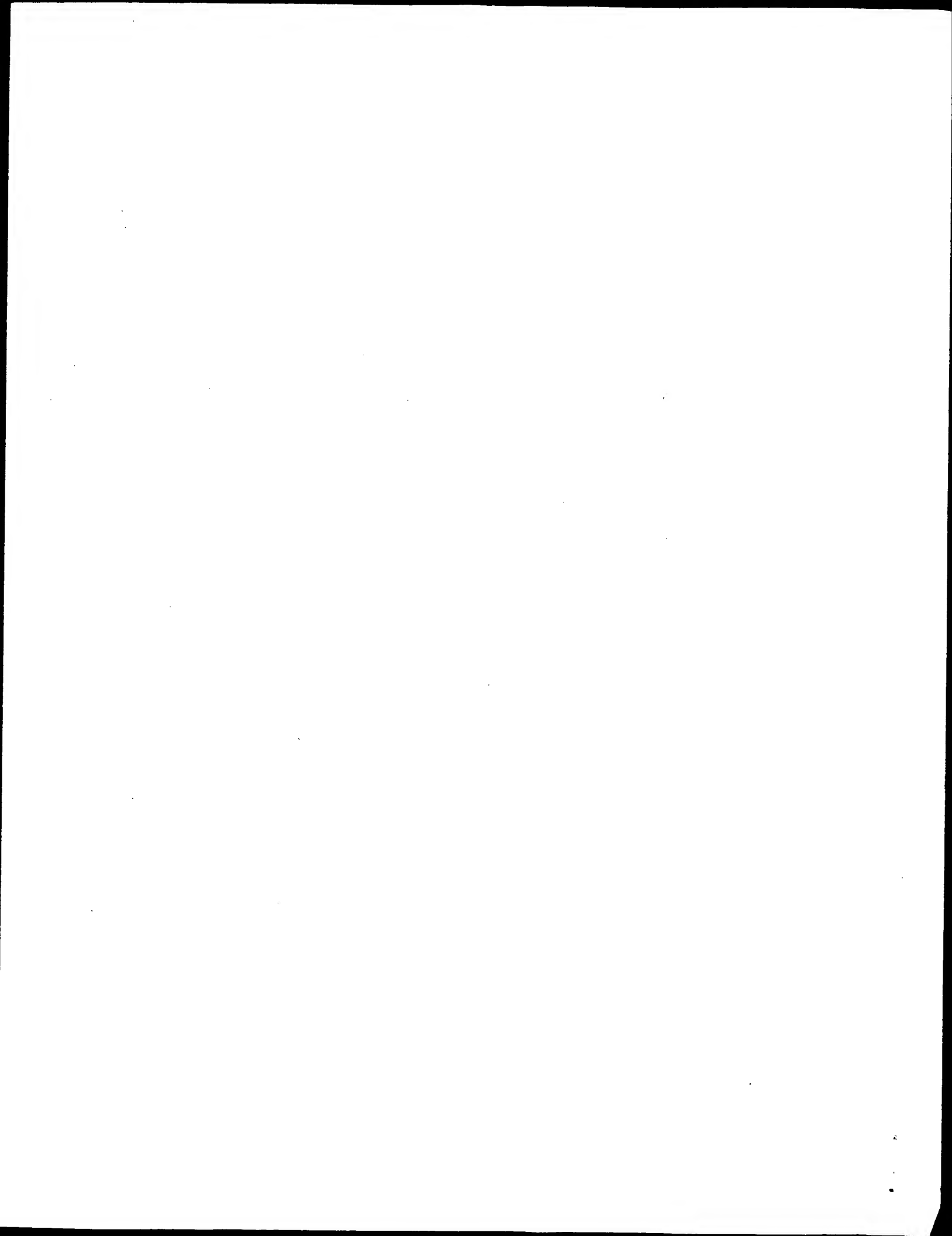
QY 61 GIPARFSGSGGTDTFLNIHPVEEDAAATYCCQSNEDPWTFFGGTKLEIK 111
Db 61 GVPARFSGSGRTDFTLTIDPVEADDAATYCCQNNEDPYTFGGTKLEIK 111

Search completed: June 28, 2001, 15:54:35
Job time: 123 sec.
```

us-09-724-406-10.rsp

---

• Fri Jun 29 08:04:19 2001



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: June 18, 2001, 15:28:27 ; Search time 19 Seconds  
(without alignments)  
352.005 Million cell updates/sec

Title: US-09-724-406-2  
Perfect score: 635  
Sequence: 1 QIQQQSGPEVYKPGASVKI.....NYGNWFAVWGQGTQVTVSA 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0401.\*  
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
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18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543.5	85.6	139	18 W29750	Anti-HMFG MAB CTMO
2	539.5	85.0	138	21 W56873	MAB CT-M-01 heavy
3	537.5	84.6	139	14 R33950	CTMO1 VH. Synthet
4	521.5	82.1	469	14 R40384	Monoclonal antibod
5	501.5	79.0	116	16 R79241	Heavy chain variab
6	497.5	78.3	122	18 W01577	Lead binding MAB 1
7	496	78.1	249	9 P80154	Biosynthetic antib
8	495	78.0	123	21 W78325	Anti-zeta-chain an
9	495	78.0	532	21 W78328	Bispecific anti-ze
10	494	77.8	119	18 W01585	Lead binding MAB 1
11	494	77.8	121	18 W07437	Anti-DNA antibody

12	490	77.2	119	19 W49814	Amino acid sequenc
13	490	77.2	138	14 R32666	Mouse C4G1 Ig heav
14	490	77.2	138	19 W49810	Variable region of
15	488.5	76.9	118	18 W27359	Heavy chain variab
16	487.5	76.8	116	17 W03742	Murine monoclonal
17	486	76.5	117	17 R88716	Mouse antibody hea
18	485.5	76.5	116	21 B10443	Murine monoclonal
19	485	76.4	136	8 P70624	Sequence encoded b
20	485	76.4	136	18 W10584	Anti-hepatitis B h
21	485	76.4	136	18 W16340	Mouse-human chimae
22	485	75.4	136	18 W10239	Chimeric anti-hepa
23	485	75.4	136	19 W47510	Human anti-hepatit
24	485	75.4	136	19 W41054	Human anti-hepatit
25	485	75.4	136	19 W47517	Human anti-hepatit
26	485	75.4	136	20 W89535	Chimeric anti-hepa
27	484.5	76.3	118	16 W79159	Human IgE receptor
28	484.5	76.3	118	18 W27356	Heavy chain variab
29	484.5	76.3	382	18 W26651	Chimeric receptor
30	484.5	76.3	403	18 W26648	Chimeric receptor
31	484.5	76.3	473	18 W26646	Chimeric receptor
32	484.5	76.3	514	18 W26647	Chimeric receptor
33	484.5	76.3	651	18 W26649	Chimeric receptor
34	484.5	76.3	692	18 W26650	Chimeric receptor
35	484	76.2	555	22 B19871	Activating polypep
36	484	76.2	565	22 B19873	Activating polypep
37	484	76.2	577	22 B19872	Activating polypep
38	484	76.2	704	22 B19888	MLV envelope glyco
39	483.5	76.1	139	15 B53328	KM-796 heavy chain
40	483.5	76.1	139	20 Y28384	Anti-GM2 heavy cha
41	483.5	76.1	139	20 Y28356	Antibody chain use
42	483	76.1	117	9 P80148	Biosynthetic antib
43	481.5	75.8	120	12 R13721	Control fusion pro
44	480.5	75.7	118	13 R22420	Murine heavy chain
45	480.5	75.7	118	15 R54757	Mouse HMFG1 heav

## ALIGNMENTS

RESULT 1

ID W29750 standard; Protein; 139 AA.

AC W29750:

XX 14-JAN-1998 (first entry)

DT Anti-HMFG MAB CTMO1 heavy chain variable region.

DE Humanised antibody; CDR-grafted antibody; chimeric antibody; CTMO1;  
KW complementarity determining region; human milk fat globule; HMFG;  
KW monoclonal antibody; MAB; mouse; cancer; breast cancer;  
KW ovary carcinoma; lung cancer; uterus cancer; diagnosis; therapy.

XX Mus musculus.

XX Key Location/Qualifiers  
XX Peptide 1..19  
XX Misc-difference 344 /label= Leader\_peptide  
XX FT "encoded by ACG"

XX EP781845-A2.

XX 02-JUL-1997.

XX 24-SEP-1992; 92EP-0308680.

XX 26-SEP-1991; 91GB-0020467.

XX (CLLT ) CELLTech THERAPEUTICS LTD.

XX Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;



XX The sequences given in R33950-51 represent the heavy and light chain  
 CC variable domains of CTMO1 respectively. The DNA encoding these  
 CC peptides was isolated by PCR using the primer sequences given in  
 CC Q38879-80. Examination of these amino acid sequences revealed  
 CC considerable homology with other characterised immunoglobulin genes.  
 CC The murine monoclonal antibody (WAB), CTMO1, was confirmed to be an  
 CC IgG-kappa antibody. CTMO1 was used in the production of a humanised  
 CC antibody for in vivo diagnosis and therapy of carcinomas of ovary,  
 CC breast, uterus and lung.  
 XX Sequence 139 AA;

Query Match 84.6%; Score 537.5; DB 14; Length 139;  
 Best Local Similarity 86.7%; Pred. No. 1.7e-36;  
 Matches 104; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

QY 1 QIQLOQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60  
 DB 20 QIQLOQSGPEVVKPGASVKISKASGYFTDYINWVKQKPGQGLEWIGWIDPGSGNTKY 79  
 QY 61 NEKFKGKATLTVDTSSTAFMQSLSTSEDTAVYFCANYGNYWFA--YWGQGTQVTVSA 117  
 DB 80 NEKFKGKATLTVDTSSTAFMQSLSTSEDTAVYFCAREKTYTYYAMDYWGQGTSTVSA 139

## RESULT 4

R40384

ID R40384 standard; Protein: 469 AA.

AC R40384;

XX R40384;

DT 08-FEB-1994 (first entry)

XX Monoclonal antibody M(alpha)2-3 Heavy-chain.

DE anti-snake small neurotoxin antibody; heavy chain; IgG2;

KW immunoglobulin; bispecific bivalent antibody; cell-targetting;

KW cytotoxic agent.

XX

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= signal\_peptide

FT Region 20..139

FT /label= variable

FT Region 140..236

FT /label= constant

FT Region 237..252

FT /label= joining

FT Region 253..362

FT /label= constant

FT Region 363..469

FT /label= constant

XX EP556111-A.

XX

XX 18-AUG-1993.

XX

XX 09-FEB-1993; 93EP-0400323.

XX

XX 11-FEB-1992; 92FR-0001505.

XX

XX (BOUL/) BOULAIN J.

XX (CONS ) COMMISSARIAT ENERGIE ATOMIQUE.

XX

XX Boulain J, Ducancel F, Gillet D, Menez A;

XX WPI; 1993-260351/33.

XX N-PSDB; Q48037.

XX

XX New immunoglobulin hybrid proteins - with immunoglobulin

XX fragments linked to dimeric protein, for diagnostic or

PT

PT therapeutic use

XX

XX Example 1; Fig 3A; 37pp; French.

XX

CC A fragment of the heavy chain (VH + CH1) from the anti-snake small

CC neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from

CC hybridoma-derived cDNA using primers Q48039 and Q48040. A light

CC chain fragment (VL + CL) was amplified from the same source using

CC primers Q48041 and Q48042. The two amplified fragments were

CC inserted into the same vector; the H-chain fragment was inserted

CC (in-frame) between codons 6-7 of the phoA coding sequence and the

CC L-chain fragment was inserted into a cassette which contained a

CC phoA S-D sequence, a signal peptide and the first 6 codons of phoA.

CC The cassette was positioned between the termination codon and

CC the transcription termination sequence of phoA. The fusion

CC construct is expected to encode a hybrid protein comprising two

CC identical Ab-derived units. The invention also covers hybrid

CC proteins containing two different Ab-derived units (i.e. to produce

CC bispecific antibodies). When a toxic protein is used in place of

CC phoA, the hybrid molecules can be used as cell-targetting

CC therapeutic agents.

XX

SQ Sequence 469 AA;

Query Match 82.1%; Score 521.5; DB 14; Length 469;

Best Local Similarity 83.3%; Pred. No. 1.3e-36;

Matches 100; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60

DB 20 QIQLOQSGPEVVKPGASVKISKASGYFTDYINWVKQKPGQGLEWIGWYPGSGNTKY 79

QY 61 NEKFKGKATLTVDTSSTAFMQSLSTSEDTAVYFCANYGNYWFA--YWGQGTQVTVSA 117

DB 80 NEKFKGKATLTVDTSSTAFMQSLSTSEDTAVYFCAREKATLIDYWGQGTSTVSS 139

## RESULT 5

R79241

ID R79241 standard; Protein: 116 AA.

AC R79241;

XX

XX 21-DEC-1995 (first entry)

XX

XX Heavy chain variable region for monoclonal antibody 4A10.

XX Monoclonal antibody; heavy metal; mercury; variable region;

XX heavy chain.

XX

XX Synthetic.

XX

XX WO9520607-A.

XX

XX 03-AUG-1995.

XX

XX 27-JAN-1995; 95WO-US01199.

XX

XX 27-JAN-1994; 94US-0187407.

XX

XX (BION-) BIONEERASKA INC.

XX

XX Lopez O, Wagner FW, Wylie DE;

XX

XX WPI; 1995-275415/36.

XX N-PSDB; Q97498.

XX

XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from

XX monoclonal antibodies, used for detecting, removing, adding or

XX neutralising heavy metals

XX

XX Claim 13; Page 54; 106pp; English.

PS

XX	DNA encoding heavy metal binding polypeptide sequences - used for
PT	detecting, removing, adding or neutralising heavy metals, such as
PT	lead cations
XX	
PS	Claim 12; Page 58; 125pp; English.
XX	
CC	The present sequence represents the heavy chain variable region for
CC	monoclonal antibody (MAb) 1254, which immunoreacts with a lead cation.
CC	The sequence was derived from RNA isolated from mouse hybridoma cells.
CC	The protein can be used for binding heavy metals, such as lead cations
CC	. It can be used for detecting, removing, adding or neutralising the
CC	heavy metals in biological and inanimate systems. It can be used in
CC	e.g. aqueous liquid systems, in biological or environmental systems or
CC	in such compositions as perfumes, cosmetics, pharmaceuticals, health
CC	care products, skin treatment products, pesticides, herbicides,
CC	solvents used in the production of semi-conductor and integrated
CC	circuit components and production materials for electronic components.
CC	The products can provide for applications involving minute amounts of
CC	specific heavy metals.
XX	
XX	Sequence 122 AA:
SO	

Query Match 78.3%; Score 497.5; DB 18; Length 122;  
Best Local Similarity 77.0%; Pred. No. 3.5e-35;  
Matches 94: Conservative 9; Mismatches 14; Indels 5;

```
QY      1 QIQLOQSPEVVKPGASVKISCKASGYTFDYIITWVKQKPGQGLEWGIIYPGSGNTKY   60  
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db      1 qvqlqgsaaqlvkpqasvlksckasytfteylhwkarsqaalewiawfypqsaslky    60
```

**QY** 61 NEKFKGKATLTVDTSSSTAFMQLSSLTSEDVAVFCA---NYGNV--WFAYWGQGQTIV 115  
||||| ||||| ||||| :||| ||||| :||||| ||||| ||||| ||||| |||||  
**Pb** 61 nekfkdkatltdkssstvymlsrlltsedsavvfcarheqvgqvawfaywggqltv 120

Qy 116 SA 117  
11  
Db 121 sa 122

RESULTS

P80154  
ID P80154 standard: protein: 249 AA

XX  
AC P80154.

01-JAN-1980 (first entry)

XX Biosynthetic antibody binding site. DE

AA Biosynthetic antibody binding site; framework region; assay; imaging;  
KW KW multifunctional protein.

PN 08809344-A.  
XX

FD 01-DEC-1966.  
XX

XX  
PE 19-MAY-1988; 88WU-US01/37.

PR  
XX  
21-MAY-1987; 8705-0032800.

PA (CREA<sup>-</sup>) CREATINE BIOMOLEC  
XXXX  
XX

DR WPI; 1988-3339Z  
DR N-PSDB: N80180.

Recombinant multifunctional

PT sequence for DI  
PT solid support.

VV



us-09-724-406-2.rag

Fri Jun 29 08:04:38 2001

XX The present invention describes a nucleic acid molecule (I) encoding at  
CC least one complementary determining region (CDR) of a variable region of  
CC an antibody which specifically interacts with the extracellular domain of  
CC the human zeta-chain. The antibody whose CDR of a variable region is  
CC encoded by (I), is obtained by immunising a rat with Jurkat cells and  
CC subsequently with a conjugate comprising a carrier molecule and a  
CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The  
CC anti-zeta-chain antibody is useful for the treatment and prevention of  
CC autoimmune diseases, immune deficiencies, T-cell malignancies,  
CC infectious diseases and the suppression of immune response preferably in  
CC order to avoid graft rejection after organ transplantation, malignancies,  
CC or viral infections. The antibody, and fragments of it, can be useful for  
CC the enhancement or suppression of NK-cell dependent immunity or for the  
CC treatment of NK-cell derived malignancies. It can also be useful for the  
CC determination of zeta-chain or eta-chain expression on NK-cells,  
CC T-lymphocytes or their precursors. The present sequence represents the  
CC VH-region of the anti-zeta-chain antibody 2-B-5, produced by rats from  
CC the present invention.

XX Sequence 123 AA;

Query Match 78.0%; Score 495; DB 21; Length 123;  
Best Local Similarity 74.8%; Pred. No. 5.8e-35;  
Matches 92; Conservative 13; Mismatches 12; Indels 6; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITWVKQPGGLEWIGWYPCSGNTKY 60  
DB 1 qvqlqqggaelpkpgasvmscksgyftfnyihwksghgkslewlgwlypgngntky 60  
QY 61 NEKFKGKATLTVDTSSSTAFMQLSSLTSEDYAYFCANYGNWY-----FAYWGQGTQVT 114  
DB 61 nqkfngkatltvdkssstaysmqlssltssdsavvyfcarythyyfydwhgbsvtsvss 120  
QY 115 VSA 117  
DB 121 vsa 123

RESULT 9  
Y78328  
ID Y78328 standard; Protein: 532 AA.

XX Y78328;  
XX 04-MAY-2000 (first entry)  
XX Bispecific anti-zeta-chain/anti-EpCAM antibody protein sequence.  
XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;  
XX complementary determining region; CDR; autoimmune disease; cytostatic;  
XX immune deficiency; T-cell malignancy; infectious disease; antiviral;  
XX immunosuppressive; antimicrobial; immune response modulator; NK-cell.  
XX Rattus norvegicus.  
XX Synthetic.  
XX WO200003016-A1.  
XX 20-JAN-2000.  
XX 09-JUL-1999; 99WO-EP04838.  
XX 10-JUL-1998; 98EP-0112867.  
XX (CONN-) CONNEX GMBH.  
XX Reiter C;  
XX WPI; 2000-160926/14.  
XX N-PSDB; 288358.  
XX

PS Disclosure; ; 15pp; English.  
XX The biosynthetic antibody binding site forms part of a recombinant  
XX multifunctional protein which also comprises an effector protein, an AA  
XX acid sequence capable of sequestering an ion, or a sequence capable of  
XX binding to a solid support. The BABS comprises the framework region from  
XX murine anti-digoxin monoclonal antibody 26-10 heavy chain variable region  
XX and the complementarity determining region from G-loop-4 heavy chain  
XX variable region and has lysozyme specificity. The effector protein is an  
XX enzyme, toxin, receptor, binding site, growth factor, cytokine  
XX or antimetabolite. The sequence capable of sequestering an ion is  
XX calmodulin or metallothionein. The sequence capable of binding to solid  
XX support is streptavidin or a protein A fragment. The protein may be used  
XX for, eg specific binding assays, affinity purification, biocatalysts, drug  
XX targeting, imaging and immunological treatment of oncogenic etc.  
XX diseases. The protein offers fewer cleavage sites to circulating  
XX proteolytic enzymes and have improved stability. They reach target organs  
XX rapidly and are cleared quickly from the body. They also have reduced  
XX immunogenicity.

XX Sequence 249 AA;

Query Match 78.1%; Score 496; DB 9; Length 249;  
Best Local Similarity 74.4%; Pred. No. 9.5e-35;  
Matches 87; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITWVKQPGGLEWIGWYPCSGNTKY 60  
DB 3 evqlqqgpeelpkpgasvmscksgyftfnyihwksghgkslewlgwlypgngntky 62  
QY 61 NEKFKGKATLTVDTSSSTAFMQLSSLTSEDYAYFCANYGNWYFAYWGQGTQVTVA 117  
DB 63 nenfkgtatltvdkssstaysmqlssltssdsavvyfcarythyyfydwhgbsvtsvss 119

RESULT 8  
Y78325  
ID Y78325 standard; Protein: 123 AA.

XX Y78325;  
XX 04-MAY-2000 (first entry)  
XX Anti-zeta-chain antibody 2-B-5 VH-region protein sequence.  
XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;  
XX complementary determining region; CDR; autoimmune disease; cytostatic;  
XX immune deficiency; T-cell malignancy; infectious disease; antiviral;  
XX immunosuppressive; antimicrobial; immune response modulator; NK-cell.  
XX Rattus norvegicus.  
XX WO200003016-A1.  
XX 20-JAN-2000.  
XX 09-JUL-1999; 99WO-EP04838.  
XX 10-JUL-1998; 98EP-0112867.  
XX (CONN-) CONNEX GMBH.  
XX Reiter C;  
XX WPI; 2000-160926/14.  
XX N-PSDB; 288323.  
XX New oligonucleotide, polypeptide, antibody useful for treating  
XX autoimmune disease, immune deficiencies, T-cell malignancies and  
XX infectious diseases -  
XX Claim 8; Fig 6; 79pp; English.  
PS

PT New oligonucleotide, polypeptide, antibody useful for treating  
 PT autoimmune disease, immune deficiencies, T-cell malignancies and  
 XX infectious diseases -  
 PS Example 9; Page 74-76; 79pp; English.  
 XX  
 CC The present invention describes a nucleic acid molecule (I) encoding at  
 CC least one complementary determining region (CDR) of a variable region of  
 CC an antibody which specifically interacts with the extracellular domain of  
 CC the human zeta-chain. The antibody whose CDR of a variable region is  
 CC encoded by (I), is obtained by immunising a rat with Jurkat cells and  
 CC subsequently with a conjugate comprising a carrier molecule and a  
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The  
 CC anti-zeta-chain antibody is useful for the treatment and prevention of  
 CC autoimmune diseases, immune deficiencies, T-cell malignancies, and  
 CC infectious diseases and the suppression of immune response preferably in  
 CC order to avoid graft rejection after organ transplantation, malignancies,  
 CC the enhancement or suppression of NK-cell dependent immunity or for the  
 CC treatment of NK-cell derived malignancies. It can also be useful for the  
 CC determination of zeta-chain or eta-chain expression on NK-cells, for  
 CC T-lymphocytes or their precursors. The present sequence represents a  
 CC bispecific anti-zeta-chain/anti-EpCAM antibody, from an example from  
 CC the present invention.  
 XX  
 SQ Sequence 532 AA;

Query Match 78.0%; Score 495; DB 21; Length 532;  
 Best Local Similarity 74.8%; Pred. No. 2.4e-34;  
 Matches 92; Conservative 13; Mismatches 12; Indels 5; Gaps 1;  
 QY 1 QIQLOQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPCSGNTKY 60  
 Db 142 qvqlqsgaelvkgpsvskiskasgyfttsydmhwikqpgnglewigyppgngntky 201  
 QY 61 NEKFKGKATLTVDSSSTAFWQLSSLTSEDYAVFCANTGNVW-----FAYWGQGTQV 114  
 Db 202 ndkfngkatltadksstaymqlssltedsavycardwhyssyrirpfaywggtltv 261  
 QY 115 VSA 117  
 II:  
 Db 262 vss 264

RESULT 10  
 W01585  
 ID W01585 standard; Protein; 119 AA.  
 XX  
 AC W01585;  
 XX  
 DT 22-AUG-1997 (first entry)  
 DE  
 XX Lead binding MAb 11D11 heavy chain variable region.  
 KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;  
 KW pharmaceutical; health care; skin treatment; pesticide; herbicide;  
 KW heavy metal.  
 XX  
 OS Mus musculus.  
 XX  
 PN W09639518-A1.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 05-JUN-1996; 96WO-US09258.  
 XX  
 PR 10-OCT-1995; 95US-0541373.  
 PR 05-JUN-1995; 95US-0462798.  
 XX  
 PA (BION-) BIONEERASKA INC.  
 XX  
 PI Lopez O, Murray PJ, Wylie DE;

XX WPI; 1997-043140/04.  
 DR N-PSDB; T58259.  
 XX  
 PT DNA encoding heavy metal binding polypeptide sequences - used for  
 PT detecting, removing, adding or neutralising heavy metals, such as  
 PT lead cations  
 XX  
 PS Claim 12; Page 73; 125pp; English.  
 XX  
 CC The present sequence represents the heavy chain variable region for  
 CC monoclonal antibody (MAb) 11D11, which immunoreacts with a lead cation.  
 CC The sequence was derived from RNA isolated from mouse hybridoma cells.  
 CC The protein can be used for binding heavy metals, such as lead cations.  
 CC It can be used for detecting, removing, adding or neutralising the  
 CC heavy metals in biological and inanimate systems. It can be used in  
 CC e.g. aqueous liquid systems, in biological or environmental systems or  
 CC in such compositions as perfumes, cosmetics, pharmaceuticals, health  
 CC care products, skin treatment products, pesticides, herbicides, and  
 CC solvents used in the production of semi-conductor and integrated  
 CC circuit components and production materials for electronic components.  
 CC The products can provide for applications involving minute amounts of  
 CC specific heavy metals.  
 XX  
 SQ Sequence 119 AA;

Query Match 77.8%; Score 494; DB 18; Length 119;  
 Best Local Similarity 76.5%; Pred. No. 6.8e-35;  
 Matches 91; Conservative 14; Mismatches 12; Indels 2; Gaps 1;  
 QY 1 QIQLOQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPCSGNTKY 60  
 Db 1 qvqlqsgaelvkgpsvskiskasgyfttsydmhwikqpgnglewigyppgngntky 201  
 QY 61 NEKFKGKATLTVDSSSTAFWQLSSLTSEDYAVFCANTGNVW-----FAYWGQGTQV 114  
 Db 61 nekfgkatltadksstaymqlssltedsavycardwhyssyrirpfaywggtltv 261  
 II:  
 RESULT 11  
 W07437  
 ID W07437 standard; Protein; 121 AA.  
 XX  
 AC W07437;  
 XX  
 DT 12-AUG-1997 (first entry)  
 DE  
 XX Anti-DNA antibody 4b2 group heavy chain variable region.  
 KW Heavy chain; variable region; anti-DNA; monoclonal; antibody;  
 KW 4b2 group; hairpin; diagnosis; inflammatory glomerulonephritis;  
 KW systemic lupus erythematosus; screening; treatment; prevention;  
 KW SLE; disease; consensus; putative.  
 XX  
 OS Synthetic.  
 XX  
 FH Key  
 FT Region  
 FT 1..30  
 FT /label= framework\_I  
 FT 31..35  
 FT /label= CDR\_I  
 FT 36..49  
 FT /label= framework\_II  
 FT 50..66  
 FT /label= CDR\_II  
 FT 67..98  
 FT /label= framework\_III  
 FT 99..110  
 FT /label= CDR\_III  
 FT 111..121  
 FT /label= J\_region  
 XX

```

PN WO9636361-A1.
XX
PD 21-NOV-1996.
XX
XX 16-MAY-1996; 96WO-US07113.
XX
XX 18-MAY-1995; 95US-0443540.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Glick GD, Swanson PC;
PI
XX WPI; 1997-011854/01.
DR
DR N-PSDB; T43806.
XX
XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT develop prods. for diagnosis and treatment of disorders, e.g.
PT glomerulonephritis or systemic lupus erythematosus
XX
XX Example; Fig 9; 102pp; English.
XX
XX The present sequence is the heavy chain variable region of the
CC group 4b2 putative consensus anti-DNA monoclonal antibody (MAB),
CC which has a high affinity for single stranded DNA, low or no
CC affinity for double stranded DNA and specifically binds a DNA
CC hairpin. The MAB can be used to diagnose disorders associated with the
CC pathological complexation of DNA, e.g. inflammatory
CC glomerulonephritis and systemic lupus erythematosus. It can also be
CC used to generate reagents to screen for pharmaceutical agents, and
CC treat and/or prevent an above disorder.
CC The sequence was derived by aligning homologous anti-DNA MAB,
CC whose sequences have been published, as well as several MAB of
CC other specificities obtained from a database search.
XX
XX Sequence 121 AA;

Query Match 77.8%; Score 494; DB 18; Length 121;
Best Local Similarity 78.3%; Pred. No. 6.9e-35;
Matches 94; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QIQLQQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPCSGNTKY 60
Db 1 qvqlqsgaelarpasvsklsckasgyftfsgiswvgrtgqglewlgelypgsgntcy 60
Qy 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDPAVYFCANYGNY----WFAYWGQGTQVTVS 116
Db 61 nekfkgtatltdksssttymqsltsdsavycarqsyysvyswfwywgqgtltvts 120

RESULT 12
W49814
ID W49814 standard; Protein; 119 AA.
XX
XX W49814;
AC
XX
XX 24-SEP-1998 (first entry)
XX
XX Amino acid sequence of the mouse antibody C4G1 mature heavy chain.
DE
XX Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody;
KW inhibition; antigen; cardiovascular disease; thromboembolic disorder;
KW cancer; acute myocardial infarction; unstable angina; stroke;
KW transient ischemic episode; pulmonary embolism; deep vein thrombosis;
KW extracorporeal cardiopulmonary circulation.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH 31..35
FT Domain /note= "complementarity determining region"
FT 50..66
FT Domain /note= "complementarity determining region"
FT

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---

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FT Domain 99..108
XX /note= "complementarity determining region"
XX
XX US5777085-A.
XX
XX 07-JUL-1998.
XX
XX 17-MAY-1995; 95US-0458516.
XX
XX 03-MAY-1993; 93US-0059159.
XX 20-DEC-1991; 91US-0812111.
XX 09-JUN-1992; 92US-0895952.
XX 11-SEP-1992; 92US-0944159.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Co MS, Tso JY;
PI
XX WPI; 1998-398136/34.
XX
XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from
PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
PT treating cardiovascular and thromboembolic disorders.
XX
XX Claim 1; Fig 5E; 35pp; English.
XX
XX This is the amino acid sequence of the humanised antibody C4G1 heavy
CC chain, used in the method of the invention involving the creation
CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
CC platelet aggregation and also the releasing reaction of platelets. The
CC Ig can be used for treating cardiovascular diseases and thromboembolic
CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets.
XX
XX Sequence 119 AA;

Query Match 77.2%; Score 490; DB 19; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.5e-34;
Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 2;

Qy 1 QIQLQQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPCSGNTKY 60
Db 1 qvqlqsgaelvpgtsrvsvckasgyaftnylliewktrpgqglewlgvlypgsgntny 60
Qy 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDPAVYFCANY-GNY-WFAYWGQGTQVTVSA 117
Db 61 nekfkgtatltdksssttymqsltsdsavycarrdngywgfwywgtrgtltvtsa 119

RESULT 13
R39266
ID R39266 standard; Protein; 138 AA.
XX
XX R39266;
AC
XX
XX 29-NOV-1993 (first entry)
XX
XX Mouse C4G1 Ig heavy-chain.
DE
XX
XX Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;
KW monoclonal antibody; platelet agglutination; humanised antibody.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1..20
FT Peptide /label= signal_peptide
FT

```



KW Complementarity determining region; CDR: murine; mouse; human;  
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;  
 KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;  
 KW chimeric; treatment; prevention; disease; allergy; CRA4.

XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Mus spp.  
 OS Synthetic.

PN JP09191886-A.

XX  
 PD 29-JUL-1997.

XX  
 PF 19-JAN-1996; 96JP-0024816.

XX  
 PR 19-JAN-1996; 96JP-0024816.

XX (ASAK ) ASahi BREWERIES LTD.

PA (NIKK-) NIKKA WHISKEY KK.

PA (TORI ) TORII YAKUHIIN KK.

PA (TSUR/) TSURA T.

XX  
 DR WPI; 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human

PT high-affinity IgE receptor - useful medicinally and have low

PT antigenicity in humans

XX Claim 8; Page 16; 26pp; Japanese.

XX The present sequence, the heavy chain variable region of a  
 CC chimeric human CRA4 antibody (Ab), comprises complementarity  
 CC determining regions (CDR) from a murine, anti-human high affinity  
 CC immunoglobulin E (IgE) receptor, monoclonal Ab (MAb). The  
 CC humanised chimeric MAb can be used to treat or prevent diseases,  
 CC specifically allergies, associated with the receptor, and has very  
 CC low antigenicity in humans.

XX Sequence 118 AA;

Query Match 76.9%; Score 488.5; DB 18; Length 118;

Best Local Similarity 78.8%; Pred. No. 2e-34;

Matches 93; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYTFTDYITWVKRPGGLEWIGWYPGSGNTKY 60

Db 1 qvqlqsgpelvkgasvriksasgyfttsyylhwvkqpggglewlgwlypkvntky 60

Qy 61 NEKFKGKATLVDTSSSTAFMQLSSLTSEDYNYFCANYGNW-FAYWGQGTQVTVSA 117

Db 61 nerfkgkatlttdkssstaymqllsslsedsavvfcaltaratamywgggtttvtvss 118

Search completed: June 18, 2001, 15:29:16  
 Job time: 49 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2001, 15:28:27 ; Search time 11.88 seconds  
(without alignments)  
198.394 Million cell updates/sec

Title: US-09-724-406-2

Perfect score: 635

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Issued\_Patents\_AA.\*
- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pap.\*
  - 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pap.\*
  - 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pap.\*
  - 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pap.\*
  - 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pap.\*
  - 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543.5	85.6	139	1	US-08-253-877C-8
2	543.5	85.6	139	2	US-08-452-164A-8
3	539.5	85.0	138	3	US-08-603-024-2
4	501.5	79.0	116	2	US-08-888-366-2
5	497.5	78.3	122	4	US-08-767-128-4
6	494	77.8	119	4	US-08-767-128-20
7	490	77.2	119	1	US-08-458-516-11
8	490	77.2	138	1	US-08-458-516-7
9	483.5	76.1	139	2	US-08-116-778E-1
10	483.5	76.1	139	2	US-08-438-562-1
11	483.5	75.1	139	2	US-08-483-528B-91
12	480.5	75.7	118	2	US-08-428-257A-74
13	480.5	75.7	118	4	US-07-987-284-14
14	477.5	75.2	128	1	US-08-202-047-21
15	477.5	75.2	128	3	US-08-964-690-21
16	476	75.0	121	3	US-08-881-037-65
17	475.5	74.9	139	1	US-08-253-877C-19
18	475.5	74.9	139	2	US-08-452-164A-19
19	475.5	74.9	139	3	US-08-603-024-18
20	474	74.6	119	1	US-08-458-516-10
21	474	74.6	222	1	US-08-458-516-22
22	474	74.6	235	1	US-08-458-516-23
23	474	74.6	449	1	US-08-458-516-13
24	473	74.5	121	4	US-08-579-378A-7
25	473	74.5	121	5	PCT-US93-11612-7
26	473	74.5	140	5	PCT-US93-11612-4
27	470	74.0	118	3	US-09-065-059-5

28	470	74.0	135	2	US-08-860-174A-4	Sequence 4, Appl1
29	470	74.0	274	2	US-08-860-174A-12	Sequence 12, Appl1
30	469.5	73.9	269	2	US-08-428-257A-72	Sequence 72, Appl1
31	469.5	73.9	269	2	US-08-491-988-3	Sequence 3, Appl1
32	469.5	73.9	402	2	US-08-491-988-9	Sequence 9, Appl1
33	469.5	73.9	415	2	US-08-491-988-7	Sequence 7, Appl1
34	469.5	73.9	435	2	US-08-491-988-5	Sequence 5, Appl1
35	468	73.7	140	4	US-08-579-378A-4	Sequence 4, Appl1
36	466.5	73.5	137	2	US-08-116-778E-3	Sequence 3, Appl1
37	466.5	73.5	137	2	US-08-438-562-3	Sequence 3, Appl1
38	466.5	73.5	137	2	US-08-483-528B-93	Sequence 93, Appl1
39	466	73.4	119	4	US-08-767-128-10	Sequence 10, Appl1
40	465.5	73.3	135	1	US-08-137-117D-27	Sequence 27, Appl1
41	465.5	73.3	135	2	US-08-436-717-27	Sequence 27, Appl1
42	465.5	73.3	137	1	US-08-392-419-2	Sequence 2, Appl1
43	465.5	73.3	139	1	US-08-137-117D-35	Sequence 35, Appl1
44	465.5	73.3	139	2	US-08-436-717-35	Sequence 35, Appl1
45	465	73.2	119	2	US-08-553-497A-8	Sequence 8, Appl1

## ALIGNMENTS

RESULT 1  
US-08-253-877C-8  
; Sequence 8, Application US/08253877C  
; Patent No. 5773001  
; GENERAL INFORMATION:  
; APPLICANT: Hamann, Philip R.  
; APPLICANT: Hinman, Lois  
; APPLICANT: Hollander, Irwin  
; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tscu, Hwei-Ru  
; APPLICANT: Weiss, Martin J.  
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/253,877C  
; FILING DATE: 03-JUN-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 32,368  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3246  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 139 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-253-877C-8

Query Match 85.6%; Score 543.5; DB 1; Length 139;  
Best Local Similarity 87.5%; Pred. No. 2.4e-44;  
Matches 105; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

; Sequence 2, Application US/08603024

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; *****  

; ZIP: 55402  

; COMPUTER READABLE FORM:  

; MEDIUM TYPE: Floppy disk  

; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/888,366
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.390USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-2

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Query Match      79.0%; Score 501.5; DB 2; Length 116;
Best Local Similarity 80.3%; Pred. No. 1.8e-40;
Matches 94; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

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QY 1 QIQLQSGPEVVKPGASVKISKASGYFTFTDYITWKQKPGQGLEWIGWYPCSGNTKY 60
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Db 61 NEKFKGKATLVDTSSSTAEMQLSSLTSEDYAVYFCARCG-YAMDYWGQGTQVTVSS 116
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```

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RESULT 5
US-08-767-128-4
; Sequence 4, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128

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```

; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-767-128-4

```

```

Query Match      78.3%; Score 497.5; DB 4; Length 122;
Best Local Similarity 77.0%; Pred. No. 4.4e-40;
Matches 94; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

```

```

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Db 1 QVQLQSGAGLVKPGASVKLSCKASGYFTFTYIIHWVKQSGQGLEWIGWYPCSGSIKY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NEKFKGKATLVDTSSSTAEMQLSSLTSEDYAVYFCA---NYGNY--WEAYWGQGTQVTV 115
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NEKFKGKATLVDTSSSTAEMQLSSLTSEDYAVYFCARHEGYGNVAVWFAWYWGQGLTVV 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 SA 117
   :||
Db 121 SA 122

```

```

RESULT 6
US-08-767-128-20
; Sequence 20, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

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us-09-724-406-2.ra1

Fri Jun 29 08:04:38 2001

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/767,128  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09258  
FILING DATE: 05-JUN-1996  
APPLICATION NUMBER: 08/541,373  
FILING DATE: 04-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/462,798  
FILING DATE: 05-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.49USF1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/371-5278  
TELEFAX: 612/332-9081  
TELEX:

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

US-08-767-128-20

Query Match 77.8%; Score 494; DB 4; Length 119;

Best Local Similarity 76.5%; Pred. No. 9.2e-40;

Matches 91; Conservative 14; Mismatches 12; Indels 2; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPGSGNTKY 60  
|:|||||:|||||:|||||:|||||:|:|:|||||:|||||:|||||:|  
DB 1 QVQLQSGVELKPGASVKISCKATGYTSSYIEWVKQKPGHLEWIGELLPGSGSTNY 60  
|:|||||:|||||:|||||:|||||:|:|:|||||:|||||:|||||:|  
QY 61 NEKFKGKATLTVDTSSTAFMQSLTSEDYAVYFCAN--YGNFYAWGQGTQVTVSA 117  
|:|||||:|||||:|||||:|||||:|:|:|||||:|||||:|||||:|  
DB 61 NEKFKGKATFTADTSSTAYMQVSSLTSEDSAVYYCARIYYGHLNMFAYWGQGLTVTVSA 119

RESULT 7

US-08-458-516-11

Sequence 11, Application US/08458516

Patent No. 5777085

GENERAL INFORMATION:

APPLICANT: Co, Man Sung

TITLE OF INVENTION: Humanized Antibodies Reactive with

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal fragment  
US-08-458-516-11

Query Match 77.2%; Score 490; DB 1; Length 119;

Best Local Similarity 78.2%; Pred. No. 2.2e-39;

Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 2;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPGSGNTKY 60  
|:|||||:|||||:|||||:|||||:|:|:|||||:|||||:|||||:|  
DB 1 QVQLQSGAELVPGTSVRVSKASGYAFTNLYIEWVKQKPGQGLEWIVPGSGSTNY 60  
|:|||||:|||||:|||||:|||||:|:|:|||||:|||||:|||||:|  
QY 61 NEKFKGKATLTVDTSSTAFMQSLTSEDYAVYFCAN--YGNFYAWGQGTQVTVSA 117  
|:|||||:|||||:|||||:|||||:|:|:|||||:|||||:|||||:|  
DB 61 NEKFKGKATLTVDKSTTAYMQVSSLTSEDSAVYFCARRDGNIGWFAIWGRGLTVTVSA 119

RESULT 8

US-08-458-516-7

Sequence 7, Application US/08458516

Patent No. 5777085

GENERAL INFORMATION:

APPLICANT: Co, Man Sung

TITLE OF INVENTION: Humanized Antibodies Reactive with

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,516

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/059,159

FILING DATE: 03-MAY-1993

ATTORNEY/AGENT INFORMATION:

```

RESULT          9
US-08-116-778E-1
: Sequence 1, Application US/08116778E
: Patent No. 5830470
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, KAZUYASU
: APPLICANT: KOIKE, MASAMICHI
: APPLICANT: SHITARA, KENYA
: APPLICANT: HANAI, NOBUO
: APPLICANT: KUNAWA, YOSHIHISA
: APPLICANT: HASEGAWA, MAMORU
: TITLE OF INVENTION: HUMANIZED ANTIBODIES
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDERHYE P.C.
: STREET: 1100 NORTH GLEBE ROAD
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: U.S.A.
: ZIP: 22201-4714
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/116,778E
: FILING DATE: 07-SEP-93
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: WILSON, MARY J.
: REGISTRATION NUMBER: 32,955
: REFERENCE/DOCKET NUMBER: 249-59
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703)816-4000
: TELEFAX: (703)816-4100
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 139 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: -19...-1

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RESULT 10
US-08-438-562-1
; Sequence 1, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUNAWA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIORITY INFORMATION:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424

```

```
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -19..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 31..35
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 50..66
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-1

Query Match 76.1%; Score 483.5; DB 2; Length 139;
Best Local Similarity 75.0%; Pred. No. 1.le-38;
Matches 90; Conservative 14; Mismatches 13; Indels 3; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISKASGYTFTDYITWVKQPGQGLEWIGWYIPNGGTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLQSGPELVKPGASVKISKASGYTFTDYNMDVKQSHGKSLWIGYIPNGGTY 79

QY 61 NEKFKGKATLTVDTSSSTAFMQLSLTSDTAVYFCANYGNVW---FAYWGQGTQVTVSA 117
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Db 80 NQKFKSKATLTVDKSSSTAYMELSLTSDSAVYICATYGHYGYMFAIWGQGLTVTVSA 139

RESULT 11
US-08-483-528B-91
; Sequence 91, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUNANA, YOSHIIHISA
; APPLICANT: HASEGAWA, MANORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
```

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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -19..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 31..35
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 50..66
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-483-528B-91

Query Match 76.1%; Score 483.5; DB 2; Length 139;
Best Local Similarity 75.0%; Pred. No. 1.le-38;
Matches 90; Conservative 14; Mismatches 13; Indels 3; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISKASGYTFTDYITWVKQPGQGLEWIGWYIPNGGTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLQSGPELVKPGASVKISKASGYTFTDYNMDVKQSHGKSLWIGYIPNGGTY 79

QY 61 NEKFKGKATLTVDTSSSTAFMQLSLTSDTAVYFCANYGNVW---FAYWGQGTQVTVSA 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKSKATLTVDKSSSTAYMELSLTSDSAVYICATYGHYGYMFAIWGQGLTVTVSA 139

RESULT 12
US-08-428-257A-74
; Sequence 74, Application US/08428257A
; Patent No. 5885808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jules E. Goldberg  
;; STREET: 261 Madison Avenue  
;; CITY: New York  
;; STATE: NY  
;; COUNTRY: USA  
;; ZIP: 10016-2391  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/428,257A  
;; FILING DATE: 07/05/95  
;; CLASSIFICATION: 514  
;; INFORMATION FOR SEQ ID NO: 74:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 118 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-428-257A-74

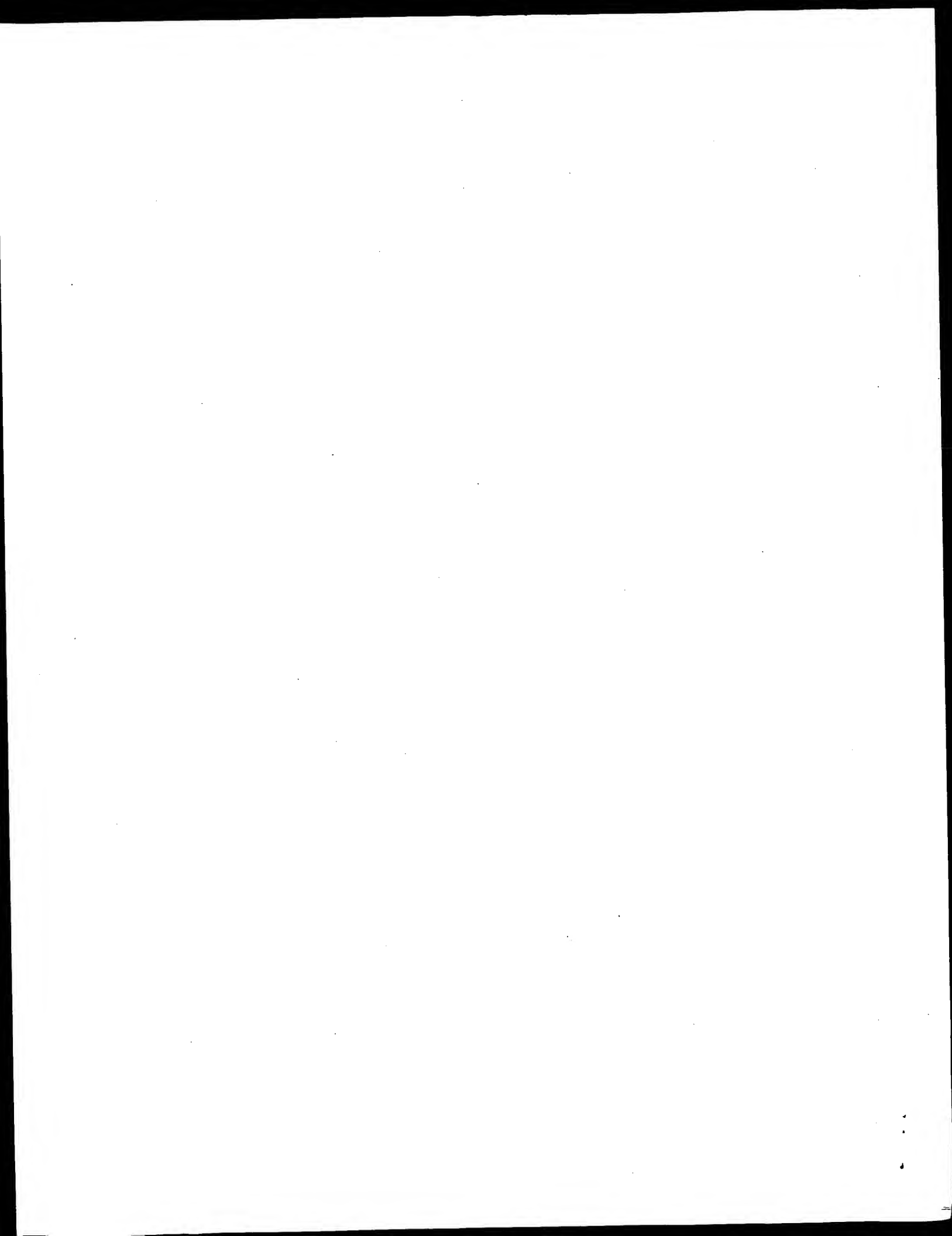
Query Match 75.7%; Score 480.5; DB 2; Length 118;  
Best Local Similarity 75.4%; Pred. No. 1.7e-38;  
Matches 89; Conservative 15; Mismatches 13; Indels 1; Gaps 1;  
QY 1 QIQLQSGPEVVKPGASVKISKASGYFTDYITWVKRPGQGLEWIGWYPGSGNTKY 60  
Db 1 QVQLQSGAELMKPGASVKISKATGYTFSAYWIEWVKRPGHGLEWIGELPGSNNSRY 60  
QY 61 NEKFGRKATLTVDTSSTAFMQLSLTSEDYAVYFCA-NYGNWYFAYWGQGTQVTVSA 117  
Db 61 NEKFGRKATFTADTSSNTAYMQLSLTSEDSAVYICRSYDFAFWYWGQGTPTVTVSA 118

RESULT 13  
US-07-987-264-14  
;; Sequence 14, Application US/07987264  
;; Patent No. 6204366  
;; GENERAL INFORMATION:  
;; APPLICANT: VERHOEYEN, MARTINE ELISA  
;; TITLE OF INVENTION: SPECIFIC BINDING AGENTS  
;; NUMBER OF SEQUENCES: 62  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
;; STREET: 1100 NEW YORK AVENUE, N.W.  
;; CITY: WASHINGTON  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20005-3918  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/987,264  
;; FILING DATE: 08-MAR-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 9019553.8  
;; FILING DATE: 07-SEP-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB PCT/GB91/01511  
;; FILING DATE: 05-SEP-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: KOKULIS, PAUL N.  
;; REGISTRATION NUMBER: 16,773  
;; REFERENCE/DOCKET NUMBER: 200232/P3095USA  
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (202) 861-3000  
;; TELEFAX: (202) 822-0944  
;; TELEX: 6714627 CUSH  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 118 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-07-987-264-14  
Query Match 75.7%; Score 480.5; DB 4; Length 118;  
Best Local Similarity 75.4%; Pred. No. 1.7e-38;  
Matches 89; Conservative 15; Mismatches 13; Indels 1; Gaps 1;  
QY 1 QIQLQSGPEVVKPGASVKISKASGYFTDYITWVKRPGQGLEWIGWYPGSGNTKY 60  
Db 1 QVQLQSGAELMKPGASVKISKATGYTFSAYWIEWVKRPGHGLEWIGELPGSNNSRY 60  
QY 61 NEKFGRKATLTVDTSSTAFMQLSLTSEDYAVYFCA-NYGNWYFAYWGQGTQVTVSA 117  
Db 61 NEKFGRKATFTADTSSNTAYMQLSLTSEDSAVYICRSYDFAFWYWGQGTPTVTVSA 118  
RESULT 14  
US-08-202-047-21  
;; Sequence 21, Application US/08202047  
;; Patent No. 5800815  
;; GENERAL INFORMATION:  
;; APPLICANT: CHESNUT, Robert W.  
;; APPLICANT: POLLEY, Margaret J.  
;; APPLICANT: PAULSON, James C.  
;; APPLICANT: JONES, S. Tarran  
;; APPLICANT: SALDANHA, Jose W.  
;; APPLICANT: BENDIG, Mary M.  
;; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses  
;; NUMBER OF SEQUENCES: 45  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend Kourie and Crew  
;; STREET: One Market Plaza, Steuart Tower, Suite 2000  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/202,047  
;; FILING DATE: 25-FEB-1994  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 14137-77  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-326-2400  
;; TELEFAX: 415-326-2422  
;; INFORMATION FOR SEQ ID NO: 21:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 128 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FEATURE:  
;; NAME/KEY: Protein  
;; LOCATION: 1..128  
;; OTHER INFORMATION: /label= MOUSE\_IIA









Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query %			ID	Description
	Score	Match	Length		
1	549	86.5	246	2	S38950
2	549	86.5	446	2	S40295
3	531	83.6	138	2	S21810
4	521.5	82.1	469	2	S37483
5	519	81.7	109	2	PH0997
6	507.5	79.9	115	2	A54378
7	503	79.2	111	2	PH0998
8	499.5	78.7	112	2	PL0245
9	498.5	78.5	120	2	G28195
10	496.5	78.2	137	2	E29380
11	492	77.5	119	2	E30562
12	491.5	77.4	110	2	PL0244
13	488.5	76.9	120	2	F28195
14	483	76.1	116	2	S20645
15	483	76.1	119	2	C30562
16	481.5	75.8	137	2	F29380
17	480.5	75.7	112	2	S26473
18	480.5	75.7	135	2	A30577
19	480	75.6	138	2	E32513
20	478.5	75.4	107	2	PL0240
21	478	75.3	119	2	C30562
22	476.5	75.0	107	2	PL0241
23	476	75.0	107	2	PH0999
24	475	74.8	117	2	S19366
25	470.5	74.1	116	2	S53751
26	469	73.9	109	2	PH1001
27	469	73.9	118	2	S38565
28	469	73.9	140	2	PH1482
29	468.5	73.8	107	2	PL0243

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RESULT      2
40295      g gamma-2a chain (mab735) - mouse
Species: Mus musculus (house mouse)
Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
Accession: S40295
Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Weisgerber, C.;
Submitted to the EMBL Data Library, January 1993
Description: Primary structure of the murine monoclonal IgG2a antibody mab735 again
Reference number: S40295
Accession: S40295
Molecule type: protein
Residues: 1-446 <KLE>
Genetics:
Map position: 12
Superfamily: immunoglobulin C region; immunoglobulin homology
Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
1-446/Product: Ig gamma-2a chain #status experimental <MAB>
1-117/Domain: V-D-C region <VDJ>
118-446/Domain: C region <CH2>

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Fri Jun 29 08:04:39 2001

F:118-214/Domain: C1 region &lt;CH1&gt;

F:215-230/Region: hinge

F:231-340/Domain: C2 region &lt;CH2&gt;

F:341-446/Domain: C3 region &lt;CH3&gt;

F:360-427/Domain: immunoglobulin homology &lt;IMM&gt;

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96,144-199,261-321,367-425/disulfide bonds: #status predicted

F:132/disulfide bonds: interchain (to light chain) #status predicted

F:224,227,229/disulfide bonds: interchain #status predicted

F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 86.5%; Score 549; DB 2; Length 446;

Best Local Similarity 86.3%; Pred. No. 1e-40;

Matches 101; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 QIOLQSGPEVVKPGASVKISKASGYTFDYITWVKQPGGLEWIGWYPGSGNTKY 60

Db 1 QIOLQSGPELVKPGASVKISKASGYTFDYITWVKQPGGLEWIGWYPGSGNTKY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCANYNFYFAYWGQGTQVTVSA 117

Db 61 NEKFKGKATLTVDTSSTAYMQLSLTSEDYAVFCARGGKFAMDYWGQGTSTVSS 117

RESULT 3

S21810

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S21810

R:Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.

Submitted to the EMBL Data Library, January 1991

A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chain

A:Reference number: S21810

A:Accession: S21810

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 &lt;OST&gt;

A:Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA0257.1; PID:g54164

C:Genetics:

A:Introns: 15/3

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 83.6%; Score 531; DB 2; Length 138;

Best Local Similarity 84.9%; Pred. No. 1.2e-39;

Matches 101; Conservative 8; Mismatches 8; Indels 2; Gaps 2;

QY 1 QIOLQSGPEVVKPGASVKISKASGYTFDYITWVKQPGGLEWIGWYPGSGNTKY 60

Db 20 QVQLQSGPELVKPGASVKISCKASGYTFDYITWVKQPGGLEWIGWYPGSNVNTKY 79

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCA-NYG-NYFAYWGQGTQVTVSA 117

Db 80 NEKFKGKATLTADSSSTAYMQLSLTSEDYAVFCARNYGSYGLAYWGQGLTVTVSA 138

RESULT 4

S37483

Ig gamma-2a chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S37483

R:Ducancel, F.F.D.

Submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-469 &lt;DUC&gt;

A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 521.5; DB 2; Length 469;  
 Best Local Similarity 83.3%; Pred. No. 2.7e-38;  
 Matches 100; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISKASGYTFDYITWVKQPGGLEWIGWYPGSGNTKY 60

Db 20 QIOLQSGPELVKPGASVKISKASGYTFDYITWVKQPGGLEWIGWYPGSGNTKY 79

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCANYNFYFAYWGQGTQVTVSA 117

Db 80 NEKFKGKATLTVDTSSTAYMQLSLTSEDYAVFCARGATATLLDYGQGTTLTVSS 139

RESULT 5

PH0997

Ig heavy chain V region (clone 17s-c2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH0997

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0997

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-109 &lt;TIL&gt;

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 81.7%; Score 519; DB 2; Length 109;

Best Local Similarity 88.1%; Pred. No. 1.1e-38;

Matches 96; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISKASGYTFDYITWVKQPGGLEWIGWYPGSGNTKY 60

Db 1 QIOLQSGPELVKPGASVKISKASGYTFDYITWVKQPGGLEWIGWYPGSGNTKY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCANYNFYFAYW 107

Db 61 NEKFKGKATLTVDTSSTAYMQLSLTSEDYAVFCARRGRSVYFDYW 109

RESULT 6

A54378

Ig heavy chain V region anti-triplex DNA - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999

C:Accession: A54378

R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluor

A:Reference number: A54378; MUID:94165109

A:Accession: A54378

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-115 &lt;AGA&gt;

A:Cross-references: GB:S68981; NID:g545744; PIDN:AAB30095.1; PID:g545745

A:Experimental source: spleen and myeloma cell line MOPC 315.43

A:Note: sequence inconsistent with nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:144172, NCBIIP:144173)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 79.9%; Score 507.5; DB 2; Length 115;  
 Best Local Similarity 80.9%; Pred. No. 1.1e-37;  
 Matches 93; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 1 QIQLQSGPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60  
 DB 1 EVQLQSGPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVYFCANYGNYWFA---NYWFGQGTQVTS 114  
 DB 61 NEKFKGKATLTADKSSSTAYMQLSLTSEDSAVYFCARSGGGLGYWGQGTTLT 115

RESULT 7  
 PH0998  
 Ig heavy chain V region (clone 165.3) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PH0998  
 R:Trillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell  
 A:Reference number: PH0971; MUID:92381444  
 A:Accession: PH0998  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <F1L>  
 A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 503; DB 2; Length 111;  
 Best Local Similarity 84.7%; Pred. No. 2.7e-37;  
 Matches 94; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 QIQLQSGPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60  
 DB 1 QIQLQSGPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVYFCANYGNYWFA---YW 107  
 DB 61 NEKFKGKATLTVDTSSTAYMQLSLTSEDSAVYFCARGDILLRLIDY 111

RESULT 8  
 PL0245  
 Ig heavy chain V region (anti-DNA, Dp17VH) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C:Accession: PL0245  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
 J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: PL0231; MUID:9011618  
 A:Accession: PL0245  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-23/Region: framework 1  
 F:8-91/Domain: immunoglobulin homology <IMM>  
 F:24-28/Region: complementarity-determining 1  
 F:29-42/Region: framework 2  
 F:43-59/Region: complementarity-determining 2  
 F:60-91/Region: framework 3  
 F:92-102/Region: complementarity-determining 3  
 F:103-112/Region: framework 4

Query Match 78.7%; Score 499.5; DB 2; Length 112;  
 Best Local Similarity 83.0%; Pred. No. 5.5e-37;  
 Matches 93; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

QY 8 GPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKYNEKEFGK 67  
 DB 1 GPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKYNEKEFGK 60

QY 68 ATLTVDTSSTAFMQLSLTSEDYAVYFCANYG---NYWFGQGTQVTS 116  
 DB 61 ATLTEDTSSTAYMQLSLTSEDSAVYFCVRNGLRRRAFYWQGTQVTS 112

RESULT 9  
 G28195  
 Ig heavy chain V region (anti-haloperidol antibody B) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 23-Jul-1999  
 C:Accession: G28195  
 R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
 J. Biol. Chem. 263, 4059-4063, 1988  
 A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino aci  
 A:Reference number: A28195; MUID:88153717  
 A:Accession: G28195  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <SHE>  
 A:Cross-references: GB:M19772; NID:9195520; PIDN:AAA38340.1; PID:9195521  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 498.5; DB 2; Length 120;  
 Best Local Similarity 77.5%; Pred. No. 7.2e-37;  
 Matches 93; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QIQLQSGPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60  
 DB 1 QVQLQSGPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIPGSGNTKY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVYFCANYGNYWFA---AYWQGTQVTS 117  
 DB 61 NEKFKGKATLTADKSSSTAYMQLSLTSEDSAVYFCAREGSTEYDEADYWGXTLTVS 120

RESULT 10  
 E29380  
 Ig heavy chain precursor V region (AC-1001) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 23-Jul-1999  
 C:Accession: E29380  
 R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
 J. Biol. Chem. 263, 13579-13583, 1987  
 A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variab  
 A:Reference number: A92612; MUID:88007582  
 A:Accession: E29380  
 A:Molecule type: mRNA  
 A:Residues: 1-137 <CHE>  
 A:Cross-references: GB:M17164; GB:J02815; NID:9195411; PIDN:AAA38295.1; PID:9195412  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 496.5; DB 2; Length 137;  
 Best Local Similarity 78.8%; Pred. No. 1.2e-36;  
 Matches 93; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 QIQLQSGPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60  
 DB 20 QVQLQSGPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 79

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVYFCA-NYGNWFWYWGQGTQVTS 117



J. Immunol. 142, 888-893, 1989  
 A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi  
 A:Reference number: A30562; MUID:89110066  
 A:Accession: C30562  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <SIK>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 483; DB 2; Length 119;  
 Best Local Similarity 76.5%; Pred. No. 1.6e-35;  
 Matches 91; Conservative 13; Mismatches 13; Indels 2; Gaps 1;  
 Oy 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITWVKQPGGLEWIGWIYPGSGNTKY 60  
 Db 1 QVQLQSGAEIMKPGASVKISCKATGYTFSSYIEWVKQPGHGLEWIGIILPGSGTNY 60  
 Oy 61 NEKFKKATLTVDTSSTAFMQLSSLTSEDYVFCAN--YGNVWFAYWGQGTQVTVSA 117  
 Db 61 NEKFKKATFTADTSSNTAFMQLSSLTSEDSAVYICARHYGSSSPAYWGQGLTVTVSA 119

Search completed: June 18, 2001, 15:30:16  
 Job time: 94 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:28:57 ; Search time 9.63 seconds  
(without alignments)  
416.188 Million cell updates/sec

Title: US-09-724-406-2

Perfect score: 635

Sequence: 1 QIQLQSGPEVVKPGASVKI.....NYGNWFAYWGQGTQVTVSA 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	73.5	120	1	HV03_MOUSE
2	466.5	73.5	139	1	HV07_MOUSE
3	453	71.3	117	1	HV12_MOUSE
4	452	71.2	140	1	HV02_MOUSE
5	451	71.0	117	1	HV13_MOUSE
6	451	71.0	117	1	HV52_MOUSE
7	450	70.9	138	1	HV48_MOUSE
8	437.5	68.9	118	1	HV51_MOUSE
9	436.5	68.7	137	1	HV11_MOUSE
10	427	67.2	121	1	HV01_MOUSE
11	418.5	65.9	120	1	HV50_MOUSE
12	415	65.4	136	1	HV15_MOUSE
13	412	64.9	117	1	HV09_MOUSE
14	405	63.8	117	1	HV06_MOUSE
15	405	63.8	117	1	HV14_MOUSE
16	403	63.5	117	1	HV04_MOUSE
17	399	62.8	117	1	HV05_MOUSE
18	396	62.4	117	1	HV10_MOUSE
19	396	62.4	117	1	HV49_MOUSE
20	386.5	60.9	147	1	HV1C_HUMAN
21	364	57.3	117	1	HV1B_HUMAN
22	356	56.1	117	1	HV1G_HUMAN
23	342.5	53.9	114	1	HV00_MOUSE
24	329	51.8	117	1	HV1A_HUMAN
25	325	51.2	142	1	HV01_RAT
26	320.5	50.5	119	1	HV40_MOUSE
27	320.5	50.5	136	1	HV16_MOUSE
28	319	50.2	144	1	HV43_MOUSE
29	313.5	49.4	119	1	HV37_MOUSE
30	311.5	49.1	122	1	HV3G_HUMAN
31	309.5	48.7	126	1	HV3K_HUMAN
32	308.5	48.6	124	1	HV1D_HUMAN
33	306.5	48.3	119	1	HV38_MOUSE

34 306.5 48.3 120 1 HV1H\_HUMAN P80421 homo sapien  
35 306 48.2 115 1 HV32\_MOUSE P01801 mus musculus  
36 305 48.0 117 1 HV41\_MOUSE P01811 mus musculus  
37 304 47.9 121 1 HV3J\_HUMAN P01771 homo sapien  
38 302.5 47.6 122 1 HV3A\_HUMAN P01762 homo sapien  
39 301 47.4 113 1 HV30\_MOUSE P01799 mus musculus  
40 299 47.1 118 1 HV39\_MOUSE P01809 mus musculus  
41 299 47.1 137 1 HV46\_MOUSE P01822 mus musculus  
42 298 46.9 115 1 HV33\_MOUSE P01802 mus musculus  
43 297 46.8 117 1 HV42\_MOUSE P01812 mus musculus  
44 296 46.6 113 1 HV27\_MOUSE P01796 mus musculus  
45 295 46.5 113 1 HV29\_MOUSE P01798 mus musculus

## ALIGNMENTS

RESULT 1  
HV03\_MOUSE STANDARD; PRT; 120 AA.  
AC HV03\_MOUSE  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION 36-65.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83131846; PubMed=6186498;  
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,  
RA Marshak-Rothstein A.;  
RT "The genetic basis of antibody production: the dominant anti-arsonate  
RT idotype response of the strain A mouse.";  
RL Eur. J. Immunol. 12:1023-1032(1982).  
CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS  
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
CC SEGMENT, JH2.  
DR PIR: A02028; HVM5G7.  
DR InterPro: IPR003006; -.  
DR Pfam: PF00047; ig; 1.  
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 73.5%; Score 467; DB 1; Length 120;  
Best Local Similarity 73.3%; Pred. No. 4.5e-40;

Matches 88; Conservative 14; Mismatches 14; Indels 4; Gaps 1;

QY 2 IOLOQSGPEVVKPGASVKISCKASGYTFDYITVWKQPGGLEWIGWYPSGNTKYN 61  
Db 1 VLOQSGAEELVRAGSSVRKMSKASGYTFYSINLVKQPGGLEWIGWYPSGNTKYN 60  
QY 62 EKFKGKATITVDTSSTAFPMQLSLTSEDYVYFCANY----GNWYFAYWGQGTQVTVSA 117  
Db 61 EKFKGKATITVDTSSTAFPMQLSLTSEDYVYFCARSYVYGSYFYDYWGQGTQVTVSS 120

## RESULT 2

HV07\_MOUSE STANDARD; PRT; 139 AA.  
ID HV07\_MOUSE  
AC P01751; P01752;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6789376;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NpB family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -!- MISCELLANEOUS: THE BL-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
CC (NPB ANTIBODIES).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J00529; AAA38170.1; -  
DR PIR; A02034; MHMS18.  
DR InterPro; IPR003006; -  
DR Pfam; PF00047; Ig; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BL-8/186-2.  
FT DOMAIN 20 49 FRAMEWORK 1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 55 68 FRAMEWORK 2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 86 117 FRAMEWORK 3.  
FT DOMAIN 118 124 D SEGMENT.  
FT DOMAIN 125 139 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 139 139  
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

Query Match 73.5%; Score 466.5; DB 1; Length 139;  
Best Local Similarity 73.3%; Pred. No. 6e-40;  
Matches 88; Conservative 14; Mismatches 15; Indels 3; Gaps 1;  
QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQKPGGLEWIGWIPGSGNTKY 60  
Db 20 QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYMMHWKQRFGRGLEWIGRIDPNSGGTKY 79  
QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSDTAVYFCAN---YGNVWFAYWGQGTQVTVSA 117  
Db 80 NEKFKSKATLTVDKPSSTAYMQLSLTSDTSADVYCYARYDYGSSYFDYWGQGTTLTVSS 139  
RESULT 3  
HV12\_MOUSE STANDARD; PRT; 117 AA.  
ID HV12\_MOUSE  
AC P01756;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION MOPC 104E.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83075344; PubMed=6816276;  
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,  
RA Hood L.E.;  
RT "Complete amino acid sequence of a mouse mu chain: homology among  
RT heavy chain constant region domains.";

RL Biochemistry 21:5415-5424(1982).  
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA  
CC PROTEIN HAS ALSO BEEN DETERMINED.  
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
DR PIR; A02039; MHMS4E.  
DR InterPro; IPR003006; -  
DR Pfam; PF00047; Ig; 1.  
KW Immunoglobulin V region; Glycoprotein.  
FT DISULFID 22 96 BY SIMILARITY.  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .).  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;  
Query Match 71.3%; Score 453; DB 1; Length 117;  
Best Local Similarity 71.8%; Pred. No. 1.1e-38;  
Matches 84; Conservative 16; Mismatches 17; Indels 0; Gaps 0;  
QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQKPGGLEWIGWIPGSGNTKY 60  
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYIMKWKQSHGKSLWIGDINPNNGGTSY 60  
QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSDTAVYFCAN---YGNVWFAYWGQGTQVTVSA 117  
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDTSADVYCYARYDYFDVWGAGTTTVTSS 117  
RESULT 4  
HV02\_MOUSE STANDARD; PRT; 140 AA.  
ID HV02\_MOUSE  
AC P01746;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/J;  
RX MEDLINE=82152818; PubMed=6801765;  
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,  
RA Capra J.D.;  
RT "Somatic mutation in genes for the variable portion of the  
RT immunoglobulin heavy chain.";  
RL Science 216:309-311(1982).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J00493; AAA38128.1; -  
DR PIR; A02028; HVMSG7.  
DR InterPro; IPR003006; -  
DR Pfam; PF00047; Ig; 1.  
KW Immunoglobulin V region; Antiarsenate antibody; Hybridoma; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.  
FT NON\_TER 140 140  
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;  
Query Match 71.2%; Score 452; DB 1; Length 140;  
Best Local Similarity 71.9%; Pred. No. 1.7e-38;  
Matches 87; Conservative 15; Mismatches 15; Indels 4; Gaps 2;  
QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQKPGGLEWIGWIPGSGNTKY 60



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Db 20 EVQLQSGAELVRAGSSVKMSCKASGYTFYSGINWVKRPGQGLEWIGVINGVINY 79
Qy 61 NEKFKGKATLVDSSTAFMQLSSLTSEDYAVYFCA--NY--GNVWFAYWGQGTQVTVS 116
Db 80 NEKFKGKATLVDSSTAFMQLSSLTSEDYAVYFCA--NY--GNVWFAYWGQGTQVTVS 139
Qy 117 A 117
Db 140 S 140

RESULT 5
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Cleveland B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RL rearrangements in heavy chain v-region gene segments.";
CC Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A26242; MMS35.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

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Query Match 71.0%; Score 451; DB 1; Length 117;
Best Local Similarity 71.8%; Pred. No. 1.8e-38;
Matches 84; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKRPGQGLEWIGVINGVINGY 60
Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYIMKWKQSHGKSLWIGDINPNNGTYS 60
Qy 61 NEKFKGKATLVDSSTAFMQLSSLTSEDYAVYFCA--NY--GNVWFAYWGQGTQVTVS 117
Db 61 NQKFKGKATLVDSSTAFMQLSSLTSEDYAVYFCA--NY--GNVWFAYWGQGTQVTVS 117

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RESULT 6
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;

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RT "Developmentally controlled and tissue-specific expression of
RL unarranged VH gene segments.";
Cell 40:271-281(1985).
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DR EMBL: M13787; AAA38499.1; -.
DR PIR: A02029; HVM5AL.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

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Query Match 71.0%; Score 451; DB 1; Length 117;
Best Local Similarity 85.8%; Pred. No. 1.8e-38;
Matches 83; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKRPGQGLEWIGVINGVINGY 60
Db 20 QVQLQSGPELVKPGALVKISCKASGYTFDYINWVKRPGQGLEWIGVINGVINGY 79
Qy 61 NEKFKGKATLVDSSTAFMQLSSLTSEDYAVYFCA 97
Db 80 NEKFKGKATLVDSSTAFMQLSSLTSEDYAVYFCA 116

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RESULT 7
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HVM5T7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.

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FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 70.98; Score 450; DB 1; Length 138;
Best Local Similarity 71.4%; Pred. No. 2.6e-38;
Matches 85; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQPGQGLEWIGWYFGSGNTKY 60
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQQGAEVVKPGASVKLSCKASGHTFTYHWVKQPGQGLEWIGINPNNGRSNY 79
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NEKFKGKATLTVDTSSSTAFMQLSSLTSEDTAVYFCANYGNY--WFAYWGQGTQVTVSA 117
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKFKKATLTVDKSSSTAYMQLSSLTSEDTAVYFCARSDGYDFWVYWGQGLTVTFS 138
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig. 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 68.9%; Score 437.5; DB 1; Length 118;
Best Local Similarity 71.2%; Pred. No. 4e-37;
Matches 84; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQPGQGLEWIGWYFGSGNTKY 60
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQSGPELVKPGASVKISKASGYTFTDYMNWVKSHGCKSLWIGDINPNNGTSY 60
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NEKFKGKATLTVDTSSSTAFMQLSSLTSEDTAVYFCANYGNYWFAYWGQGTQVTVSA 117
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKGKATLTVDKSSSTAYMELRSLSLTSEDTAVYFCARGYGYDFVWGTGTTVTVSS 118
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig. 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 68.7%; Score 436.5; DB 1; Length 137;
Best Local Similarity 70.6%; Pred. No. 5.8e-37;
Matches 84; Conservative 12; Mismatches 20; Indels 3; Gaps 2;

QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQPGQGLEWIGWYFGSGNTKY 60
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQQGAEVVKPGASVKLSCKASGYTFTSYLMHWVNRGRGLEWIGRIDPNSGGTTY 79
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NEKFKGKATLTVDTSSSTAFMQLSSLTSEDTAVYFCANYGNYWFAYWGQGTQVTVSA 117
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKFRKATLTVDKPSSTAYMQLSSLTSEDTAVYFCARYRLGRY-FDYWGQGTTLTVSS 137
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
HV01_MOUSE STANDARD; PRT; 121 AA.
ID HV01_MOUSE
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";

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RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR: A02037; GVMS11.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT NON_TER 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 67.2%; Score 427; DB 1; Length 121;
Best Local Similarity 67.2%; Pred. No. 4.6e-36;
Matches 82; Conservative 16; Mismatches 18; Indels 6; Gaps 2;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITVWVKPGQGLEWIGWYPGSGNTKY 60
DB 1 EAOLQSGAELVRPGTSVKISCKAAGYTFNWIWGVKRPGRHGLEWIGDIYPPGGFTNY 60
QY 61 NEKFKGKATLTVDTSSTAFMQLSSTSEDTAVYFCANY-----WFAWYWGQGTQVTV 115
DB 61 NDNLKGRATLTADTSSSTAYIQLSSTSEDSAIYHCAR-GIYNNSPYFDSWGQGTTLTV 119
QY 116 SA 117
DB 120 SS 121

RESULT 11
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02037; MHMS15.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 65.9%; Score 418.5; DB 1; Length 120;
Best Local Similarity 65.0%; Pred. No. 3.2e-35;
Matches 78; Conservative 17; Mismatches 22; Indels 3; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITVWVKPGQGLEWIGWYPGSGNTKY 60
DB 1 EAOLQSGAELVRPGTSVKISCKAAGYTFNWIWGVKRPGRHGLEWIGDIYPPGGFTNY 60
QY 61 NEKFKGKATLTVDTSSTAFMQLSSTSEDTAVYFCANY-----WFAWYWGQGTQVTVSA 117
DB 61 NDNLKGRATLTADTSSSTAYIQLSSTSEDSAIYHCAR-GIYNNSPYFDSWGQGTTLTV 119

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DB 61 NEKFKSKATLTVDKSSSATYMQLSPTSDSAVYCARWDYEGDRYFDVWGTGTTVTSS 120

RESULT 12
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222252; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RL by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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CC -----
CC EMBL: J00494; AAA38130.1; -.
CC PIR: A02042; HVMSB1
CC InterPro: IPR003006; -.
CC Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 65.4%; Score 415; DB 1; Length 136;
Best Local Similarity 68.6%; Pred. No. 8.2e-35;
Matches 81; Conservative 13; Mismatches 22; Indels 2; Gaps 2;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITVWVKPGQGLEWIGWYPGSGNTKY 60
DB 20 QVQLQSGPEVVRPGVSVKISCKSGYTFDYAMHWKQSHAKSLEWIGVISTYNGNTSY 79
QY 61 NEKFKGKATLTVDTSSTAFMQLSSTSEDTAVYFCAN-YGNYWFAWYWGQGTQVTVSA 117
DB 80 NOKFKGKATMTVDKSSSTVHMLARLTSEDSANLYCARYGNY-FDYWGQGTTLTVSS 136

RESULT 13
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;

```

Fri Jun 29 08:04:40 2001

us-09-724-406-2.rsp

RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.,  
 RT "Heavy chain variable region contribution to the NPb family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region."  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
 DR PIR: B02034; HVMS61.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig: 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 64.9%; Score 412; DB 1; Length 117;  
 Best Local Similarity 79.4%; Pred. No. 1.4e-34;  
 Matches 77; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYTFDYITWVKRPGQGLEWIGWYPGSGNTKY 60  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 Db 20 QVLOQPGAEIVKPGASVKISCKASGYTFDYITWVKRPGQGLEWIGRIDPNSSGTTY 79  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 QY 61 NEKFKGKATLTVDTSSTAFMOLSLTSEDYAVFYCA 97  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 Db 80 NEKFKGKATLTVDTSSTAFMOLSLTSEDYAVFYCA 116  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|

RESULT 14  
 HV06\_MOUSE  
 ID HV06\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01750;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION 102 PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.,  
 RT "Heavy chain variable region contribution to the NPb family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region."  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
 DR PIR: A02032; HVMS02.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig: 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 63.8%; Score 405; DB 1; Length 117;  
 Best Local Similarity 77.1%; Pred. No. 7e-34;  
 Matches 74; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 2 QIOLQSGPEVVKPGASVKISCKASGYTFDYITWVKRPGQGLEWIGWYPGSGNTKY 61  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 Db 21 VLOQPGAEIVKPGASVKISCKASGYTFDYITWVKRPGQGLEWIGRIDPNSSGTTY 80  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 QY 62 EKEFGKATLTVDTSSTAFMOLSLTSEDYAVFYCA 97  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 Db 81 QKEFGKATLTVDTSSTAFMOLSLTSEDYAVFYCA 116  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|

RESULT 15  
 HV14\_MOUSE  
 ID HV14\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01758;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION 108A PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81245215; PubMed=6789211;  
 RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.,  
 RT "Diversity of germ-line immunoglobulin VH genes."  
 RL Nature 292:426-430(1981).

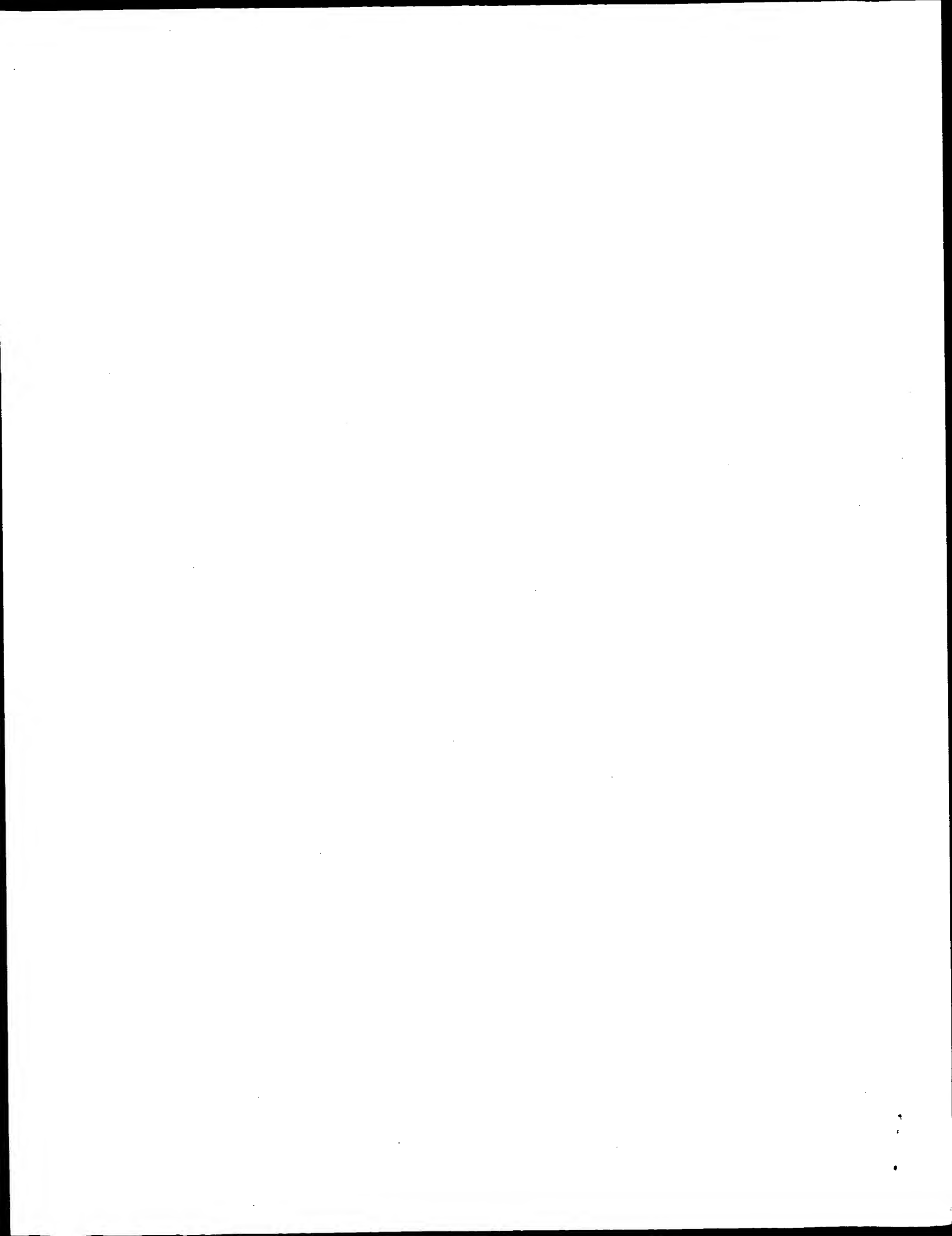
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 CC -----  
 CC EMBL: J00488; AAA38519.1;  
 DR PIR: A02041; HVMS8A.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig: 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 63.8%; Score 405; DB 1; Length 117;  
 Best Local Similarity 77.3%; Pred. No. 7e-34;  
 Matches 75; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYTFDYITWVKRPGQGLEWIGWYPGSGNTKY 60  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 Db 20 EVLOQSGPEVVKPGASVKISCKASGYTFDYITWVKRPGQGLEWIGWYPGSGNTGY 79  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 QY 61 NEKFKGKATLTVDTSSTAFMOLSLTSEDYAVFYCA 97  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|  
 Db 80 NOKFKGKATLTVDNSSSTAYMELSLTSEDYAVFYCA 116  
 :||||| :|:|||||:|||||:|: :|:|||||:|||||:|:| :|:|

Search completed: June 18, 2001, 15:30:28  
 Job time: 91 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:28:27 ; Search time 23.23 Seconds  
(without alignments)  
666.366 Million cell updates/sec

Title: US-09-724-406-2  
Perfect score: 635  
Sequence: 1 QIOLQSGPEVVKPGASVKI.....NYGNWFAYWGQGTQVTVSA 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query %	Length	DB ID	Description
1	470	74.0	117	11	Q9QXF0	Q9qxf0 mus musculus
2	460	72.4	117	11	Q9QXE9	Q9qxe9 mus musculus
3	434.5	68.4	109	11	Q9JL75	Q9jl75 mus musculus
4	434.5	68.4	118	11	Q9Z1C4	Q9z1c4 mus musculus
5	424.5	66.9	110	11	Q9JL83	Q9jl83 mus musculus
6	420	66.1	119	4	Q9UL94	Q9ul94 homo sapien
7	419.5	66.1	110	11	Q9JL77	Q9jl77 mus musculus
8	417	65.7	117	11	Q9Z1C6	Q9z1c6 mus musculus
9	411.5	64.8	114	11	Q9JL81	Q9jl81 mus musculus
10	404	63.6	119	5	Q9CY22	Q9cy22 schistosoma
11	401.5	63.2	124	4	Q9UL92	Q9ul92 homo sapien
12	394	62.0	125	4	Q9UL95	Q9ul95 homo sapien
13	384	60.5	109	11	Q9JL85	Q9jl85 mus musculus
14	377.5	59.4	116	4	Q9UL89	Q9ul89 homo sapien
15	365	57.5	157	4	Q9JL89	Q9jl89 mus musculus
16	353	55.6	150	4	Q9JL89	Q9jl89 mus musculus
17	343	54.0	102	11	Q9JL79	Q9jl79 mus musculus
18	338	53.2	119	4	Q9UL73	Q9ul73 homo sapien
19	320.5	50.5	298	11	Q9QVF0	Q9qvf0 mus musculus

20	314	49.4	116	4	Q9UL93	Q9ul93 homo sapien
21	310	48.8	113	4	Q9UL90	Q9ul90 homo sapien
22	305.5	48.1	147	4	Q9Y509	Q9y509 homo sapien
23	304.5	48.0	112	4	Q9HCC1	Q9hcc1 homo sapien
24	303.5	47.8	124	6	Q9N0W6	Q9n0w6 oryctolagus
25	301.5	47.5	124	6	Q9N0W4	Q9n0w4 oryctolagus
26	300.5	47.3	118	4	Q9UL72	Q9ul72 homo sapien
27	297.5	46.9	150	4	Q9JL72	Q9jl72 homo sapien
28	292	46.0	121	4	Q9UL71	Q9ul71 homo sapien
29	292	46.0	131	4	Q9UL88	Q9ul88 homo sapien
30	287.5	45.3	122	4	Q9UL84	Q9ul84 homo sapien
31	284.5	44.8	118	4	Q9UL91	Q9ul91 homo sapien
32	284.5	44.8	437	11	Q9UL91	Q9ul91 homo sapien
33	264	41.6	112	4	Q9UGP3	Q9ugp3 mus musculus
34	259	40.8	104	4	Q9UL87	Q9ul87 mus musculus
35	252	39.7	95	4	Q9UL86	Q9ul86 mus musculus
36	247.5	39.0	122	4	Q9UL75	Q9ul75 mus musculus
37	240	37.8	121	4	Q9UL96	Q9ul96 mus musculus
38	198	31.2	118	4	Q9UL74	Q9ul74 mus musculus
39	194.5	30.6	88	4	Q9JL73	Q9jl73 mus musculus
40	192.5	30.3	78	4	Q9JL73	Q9jl73 mus musculus
41	190.5	30.0	81	4	Q9JL73	Q9jl73 mus musculus
42	189	29.8	76	4	Q9JL73	Q9jl73 mus musculus
43	187	29.4	82	4	Q9JL73	Q9jl73 mus musculus
44	184	29.0	75	4	Q9JL73	Q9jl73 mus musculus
45	183	28.8	77	4	Q9JL73	Q9jl73 mus musculus

## ALIGNMENTS

RESULT	ID	Q9QXF0	PRELIMINARY;	PRT;	117 AA.
AC	Q9QXF0				
DT	01-MAY-2000	(TREMREL. 13, Created)			
DT	01-MAY-2000	(TREMREL. 13, Last sequence update)			
DT	01-MAY-2000	(TREMREL. 16, Last annotation update)			
DE	IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Clemens A., Rademackers A., Specht C., Koelsch E.;				
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AJ225171; CAB65236.1; -				
DR	InterPro: IPR003006; -				
DR	InterPro: IPR003596; -				
DR	Pfam: PF00047; ig; 1.				
DR	SMART: SM00406; IGV; 1.				
FT	NON_TER 1				
FT	NON_TER 117				
SQ	SEQUENCE	117 AA; 13060 MW; D816AD0858A7E4C CRC64;			
Query Match 74.0%; Score 470; DB 11; Length 117;					
Best Local Similarity 73.5%; Pred. No. 2.3e-41;					
Matches 86; Conservative 16; Mismatches 15; Indels 0; Gaps 0;					
QY	1	QIOLQSGPEVVKPGASVKISKASGYTFTDYYITWVKQKPGGLEWIGVYGGSGNTKY 60			
Db	1	EVOLQSGPEVVKPGASVKMSKASGYTFTDYYIMKWKQSHGKSLWIGDINPNNGTSY 60			
QY	61	NEFKFKATLIVDTSSSTAFMOLSLTSEDYAVFCANYGNWFAYWGQGTQVTVSA 117			
Db	61	NEFKFKATLIVDKSSSTAYMQLSLTSEDYAVFCANYGNWFAYWGQGTQVTVSA 117			
RESULT	2				
Q9QXE9					
ID	Q9QXE9	PRELIMINARY;	PRT;	117 AA.	

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AC Q9X9E9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1;
DR InterPro; IPR003006;
DR InterPro; IPR003596;
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 72.4%; Score 460; DB 11; Length 117;
Best Local Similarity 73.5%; Pred. No. 2.5e-40;
Matches 86; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 QIQLQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60
Db 1 EVQLQQSGPELVKPGASVKMSKASGYFTDYIMKWKQYKQSHGKSLGIDINPNNGTSY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFYFCANYNFYAYWGQGTQVTVSA 117
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYICARDRIYAMDYWGQGTSTVVS 117

RESULT 3
Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RL acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
DR EMBL; AF206031; AAF69329.1;
DR InterPro; IPR003006;
DR InterPro; IPR003596;
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 68.4%; Score 434.5; DB 11; Length 109;
Best Local Similarity 76.1%; Pred. No. 1e-37;
Matches 83; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 10 EVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKYNEKFKGRAT 69
Db 1 ELVKPGASVKMSKASGYFTSYVHWVHWKQKPGQGLEWIGYINPYNDGTYKNEKFKGRAT 60
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QY 70 LTVDTSSSTAFMQLSLTSEDYAVFYFCANYNFYAYWGQGTQVTVSA 117
Db 61 LNSDKSSSTAYMQLSLTSEDSAVYICARDGNRYGFDYWGQGTTLTVSS 109

RESULT 4
Q921C4 PRELIMINARY; PRT; 118 AA.
AC Q921C4;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/64 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
CC EMBL; U78801; AAD00293.1;
DR InterPro; IPR003006;
DR InterPro; IPR003596;
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90BEC559D31EC4FC CRC64;

Query Match 68.4%; Score 434.5; DB 11; Length 118;
Best Local Similarity 68.1%; Pred. No. 1.1e-37;
Matches 81; Conservative 16; Mismatches 19; Indels 3; Gaps 2;

QY 1 QIQLQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60
Db 1 QVQVQSGAELARHWASVKLSKASGYFTSYVHWVHWKQKPGQGLEWIGYIPGQDTSY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFYFCANYNFYAYWGQGTQVTVSA 117
Db 61 TQKFRGKATLTADKSSSTAYMQLSLTSEDSAVYICARRTVGGY-EDYWGQGTTLTVSS 118

RESULT 5
Q9JL83 PRELIMINARY; PRT; 110 AA.
AC Q9JL83;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RL acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
DR EMBL; AF206023; AAF69321.1;
DR InterPro; IPR003006;
DR InterPro; IPR003596;
DR
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DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 FT NON\_TER 110  
 SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 66.9%; Score 424.5; DB 11; Length 110;  
 Best Local Similarity 74.1%; Pred. No. 1.1e-36;  
 Matches 83; Conservative 10; Mismatches 14; Indels 5; Gaps 2;  
 QY 9 PEVVRPGASVKISCKASGYTFDYITVWKQPGQGLEWIGWYPSGNTKYNEKFKGKA 68  
 Db 1 PELVRPGASVKISCKASGYTFSSNWNVVKLRPGQGLEWIGRIYFGDGYNGKFKGKA 60  
 QY 69 TLTVTSSTAPWQLSSLTSETAVYFCANYGNYW---FAYWGQGTQVTVSA 117  
 Db 61 TLTVTSSTAPWQLSSLTSETAVYFCAR--SNWDVRFAYWGQGLTVTVSS 110

RESULT 6  
 Q9UL94 PRELIMINARY; PRT; 119 AA.  
 AC Q9UL94;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AF035020; AAD56256.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 FT NON\_TER 119  
 SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 66.1%; Score 420; DB 4; Length 119;  
 Best Local Similarity 65.5%; Pred. No. 3.6e-36;  
 Matches 78; Conservative 15; Mismatches 24; Indels 2; Gaps 1;  
 QY 1 QIOLQSGPEVVRPGASVKISCKASGYTFDYITVWKQPGQGLEWIGWYPSGNTKY 60  
 Db 1 EVQLVESGAEEKKPGASVKVSKASGYTFGTGYMHVROAPGQGLEWGWNPNSWTTNY 60  
 QY 61 NEKFKGKATLVDTSSSTAPWQLSSLTSETAVYFCANYG--NYWFAWGQGTQVTVSA 117  
 Db 61 AQKFGKVTWKDTSISTAYMELSLRLSDDTAVYICARGGGLWFDWFGQGLTVTVSS 119

RESULT 7  
 Q9JL77 PRELIMINARY; PRT; 110 AA.  
 AC Q9JL77;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DBA/2;  
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF206029; AAR69327.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 FT NON\_TER 110  
 SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 66.1%; Score 419.5; DB 11; Length 110;  
 Best Local Similarity 73.1%; Pred. No. 3.7e-36;  
 Matches 79; Conservative 13; Mismatches 15; Indels 1; Gaps 1;  
 QY 11 VVRPGASVKISCKASGYTFDYITVWKQPGQGLEWIGWYPSGNTKYNEKFKGKATL 70  
 Db 3 LVRPGASVKISCKASGYTFSSNWNVVKLRPGQGLEWIGRIYFGDGYNGKFKGKATL 62  
 QY 71 TVDPTSSSTAPWQLSSLTSETAVYFCANY--GNWFAWGQGTQVTVSA 117  
 Db 63 TVDPTSSSTAPWQLSSLTSETAVYFCAR--GNWFAWGQGTQVTVSS 110

RESULT 8  
 Q9Z1C6 PRELIMINARY; PRT; 117 AA.  
 AC Q9Z1C6;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Mueller J.P., Glannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,  
 RA Matis L.M., Evans M.J.;  
 RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric  
 IgG2/G4 constant regions block human leukocyte binding to porcine  
 endothelial cells";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: U78799; AAD00291.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 FT NON\_TER 117  
 SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;

Query Match 65.7%; Score 417; DB 11; Length 117;  
 Best Local Similarity 65.8%; Pred. No. 7.1e-36;  
 Matches 77; Conservative 14; Mismatches 26; Indels 0; Gaps 0;  
 QY 1 QIOLQSGPEVVRPGASVKISCKASGYTFDYITVWKQPGQGLEWIGWYPSGNTKY 60  
 Db 1 EVQLVESGAEEKKPGASVKVSKASGYTFGTGYMHVROAPGQGLEWGWNPNSWTTNY 60



OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
DR EMBL: AF035C19; AAD56255.1; -.  
DR InterPro: IPR003006; -.  
DR InterPro: IPR003596; -.  
DR Pfam: PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR NON\_TER 1  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;  
  
Query Match 62.0%; Score 394; DB 4; Length 125;  
Best Local Similarity 59.2%; Pred. No. 1.8e-33;  
Matches 74; Conservative 17; Mismatches 26; Indels 8; Gaps 1;  
  
Qy 1 QIOLQSGPWPVKPGASVKISCKASGYTFTDYITWKQKPGQGLEWIGWYFGSGNTRY 60  
Db 1 EVLVESGAEVKPGASVKSKASGYTFTGYHMHVVRAPQGLEWGWNPNSGGNY 60  
Qy 61 NEKFKGKATVTDTSSSTAFMQLSSLTSEDYAVYFCA-----YGNWYFAYGQGTQ 112  
Db 61 AOKVOGRVTTTDTTSTAYMELSLRSDDTAVYICARSQGGGRTAAAGADAFDINGQGT 120  
Qy 113 VTUSA 117  
Db 121 VTSS 125  
  
RESULT 13  
Q9JL85 PRELIMINARY; PRT; 109 AA.  
AC Q9JL85;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-MAY-1999 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA Markiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF206021; AAF69319.1; -.  
DR InterPro: IPR003006; -.  
DR InterPro: IPR003596; -.  
DR Pfam: PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR NON\_TER 1  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;  
  
Query Match 60.5%; Score 384; DB 11; Length 109;  
Best Local Similarity 65.7%; Pred. No. 1.7e-32;  
Matches 71; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

Qy 10 EVYKPGASVKISCKASGYTFTDYITWKQKPGQGLEWIGWYFGSGNTRYNEKFKCAT 69  
Db 2 ELVKPGASVKLSCTASGFNIEDTYHMHVVRAPQGLEWIGRITDPTGHSKYDPKQPKAT 61  
Qy 70 LTVDTSSSTAFMQLSSLTSEDYAVYFCAVYGNWYFAYGQGTQVTVSA 117  
Db 62 ITSDTSSNTAYIQLSSLTSEDYAVYCYVRRGAVFDYWGQGTALVSS 109  
  
RESULT 14  
Q9JL89 PRELIMINARY; PRT; 116 AA.  
AC Q9JL89;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
DR EMBL: AF035025; AAD56261.1; -.  
DR InterPro: IPR003006; -.  
DR InterPro: IPR003596; -.  
DR Pfam: PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR NON\_TER 1  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;  
  
Query Match 59.4%; Score 377.5; DB 4; Length 116;  
Best Local Similarity 63.5%; Pred. No. 8.6e-32;  
Matches 73; Conservative 17; Mismatches 22; Indels 3; Gaps 2;  
  
Qy 6 QSGDEVKPGASVKISCKASGYTFTDYITWKQKPGQGLEWIGWYFGSGNTRYNEKFK 65  
Db 2 QSGAEVKPGASVKSKASGYTFTSYAISVVRAPQGLEWGRITPIILGIANYAQKFK 61  
Qy 66 GKATITVDTSSSTAFMQLSSLTSEDYAVYFCA--NYGNWYFAYGQGTQVTVSA 117  
Db 62 GRVITADKSTAYMELSSLTSEDYAVYICASSNWGPGYFVFLWGRGTLTVSS 116  
  
RESULT 15  
O95978 PRELIMINARY; PRT; 157 AA.  
AC O95978;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE VH1 PROTEIN PRECURSOR (FRAGMENT).  
GN VH1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PERIPHERAL BLOOD;  
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,  
RA Bohlen H., Diehl V., Wolf J.;

•

CC	-!- SIMILARITY; TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
EMBL:	AJ0005570; CAA06599.1; -.
DR	InterPro; IPR003006; -. DR
DR	InterPro; IPR003596; -. DR
DR	Pfam; PF00047; Ig; 1. DR
SMART:	SMO0406; IGV; 1. DR
KW	Signal.
SIGNAL:	1 21 POTENTIAL.
FT	NON_TER 157 157
SEQ	SEQUENCE 157 AA; 117304 MW; 86986EDDA84D88B5 CRC64;

Query Match	57.5%;	Score 365;	DB 4;	Length 157;	
Best Local Similarity	57.0%;	Pred. 2.4e-30;			
Matches	69;	Conservative 19;	Mismatches 29;	Indels 4;	Gaps 1;
1	QIQLOQSGPEVVRPGASVKISCKASGYTDTYYIITWVKPQGLWETGWTYIPGSGNTKY	60			
20	QVQLVQSGAEIKRPGASVHKCTSGYVETSYIIHWVRQPGQLWMMGGIGPCVGTMC	79			
61	NEKFKGKATLTVDTSSTAFPMOLSSITSDTAYVFCANYNY---	116			
80	AERFQGLTWRTSTTTVMELSLRFEEDTAYVFCGRGWRSGNYNGHWGQGTPTVS	139			
117	A	117			
140	S	140			

Search completed: June 18, 2001, 15:29:58  
Job time: 91 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 362.28 Seconds  
(without alignments)  
0.837 Million cell updates/sec

Title: US-09-724-406-4  
Perfect score: 29  
Sequence: 1 DVTIT 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	29	100.0	346 15 AAR55059	Elk tyrosine kinases
2	29	100.0	346 16 AAR82606	Eph transmembrane
3	29	100.0	346 17 AAR91930	Human cytokine elk
4	29	100.0	346 18 AAW36055	Human elk-L protei
5	29	100.0	346 18 AAW19249	Human elk ligand p
6	29	100.0	346 19 AAW44323	Human elk-L. Homo
7	29	100.0	683 21 AAY96781	Ephrin-B1-Ephrin-B
8	29	100.0	706 18 AAW31199	Bacillus popilliae
9	28	96.6	173 16 AAR71930	Zag gene FAM bindi
10	28	96.6	200 22 AAB63700	Human gastric canc
11	28	96.6	254 21 AAG42791	Arabidopsis thalia

12	28	96.6	255	21	AAG42790	Arabidopsis thalia
13	28	96.6	328	21	AAG42789	Arabidopsis thalia
14	28	96.6	515	21	AAB10981	H. tuberculata hem
15	27	93.1	101	21	AAY93885	Amino acid sequenc
16	27	93.1	177	19	AAW48849	Mouse receptor tyr
17	27	93.1	197	21	AAB42709	Human ORFX ORF2473
18	27	93.1	275	19	AAW48847	Rat receptor tyros
19	27	93.1	398	20	AAW37578	Amino acid sequenc
20	27	93.1	472	19	AAW48848	Human receptor tyr
21	26	89.7	120	13	AAR27497	WNI 222-5 antibody
22	26	89.7	120	13	AAR27498	WNI 58-9 antibody
23	26	89.7	124	17	AAR90831	2B5 heavy chain va
24	25	86.2	58	22	AAB59288	Beta4Gal-T1 protei
25	25	86.2	76	21	AAB39058	Human secreted pro
26	25	86.2	116	17	AAW03742	Murine monoclonal
27	25	86.2	123	18	AAW28331	Staphylococcus aur
28	25	86.2	142	19	AAW85892	S. pneumoniae deri
29	25	86.2	154	21	AAW91476	Human secreted pro
30	25	86.2	162	13	AAW21140	Polypeptide encode
31	25	86.2	183	21	AAB18980	Amino acid sequenc
32	25	86.2	197	20	AAW92992	S. aureus MurB pro
33	25	86.2	207	21	AAW91632	Human secreted pro
34	25	86.2	208	12	AAW13210	Streptococcal pyro
35	25	86.2	208	14	AAW45018	Streptococcal ent
36	25	86.2	208	22	AAW67345	Streptococcus pyro
37	25	86.2	235	19	AAW62784	Streptococcus pyro
38	25	86.2	235	19	AAW62785	Mutant streptococc
39	25	86.2	235	19	AAW62786	Mutant streptococc
40	25	86.2	235	19	AAW62787	Mutant streptococc
41	25	86.2	235	19	AAW62788	Mutant streptococc
42	25	86.2	307	20	AAW92991	S. aureus MurB pro
43	25	86.2	307	21	AAW70128	Staphylococcus aur
44	25	86.2	326	22	AAW46973	S. aureus MurB pro
45	25	86.2	367	21	AAW40201	Gene 1 human secre

## ALIGNMENTS

RESULT	1
AAW55059	AAW55059 standard; Protein; 346 AA.
ID	AAW55059 standard; Protein; 346 AA.
XX	
AC	AAW55059;
XX	
DT	28-JAN-1995 (first entry)
XX	
DE	Elk tyrosine kinase receptor ligand.
XX	
KW	Vectors; elk-L protein; elk; ligands; cell growth; differentiation.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Peptide
FT	1..24
FT	/note= "signal peptide"
FT	25..346
FT	/note= "mature elk-L protein"
XX	
PN	W09411384-A.
XX	
PD	26-MAY-1994.
XX	
PF	15-NOV-1993; 93WO-US10955.
XX	
PR	13-NOV-1992; 92US-0977693.
XX	
PA	(IMMV ) IMMUNEX CORP.
XX	
PI	Baum PR, Beckmann MP, Lyman S;
XX	
DR	WPI, 1994-183415/22..
DR	N-PSDB; AAQ65486.

XX New DNA encoding ligand for elk tyrosine kinase receptor - also  
 PT related polypeptides, vectors, antibodies and probes, useful e.g.  
 PT in studying cell differentiation or growth  
 XX  
 PS Claim 7; Page 30; 35pp; English.  
 XX  
 CC The sequence is that of the elk-L protein able to bind elk, a  
 CC tyrosine kinase receptor. The DNA may be incorporated into vectors  
 CC which can be used to study the role of elk and its ligands in cell  
 CC growth and differentiation.  
 XX  
 SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 15; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 DB 131 dyyit 135  
 |||||

RESULT 2  
 AAR82606  
 ID AAR82606 standard; Protein; 346 AA.  
 XX  
 AC AAR82606;  
 DT 16-MAY-1996 (first entry)  
 XX  
 DE Eph transmembrane tyrosine kinase family ligand, Efl-3.  
 XX  
 KW Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;  
 KW neurological disorder; identification; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..29  
 FT Domain /label= signal\_peptide  
 FT /label= transmembrane\_domain  
 FT Misc-difference 159  
 FT /note= "borders main conserved regions"  
 XX  
 PN W09527060-A2.  
 XX  
 PD 12-OCT-1995.  
 XX  
 PF 04-APR-1995; 95WO-US04208.  
 XX  
 PR 21-OCT-1994; 94US-0327423.  
 PR 04-APR-1994; 94US-0222075.  
 PR 12-APR-1994; 94US-0229402.  
 PR 01-SEP-1994; 94US-0299567.  
 XX  
 PA (REG- ) REGENERON PHARM INC.  
 XX  
 PI Aldrich TH, Davis S, Gale N, Goldfarb M, Maisonnier PC;  
 PI Yancopoulos GD;  
 XX  
 DR WPI; 1995-358635/46.  
 XX  
 PT Ligands which bind Eph family receptors - used in the diagnosis of  
 PT neurological disorders  
 XX  
 PS Disclosure; Fig 2; 58pp; English.  
 XX  
 CC Efl-3 (also known as EHK-L) is an Eph transmembrane tyrosine kinase  
 CC family ligand. It has homology with B61 (Efl-1) and Efl-2. Efl-3  
 CC appears to comprise a conventional transmembrane protein with a

CC cytoplasmic domain. Efl-3 is useful for identifying other ligands  
 CC for EHK-1, -2, -3, ECK and Elk receptors. The ligands are useful in  
 CC promoting a differential function and/or influencing the phenotype,  
 CC such as growth and/or proliferation, of receptor bearing cells. They  
 CC may be used in the diagnosis, and treatment of neurological disorders.  
 XX  
 SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 16; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 DB 131 dyyit 135  
 |||||

RESULT 3  
 AAR91930  
 ID AAR91930 standard; Protein; 346 AA.  
 XX  
 AC AAR91930;  
 DT 11-DEC-1996 (first entry)  
 XX  
 DE Human cytokine elk-ligand (elk-L).  
 XX  
 KW Human; cytokine; elk-ligand; elk-L; tyrosine kinase receptor;  
 KW neurotrophic; neuroprotective; placenta; radiolabelled probe;  
 KW treatment; neural tissue; excitotoxicity; injury; disorder;  
 KW neural culture reagent; immunogenic fragment; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..24  
 FT /label= sig\_peptide  
 FT Peptide 25..346  
 FT /label= mat\_peptide  
 XX  
 PN US5512457-A.  
 XX  
 PD 30-APR-1996.  
 XX  
 PF 13-NOV-1992; 92US-0977693.  
 XX  
 PR 15-MAR-1994; 94US-0213403.  
 PR 13-NOV-1992; 92US-0977693.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Baum PR, Beckmann MP, Carpenter MK, Lyman S;  
 XX  
 DR WPI; 1996-229866/23.  
 DR N-PSDB; AAT28770.  
 XX  
 PT DNA coding for neurotrophic human elk ligand cytokine - useful as  
 PT probe to isolate other elk ligand sequences  
 XX  
 PS Claim 1; Columns 27-30; 18pp; English.  
 XX  
 CC The present sequence is the human cytokine elk-ligand (elk-L),  
 CC which binds a member of the tyrosine kinase receptor family. Elk-L  
 CC exhibits neurotrophic and neuroprotective properties, and has a  
 CC calculated mol. wt. 35180 daltons and a pI of 9.006. The elk-L  
 CC cDNA, isolated from a human placental cDNA library, can be  
 CC radiolabelled and used as a probe for isolating other mammalian  
 CC elk-L cDNA. Elk-L can be used to treat neural tissue disorders,  
 CC partic. excitotoxicity associated injuries or disorders, and as a  
 CC neural culture reagent, while immunogenic fragments of elk-L can be  
 CC used to generate specific anti-elk-L antibodies.

SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 17; Length 346;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYIIT 5  
|  
|  
|  
|  
Db 131 dyiit 135

# RESULT 4

AAW36055  
ID AAW36055 standard; Protein; 346 AA.

XX AC AAW36055;

XX DT 06-MAR-1998 (first entry)

XX DE Human elk-L protein.

XX KW Human; elk-L; cytokine; ligand; tyrosine kinase receptor; fusion protein;  
XX KW extracellular domain; immunoglobulin; neurological disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..24

FT Protein /note= "signal peptide"

FT Domain 25..346

FT Domain /note= "mature protein"

FT FT /note= "extracellular domain; this region is used to  
generate a fusion protein with the Fc portion  
of the human immunoglobulin G1"

FT Domain 238..265

FT Domain /note= "transmembrane domain"

FT Domain /note= "intracellular domain"

FT Modified-site 139..141

FT Cleavage-site /note= "Asn is N-glycosylated"

FT Cleavage-site 266..267

FT Cleavage-site /note= "KEX2 protease cleavage site"

FT Cleavage-site 267..268

FT Cleavage-site /note= "KEX2 protease cleavage site"

FT Cleavage-site 270..271

FT Cleavage-site /note= "KEX2 protease cleavage site"

XX US5670625-A.

XX PD 23-SEP-1997.

XX XX 02-JUN-1995; 95US-0460741.

XX PR 15-MAR-1994; 94US-0213403.

XX PR 13-NOV-1992; 92US-0977693.

XX PR 02-JUN-1995; 95US-0460741.

XX PA (IMMV ) IMMUNEX CORP.

XX PI Baum PR, Beckmann MP, Lyman S;

XX XX WPI; 1997-479524/44.

XX DR N-PSDB; AAT97976.

XX FT Soluble fusion proteins of human elk-L ligand and Fc immunoglobulin  
XX FT fragment - and their dimers and oligomers, useful as  
XX FT neuro-protectants and neurotrophic agents

XX PS Claim 1; Columns 27-30; 18pp; English.

XX XX This is the amino acid sequence of the human elk-L protein, a new  
CC

CC cytokine that is the ligand for the elk tyrosine kinase receptor. The  
CC extracellular domain of the protein (amino acids 1-213) is used to  
CC generate a fusion protein comprising the Fc polypeptide of the human  
CC immunoglobulin G1 (extending from the hinge region to the C-terminus).  
CC The fusion protein (which has the same activities as the natural elk-L  
CC protein) has neuroprotective and neurotrophic activity so is potentially  
CC useful for treating a wide range of neurological diseases.

XX SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 18; Length 346;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYIIT 5

Db 131 dyiit 135

# RESULT 5

AAW19249

ID AAW19249 standard; Protein; 346 AA.

XX AC AAW19249;

XX DT 18-AUG-1997 (first entry)

XX DE Human elk ligand protien.

XX KW Human; elk; ligand; elk-L; cytokine; testing; measuring;  
XX KW purification; neuroprotection; treatment; diabetic; hereditary;  
XX KW nutritional; neuropathy; neurodegenerative disease;  
XX KW tissue culture.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..24

FT Peptide /label= sig\_peptide

FT Peptide 25..346

FT Peptide /label= mat\_peptide

XX US5627267-A.

XX PD 06-MAY-1997.

XX XX 13-NOV-1992; 92US-0977693.

XX PR 15-MAR-1994; 94US-0213403.

XX PR 13-NOV-1992; 92US-0977693.

XX PR 01-JUN-1995; 95US-0458077.

XX PA (IMMV ) IMMUNEX CORP.

XX PI Baum PR, Beckmann MP, Lyman S;

XX XX WPI; 1997-271366/24.

XX DR N-PSDB; AAT69766.

XX FT Human elk ligand protein - for diagnostic or therapeutic use, e.g.  
XX FT as neuro-protective agent

XX PS Claim 1; Columns 29-32; 18pp; English.

XX CC The present sequence is a human elk ligand (elk-L) protein,  
XX CC which binds elk, has a calculated molecular weight of 35180 and an  
XX CC isoelectric point of 9.006. Elk-L is a cytokine that can be used to  
XX CC test cells for elk expression, measure the biological activity of  
XX CC elk, purify elk by affinity chromatography and as a neuroprotective  
XX CC agent to treat diabetic, hereditary and nutritional neuropathies  
XX CC and neurodegenerative diseases. It may also be added to tissue  
XX CC cultures to prolong the life of neurons. The elk-L cDNA was

0;

0;

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CC isolated from a human placental cDNA library, and is present as a  
CC cDNA insert in the recombinant vector deposited in strain  
CC ATCC 69085.  
XX  
XX  
SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 18; Length 346;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
DB 131 dyyit 135

RESULT 6  
AAW44323  
ID AAW44323 standard; Protein; 346 AA.

XX AAW44323;

XX 27-MAY-1998 (first entry)

XX Human elk-L.

XX Human; elk-L; elk ligand; cytokine; antibody; cell surface receptor;  
KW tyrosine kinase receptor; neural disease; trophic mechanism.  
XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..24  
FT Protein /label= signal  
FT 25..346  
FT /label= elk-L

XX US5728813-A.

XX 17-MAR-1998.

XX 12-NOV-1996; 96US-0747240.

XX 15-MAR-1994; 94US-0213403.

XX 13-NOV-1992; 92US-0977693.

XX 02-JUN-1995; 95US-0460741.

XX 12-NOV-1996; 96US-0747240.

XX (IMMV ) IMMUNEX CORP.

XX Baum PR, Beckmann MP, Lyman S;

XX WPI; 1998-206621/18.

XX N-PSDB; AAV15226.

XX Antibodies to elk ligand polypeptides - bind to tyrosine kinase  
XX receptors, useful for treating neural disease

XX Claim 1; Column 31-32; 17pp; English.

XX The present sequence represents human elk-L (elk ligand). The present  
XX invention describes antibodies to elk-L polypeptides. The elk-L protein  
XX is known to be neuroprotective exhibiting its effect through a trophic  
XX mechanism. Examples of diseases that may be treated with elk-L include  
XX neuropathies e.g. diabetic, hereditary and nutritional neuropathies,  
XX neurodegenerative diseases and other diseases characterised by loss of  
XX function or degeneration of neurons.

XX Sequence 346 AA;

Query Match 100.0%; Score 29; DB 19; Length 346;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

0;

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0;

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0;

0;

0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYYIT 5  
DB 131 dyyit 135

RESULT 7

AAAY96781

ID AAY96781 standard; Protein; 683 AA.

XX AC AAY96781;

XX 26-SEP-2000 (first entry)

XX Ephrin-B1-Ephrin-B1-FC fusion protein.

XX Ephrin-B1; ELK receptor; ligand; dimer; Fc domain; fusion protein;

XX Efl-6 antagonist; neurological.

XX Chimeric - Homo sapiens.

XX Chimeric - Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..29

FT /label= Signal\_peptide

FT /note= "derived from ELK-L Ectodomain 1"

FT Protein 30..237

FT /label= ELK-L\_ectodomain\_1

FT Peptide 238..240

FT /label= Bridging\_peptide

FT Protein 241..448

FT /label= ELK-L\_Ectodomain\_2

FT Peptide 449..451

FT /label= Bridging\_peptide

FT Region 452..683

FT /label= Human\_IgG1\_Fc\_region

XX WO200037642-A1.

XX 29-JUN-2000.

XX 23-DEC-1999; 99WO-US30900.

XX 23-DEC-1998; 98US-0113387.

XX (REGE-) REGENERON PHARM INC.

XX Davis SJ, Gale NW, Yaucopoulos GD, Stahl N;

XX WPI; 2000-442670/38.

XX N-PSDB; AAA51345.

XX Polynucleotide encoding a fusion polypeptide, useful for promoting  
XX differential function and influencing phenotype, comprises two subunits  
XX containing at least one copy of the receptor binding domain of a ligand  
XX Example 12; Fig 14A-E; 97pp; English.  
XX Production of homogenous forms of clustered ligands is broadly applicable  
XX to improve the affinity and/or increase the activity of a ligand as  
XX compared to the native form of the ligand. Ephrin fusion proteins have  
XX been constructed, which may be useful for treating neurological  
XX disorders. The ephrin fusion proteins are preferably capable of binding  
XX to ELK receptor and are especially Efl-6 antagonists. The fusion proteins  
XX were constructed after it was demonstrated that similar improved  
XX activities could be achieved using Tie-2 receptor ligands.  
XX Angiopoietin-1 (Ang-1) is a Tie-2 receptor ligand and is an agonist for  
XX of the Tie-2 receptor. The fibrogen domains (FD) of Ang-1 and Ang-2 are  
XX the receptor-binding domains and dimerized versions, of e.g. Ang-1-FD-Fc  
XX (Ang-1 fibrinogen domain fused to an Fc domain), can bind to the Tie-2  
XX receptor with much higher affinity than monomeric Ang-1-FD (dimerization



CC occurs between the Fc components of adjacent molecules). However,  
 CC Ang-1-FD-Fc is not able to induce phosphorylation (activate) the Tie-2  
 CC receptor on endothelial cells unless it is further clustered with goat  
 CC anti-human Fc antibodies. The novel fusion proteins, mutant versions of  
 CC Ang-1-FD and Ang-2-FD, were designed that were intrinsically more highly  
 CC clustered. Tie-2 agonist fusion proteins may be used as haematopoietic  
 CC factors. Tie-2 receptor antagonist fusion proteins may be used to  
 CC diagnose or treat, e.g. myeloproliferative or other proliferative  
 CC disorders of blood forming organs, e.g. thrombocythemias, polycythemia  
 CC and leukemias.  
 XX  
 XX

SQ Sequence 583 AA;

Query Match 100.0%; Score 29; DB 21; Length 583;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5  
 Db 131 dyvit 135  
 |||||

RESULT 8  
 AAW311199  
 ID AAW31199 standard; Protein; 706 AA.

XX AC AAW31199;

XX DT 13-FEB-1998 (first entry)

XX DE Bacillus popilliae crystal protein.

XX KW Crystal protein; beetle; Scarabaeidae; maybug; cockchafer;  
 XX KW agricultural pest; spore; Bacillus thuringiensis; cytolysing protein;  
 XX KW fusion protein; transgenic plant.

XX OS Bacillus popilliae.

XX FH Key Location/Qualifiers  
 XX FT Protein 1..706  
 XX FT /label= crystal protein

XX PN DE19642729-A1.

XX PD 24-APR-1997.

XX PF 17-OCT-1996; 96DE-1042729.

XX PR 18-OCT-1995; 95DE-1040223.

XX PA (UYHE-) UNIV HEIDELBERG.

XX PI Krieger L, Schnetter W, Zhang J;

XX DR WPI; 1997-237512/22.

XX DR N-PSDB; AAT89348.

XX PT DNA encoding Bacillus popilliae crystal protein - for production of  
 XX PT recombinant protein and transgenic plants resistant to attack by  
 XX PT beetles

XX PS Claim 8; Pages 8-11; 12pp; German.

XX This sequence represents a novel bacterial crystal protein which can be  
 CC used to control beetles of the family Scarabaeidae, especially  
 CC Melolontha spp. (e.g. maybugs, cockchafers) which are pests of  
 CC agriculture and forestry. The protein can inhibit eating, killing both  
 CC adult beetles and larvae. It can be incorporated into eradication  
 CC programmes involving Bacillus popilliae and Bacillus thuringiensis  
 CC spores, fungal spores or cytolysing proteins in the form of a fusion  
 CC protein. The DNA can also be used to produce transgenic plants that are  
 CC resistant to attack by the beetles.

XX SQ Sequence 706 AA;

Query Match 100.0%; Score 29; DB 18; Length 706;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5  
 Db 506 dyvit 510  
 |||||

RESULT 9  
 AAR71930

XX ID AAR71930 standard; Protein; 173 AA.

XX AC AAR71930;

XX DT 22-SEP-1995 (first entry)

XX DE zag gene FAM binding domain.

XX KW ZAG; fast alpha-2-macroglobulin binding protein; FAM;  
 XX KW plasma proteinase-inhibitor binding protein.

XX OS Streptococcus zooepidemicus strain V.

XX PN WO9507296-A.

XX PD 16-MAR-1995.

XX PF 06-SEP-1994; 94WO-SE00826.

XX PR 06-SEP-1993; . 93SE-0002855.

XX PA (GUSS/) GUSS B.

XX PA (JONS/) JONSSON H.

XX PA (LIND/) LINDBERG M.

XX PA (MUEL/) MUELLER H.

XX PA (RANT/) RANTAMAKI L K.

XX PI Guss B, Jonsson H, Lindberg M, Mueller H, Rantamaki LK;

XX DR WPI; 1995-123382/16.

XX DR N-PSDB; AAQ89198.

XX PT DNA encoding fast alpha 2-macroglobulin-binding proteins - used  
 XX PT to obtain prods. for sepn., detection or quantification or for  
 XX PT binding inhibition

XX PS Claim 24; Page 37; 50pp; English.

XX A phage lambda EMBL3 library of S. equi subsp. zooepidemicus V  
 CC was analyzed for fast-acting alpha-2-macroglobulin (FAM)- and  
 CC IgG-binding activity. One clone, lambda SzGL, which expressed  
 CC both activities, was analyzed to obtain DNA encoding the  
 CC FAM-binding protein, ZAG. The FAM-binding domain (R71930) in  
 CC ZAG was identified.

XX SQ Sequence 17; AA;

Query Match 96.6%; Score 28; DB 16; Length 173;  
 Best Local Similarity 80.0%; Pred. No. 95;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5

Db 156 dyvit 160  
 |||||

RESULT 10

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AAB63700
ID AAB63700 standard; Protein; 200 AA.
XX
XX AAB63700;
AC
XX
XX
DT 26-MAR-2001 (first entry)
XX
DE Human gastric cancer associated antigen protein sequence SEQ ID NO:1062.
XX
XX Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW cancer associated antigen; cytostatic; cancer vaccine.
XX
XX Homo sapiens.
OS
XX WO200073801-A2.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 26-MAY-2000; 2000WO-US14749.
PF
XX
XX 28-MAY-1999; 99US-0136526.
PR
XX 10-SEP-1999; 99US-0133454.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX Obata Y;
PI
XX WPI; 2001-025274/03.
DR
XX
XX Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer.
XX
XX Example 1; Page 675; 799pp; English.
PS
XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP), respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer.
XX
XX Sequence 200 AA;
SQ

Query Match 96.6%; Score 28; DB 22; Length 200;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYIT 5
Db 99 dyyvt 103
|||:|

RESULT 11
AAG42791
ID AAG42791 standard; Protein; 254 AA.
XX
XX AAG42791;
AC
XX
XX 18-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 53407.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX

```

OS Arabidopsis thaliana.

XX

XX PN EP1033405-A2.

XX

XX PD 06-SEP-2000.

XX

XX DF 25-FEB-2000; 2000EP-0301439.

XX

XX 25-FEB-1999; 99US-0121825.

XX

XX 05-MAR-1999; 99US-0123180.

XX

XX 09-MAR-1999; 99US-0123548.

XX

XX 23-MAR-1999; 99US-0125788.

XX

XX 25-MAR-1999; 99US-0126264.

XX

XX 29-MAR-1999; 99US-0126785.

XX

XX 01-APR-1999; 99US-0127462.

XX

XX 06-APR-1999; 99US-0128234.

XX

XX 08-APR-1999; 99US-0128714.

XX

XX 16-APR-1999; 99US-0129845.

XX

XX 19-APR-1999; 99US-0130077.

XX

XX 21-APR-1999; 99US-0130449.

XX

XX 23-APR-1999; 99US-0130510.

XX

XX 23-APR-1999; 99US-0130891.

XX

XX 28-APR-1999; 99US-0131449.

XX

XX 30-APR-1999; 99US-0132048.

XX

XX 30-APR-1999; 99US-0132407.

XX

XX 04-MAY-1999; 99US-0132484.

XX

XX 05-MAY-1999; 99US-0132485.

XX

XX 06-MAY-1999; 99US-0132486.

XX

XX 06-MAY-1999; 99US-0132487.

XX

XX 07-MAY-1999; 99US-0132863.

XX

XX 11-MAY-1999; 99US-0134256.

XX

XX 14-MAY-1999; 99US-0134218.

XX

XX 14-MAY-1999; 99US-0134219.

XX

XX 14-MAY-1999; 99US-0134221.

XX

XX 14-MAY-1999; 99US-0134370.

XX

XX 18-MAY-1999; 99US-0134768.

XX

XX 19-MAY-1999; 99US-0134941.

XX

XX 20-MAY-1999; 99US-0135124.

XX

XX 21-MAY-1999; 99US-0135353.

XX

XX 24-MAY-1999; 99US-0135629.

XX

XX 25-MAY-1999; 99US-0136021.

XX

XX 27-MAY-1999; 99US-0136392.

XX

XX 28-MAY-1999; 99US-0136782.

XX

XX 01-JUN-1999; 99US-0137222.

XX

XX 03-JUN-1999; 99US-0137528.

XX

XX 04-JUN-1999; 99US-0137502.

XX

XX 07-JUN-1999; 99US-0137724.

XX

XX 08-JUN-1999; 99US-0138094.

XX

XX 10-JUN-1999; 99US-0138540.

XX

XX 10-JUN-1999; 99US-0138847.

XX

XX 14-JUN-1999; 99US-0139119.

XX

XX 16-JUN-1999; 99US-0139452.

XX

XX 16-JUN-1999; 99US-0139453.

XX

XX 17-JUN-1999; 99US-0139492.

XX

XX 18-JUN-1999; 99US-0139454.

XX

XX 18-JUN-1999; 99US-0139455.

XX

XX 18-JUN-1999; 99US-0139456.

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XX 18-JUN-1999; 99US-0139457.

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XX 18-JUN-1999; 99US-0139458.

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XX 18-JUN-1999; 99US-0139459.

XX

XX 18-JUN-1999; 99US-0139460.

XX

XX 18-JUN-1999; 99US-0139461.

XX

XX 18-JUN-1999; 99US-0139462.

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XX 18-JUN-1999; 99US-0139463.

XX

XX 18-JUN-1999; 99US-0139750.

XX

XX 18-JUN-1999; 99US-0139763.

XX

XX 21-JUN-1999; 99US-0139817.

XX

XX 22-JUN-1999; 99US-0139899.

XX

XX 23-JUN-1999; 99US-0140353.

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XX 23-JUN-1999; 99US-0140354.

XX

XX 24-JUN-1999; 99US-0140695.

XX

XX 28-JUN-1999; 99US-0140823.

XX

XX 29-JUN-1999; 99US-0140991.

XX

PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144086.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 06-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 10-AUG-1999; 99US-0147935.  
PR 11-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 13-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 17-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.

PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
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PR 29-OCT-1999; 99US-0162142.

Query Match 96.68; Score 28; DB 21; Length 254;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYIIT 5  
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Db 249 dyvvt 253

## RESULT 12

AAG42790  
ID AAG42790 standard; Protein; 255 AA.

XX  
AC AAG42790;

XX  
DT 18-OCT-2000 (first entry)

XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53406.

XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.

XX  
OS Arabidopsis thaliana.

XX  
PN EP1033405-A2.

XX  
PD 06-SEP-2000.

XX  
PF 25-FEB-2000; 2000EP-0301439.

XX  
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Query Match 96.6%; Score 28; DB 21; Length 255;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5  
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 Db 250 dyvvt 254

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 XX AC AAG42789;  
 XX DT 18-OCT-2000 (first entry)  
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 53405.  
 XX KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX OS Arabidopsis thaliana.  
 XX PN EP1033405-A2.  
 XX PD 06-SEP-2000.  
 XX PF 25-FEB-2000; 2000EP-0301439.  
 XX PR 25-FEB-1999; 99US-0121825.  
 XX PR 05-MAR-1999; 99US-0123180.  
 XX PR 09-MAR-1999; 99US-0123548.  
 XX PR 23-MAR-1999; 99US-0125788.  
 XX PR 25-MAR-1999; 99US-0126264.  
 XX PR 29-MAR-1999; 99US-0126785.



XX PS Claim 21; Page 108-110; 163pp; German.

XX CC This invention describes a novel nucleic acid (I) containing a sequence

CC that encodes hemocyanin (II), a domain of (I) or its fragment with the

CC immunological properties of at least one domain of (II). The products of

CC the invention have cytostatic, virucide, antibacterial, antiparasitic,

CC immunomodulatory and antihypertensive activity. (I), and constructs

CC additionally containing antigen-encoding sequences, are useful in gene

CC therapy of tumors. Polypeptides encoded by (I) are useful for treating

CC parasitic or viral infections and tumors, particularly schistosomiasis

CC and carcinoma (of bladder, epithelium, ovary, breast, bronchi or

CC colon-rectum), also hypertension, as vaccines, for treating cocaine

CC misuse and very generally as carriers for pharmaceuticals, e.g.

CC cytostatics. They may also be used to generate antibodies (Ab). Probes

CC based on (I) and Ab are useful for detecting tumor-specific DNA in a cell

CC (by detecting specific binding to cellular DNA or proteins), particularly

CC where associated with the types of carcinoma listed above. Hemocyanins

CC can be produced recombinantly, relatively inexpensively and in adequate

CC amounts, eliminating the need to culture gastropods. When used as a

CC carrier, (II) significantly increases the half-life of the attached

CC pharmaceutical, by inhibiting ultrafiltration in the kidneys.

XX SQ Sequence 515 AA;

Query Match 96.6%; Score 28; DB 21; Length 515;

Best Local Similarity 80.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
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Db 490 dyyvt 494

RESULT 15

AAAY93885

ID AAY93885 standard; Protein; 101 AA.

XX AC AAY93885;

XX DT 03-OCT-2000 (first entry)

XX DE Amino acid sequence of a protein encoded by Hepatitis Y virus genome.

XX KW Hepatitis virus; Hepatitis Y virus; HYV; cell line ECACC 9110711;

XX RW vaccine.

XX OS Hepatitis Y virus.

XX PN WO200037650-A1.

XX PD 29-JUN-2000.

XX PF 16-DEC-1999; 99WO-EP10179.

XX PR 18-DEC-1998; 98EP-0204313.

XX PR 20-JAN-1999; 99EP-0200167.

XX PA (ALKU ) AKZO NOBEL NV.

XX PA Yap SH, Verslype CJC, Boender PJ, Hellings JA;

XX PI WPI; 2000-442677/38.

XX DR

XX PT Detecting non- A-G hepatitis virus, especially hepatitis Y virus, in a

PT sample, comprising contacting the cell with antibodies specific for

PT sequences in the virus genome -

XX

PS Disclosure; Page 17; 124pp; English.

XX

CC The present sequence represents a protein which is encoded by the

CC genome of the Hepatitis Y virus. The specification describes a novel

CC Hepatitis virus, Hepatitis Y virus (HYV), and a method for detecting

CC this virus in a hepatitis C negative sample. The method comprises

CC contacting the sample with antibodies from the cell line ECACC 9110711,

CC or monoclonal antibodies with the same immunoreactivity, and detecting

CC immunocomplexes formed. The methods are used to detect non A-G hepatitis

CC virus, especially hepatitis Y virus (HYV), in a sample. Proteins derived

CC from HYV can be used in vaccines, which are used to protect against HYV.

XX SQ Sequence 101 AA;

Query Match 93.1%; Score 27; DB 21; Length 101;

Best Local Similarity 80.0%; Pred. No. 86;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
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Db 94 dyyt 98

Search completed: June 28, 2001, 16:14:33

Job time: 1321 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 138.34 Seconds  
(without alignments)  
0.728 Million cell updates/sec

Title: US-09-724-406-4  
Perfect score: 29  
Sequence: 1 DYYIT 5

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	29	100.0	346	1	US-08-213-403-2
3	29	100.0	346	1	US-08-458-077-2
4	29	100.0	346	1	US-08-460-741-2
5	29	100.0	346	1	US-08-747-240-2
6	29	100.0	346	1	US-08-299-567-6
7	29	100.0	706	4	US-05-408-820-2
8	28	96.6	173	3	US-08-669-408B-8
9	27	93.1	178	4	US-08-976-255-18
10	27	93.1	275	4	US-08-976-255-16
11	27	93.1	472	4	US-08-647-144-2
12	26	89.7	120	2	US-08-647-144-2
13	26	89.7	124	1	US-08-442-542-6
14	26	89.7	124	3	US-08-765-469-6
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17	25	86.2	167	2	US-07-961-702-2
18	25	86.2	162	1	US-08-472-284-2
19	25	86.2	162	1	US-08-476-678-2
20	25	86.2	162	1	US-08-472-418-2
21	25	86.2	197	4	US-08-975-215-4
22	25	86.2	208	4	US-08-896-933-30
23	25	86.2	239	4	US-09-095-738-11
24	25	86.2	239	4	US-09-422-968-11
25	25	86.2	307	4	US-08-975-215-2
26	25	86.2	380	4	US-08-971-782-4
27	25	86.2	380	4	US-09-309-026-4

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29 25 86.2 449 1 US-08-624-663A-2 Sequence 2, Appli  
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31 25 86.2 449 3 US-09-255-748-1 Sequence 1, Appli  
32 25 86.2 459 3 US-08-971-782-2 Sequence 2, Appli  
33 25 86.2 459 4 US-09-309-026-2 Sequence 2, Appli  
34 25 86.2 553 2 US-08-586-272-2 Sequence 2, Appli  
35 25 86.2 553 3 US-09-082-969-2 Sequence 2, Appli  
36 25 86.2 575 2 US-08-766-858A-5 Sequence 5, Appli  
37 25 86.2 667 1 US-08-471-033-7 Sequence 7, Appli  
38 25 86.2 667 2 US-08-471-044-7 Sequence 7, Appli  
39 25 86.2 667 2 US-08-463-483A-7 Sequence 7, Appli  
40 25 86.2 667 2 US-08-471-046A-7 Sequence 7, Appli  
41 25 86.2 667 2 US-08-470-566B-7 Sequence 7, Appli  
42 25 86.2 667 2 US-08-469-334-7 Sequence 7, Appli  
43 25 86.2 667 3 US-09-300-529-7 Sequence 7, Appli  
44 25 86.2 713 2 US-08-987-466-3 Sequence 3, Appli  
45 25 86.2 713 2 US-08-974-565C-5 Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-09-232-446B-5  
; Sequence 5, Application US/09232446B  
; Patent No. 6228647  
; GENERAL INFORMATION:  
; APPLICANT: Voytas, Daniel F.  
; TITLE OF INVENTION: Transposable Element Protein that Directs DNA  
; TITLE OF INVENTION: Integration to Specific Chromosomal Sites  
; FILE REFERENCE: 2-98  
; CURRENT APPLICATION NUMBER: US/09/232,446B  
; PRIOR FILING DATE: 1999-01-15  
; PRIOR APPLICATION NUMBER: US 60/071,383  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 178  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-232-446B-5

Query Match 100.0%; Score 29; DB 4; Length 178;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYIT 5  
Db 168 DYYIT 172

RESULT 2  
US-08-213-403-2  
; Sequence 2, Application US/08213403  
; Patent No. 5512457  
; GENERAL INFORMATION:  
; APPLICANT: Lyman, Stewart D.  
; APPLICANT: Beckmann, M. Patricia  
; APPLICANT: Baum, Peter R  
; APPLICANT: Carpenter, Melissa  
; TITLE OF INVENTION: No. 5512457el Cytokine Designated elk Ligand  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101

us-09-724-406-4.ra1

Fri Jun 29 08:05:13 2001

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/213,403
FILING DATE: 15-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-213-403-2

Query Match 100.0%; Score 29; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 131 DYYIT 135

RESULT 4
US-08-460-741-2
Sequence 2, Application US/08460741
Patent No. 5670625
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R.
APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,741
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-741-2

Query Match 100.0%; Score 29; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 131 DYYIT 135

RESULT 3
US-08-458-077-2
Sequence 2, Application US/08458077
Patent No. 5627267
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R.
APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,077
FILING DATE: 01-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
|||||

Db 131 DYYIT 135

# RESULT 5

US-08-747-240-2  
; Sequence 2, Application US/08747240  
; Patent No. 5728813  
; GENERAL INFORMATION:  
; APPLICANT: Lyman, Stewart D.  
; APPLICANT: Beckmann, M. Patricia  
; APPLICANT: Baum, Peter R.  
; APPLICANT: Carpenter, Melissa  
; TITLE OF INVENTION: No. 5728813el Cytokine Designated elk Ligand  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,240  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/213,403  
; FILING DATE: 15-MAR-1994  
; APPLICATION NUMBER: US 07/977,693  
; FILING DATE: 13-NOV-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2807-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 346 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-747-240-2

Query Match 100.0%; Score 29; DB 1; Length 346;  
Best Local Similarity 100.0%; Pred. No. le+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
|||||

Db 131 DYYIT 135

# RESULT 6

US-08-299-567-6  
; Sequence 6, Application US/08299567  
; Patent No. 5747033  
; GENERAL INFORMATION:  
; APPLICANT: Davis, et al.  
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL  
; ACTIVITY OF EPH FAMILY LIGANDS

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-6707  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,567  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kempner, Gail M.  
; REGISTRATION NUMBER: 32,143  
; REFERENCE/DOCKET NUMBER: REG 290  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 914-345-7400  
; TELEFAX: 914-345-7721  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 346 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-299-567-6

Query Match 100.0%; Score 29; DB 1; Length 346;  
Best Local Similarity 100.0%; Pred. No. le+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
|||||

Db 131 DYYIT 135

# RESULT 7

US-09-408-820-2  
; Sequence 2, Application US/09408820  
; Patent No. 6204057  
; GENERAL INFORMATION:  
; APPLICANT: Schaeffer, Wolfgang  
; APPLICANT: Krieger, Lutz  
; APPLICANT: Zhang, Jiaming  
; TITLE OF INVENTION: Polynucleotides And The Proteins Encoded Thereby,  
; FILE OF INVENTION: Suitable For Controlling Lamellicorn Beetles  
; FILE REFERENCE: S-30403/A/UHD/GSC1996/PCT  
; CURRENT APPLICATION NUMBER: US/09/408,820  
; CURRENT FILING DATE: 1999-09-29  
; EARLIER APPLICATION NUMBER: 09/051,454  
; EARLIER FILING DATE: 1998-04-07  
; EARLIER APPLICATION NUMBER: DE 195 40 223.5  
; EARLIER FILING DATE: 1995-10-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 706  
; TYPE: PRT  
; ORGANISM: Bacillus popilliae  
; FEATURE:  
; OTHER INFORMATION: strain subspecies: melolonthae H1; stage of  
; OTHER INFORMATION: development: spore stage; cell type: sporangium  
; FEATURE:  
; OTHER INFORMATION: immediate origin: isolate from the haemolymph of  
; OTHER INFORMATION: Melolontha melolontha individuals captured on open  
; OTHER INFORMATION: ground

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us-09-724-406-4.ra1

FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(706)  
OTHER INFORMATION: mature protein crystal peptide determined by  
OTHER INFORMATION: experiment  
US-09-408-820-2

Query Match 100.0%; Score 29; DB 4; Length 706;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
| | | | |  
Db 506 DYYIT 510

RESULT 8  
US-08-669-408B-8  
Sequence 8, Application US/08669408B  
Patent No. 6100055  
GENERAL INFORMATION:  
APPLICANT: GUSS, Bengt  
APPLICANT: JONSSON, Hans  
APPLICANT: LINDBERG, Martin  
APPLICANT: MUELLER, Hans-Peter  
APPLICANT: RANTAMAKI, Liisa K.  
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING  
TITLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,408B  
FILING DATE: 03-JUL-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/SE94/00826  
FILING DATE: 06-SEP-1994  
PRIOR APPLICATION DATA: SE 9302855-3  
FILING DATE: 06-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 61743/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 173 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-669-408B-8

Query Match 96.6%; Score 28; DB 3; Length 173;  
Best Local Similarity 80.0%; Pred. No. 77;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
| | | | |  
Db 156 DYYIT 160

RESULT 9  
US-08-976-255-18  
Sequence 18, Application US/08976255  
Patent No. 6136581  
GENERAL INFORMATION:  
APPLICANT: Jono, Keith E.  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: KINASE GENES AND USES  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,255  
FILING DATE: No. 6136581ember 21, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/031,675  
FILING DATE: No. 6136581ember 22, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 229/182  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-976-255-18

Query Match 93.1%; Score 27; DB 4; Length 170;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
| | | | |  
Db 132 DYYIT 136

RESULT 10  
US-08-976-255-16  
Sequence 16, Application US/08976255  
Patent No. 6136581  
GENERAL INFORMATION:  
APPLICANT: Jono, Keith E.  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: KINASE GENES AND USES  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon

```

; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-976-255-16

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Query Match 93.1%; Score 27; DB 4; Length 275;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYYIT 5
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Db 230 DYYLT 234
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RESULT 11
US-08-976-255-17
; Sequence 17, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-976-255-17

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Query Match 93.1%; Score 27; DB 4; Length 472;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYYIT 5
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Db 295 DYYLT 299
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RESULT 12
US-08-647-144-2
; Sequence 2, Application US/08647144
; Patent No. 5858728
; GENERAL INFORMATION:
; APPLICANT: Gram, Hermann
; APPLICANT: Di Padova, Franco
; APPLICANT: Barclay, George R.
; APPLICANT: Foxton, Ian R.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST LPS CORE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5858728th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,144
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/119,046
; FILING DATE: 10-SEP-1993
; APPLICATION NUMBER: EP 92/00380
; FILING DATE: 22-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids

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RESULT 14  
US-08-442-542-6  
; Sequence 6, Application US/08442542  
; Patent No. 5686600  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine B.  
; APPLICANT: Koziel, Michael G.  
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut  
; TITLE OF INVENTION: Proteins and their Use  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,542  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/267,641  
; FILING DATE: 28-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: CGC 1750  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8615  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-442-542-6  
  
Query Match 89.7%; Score 26; DB 1; Length 124;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYYIT 5  
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Db 31 DYYMT 35

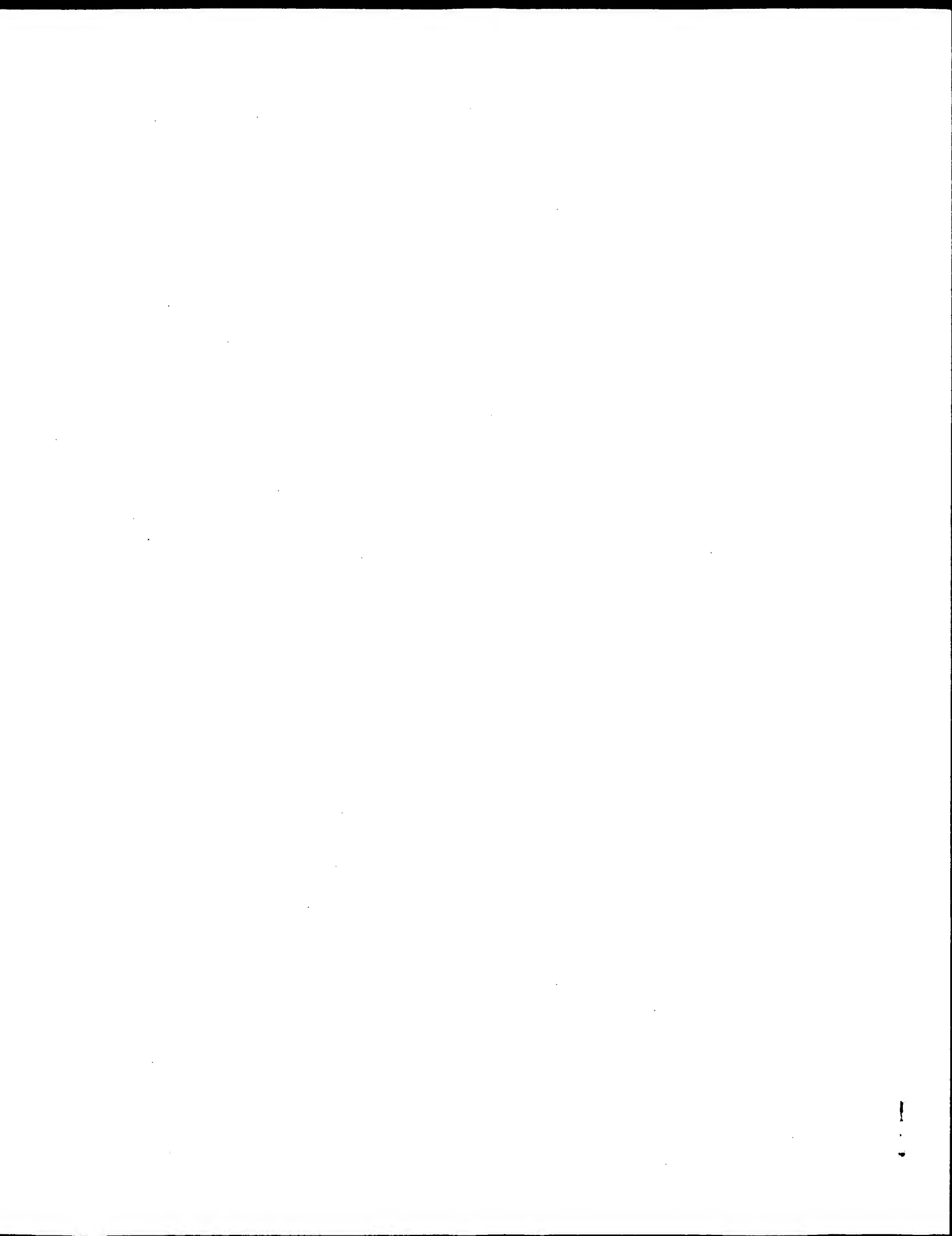
US-08-647-144-2  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-647-144-2  
  
Query Match 89.7%; Score 26; DB 2; Length 120;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYYIT 5  
|||:|  
Db 31 DYYMT 35

RESULT 13  
US-08-647-144-4  
; Sequence 4, Application US/08647144  
; Patent No. 5858728  
; GENERAL INFORMATION:  
; APPLICANT: Gram, Hermann  
; APPLICANT: Di Padova, Franco  
; APPLICANT: Barclay, George R.  
; APPLICANT: Poxton, Ian R.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST LPS CORE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: Post Office Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5858728th Carolina  
; COUNTRY: U.S.A.  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/647,144  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/119,046  
; FILING DATE: 10-SEP-1993  
; APPLICATION NUMBER: EP 92/00380  
; FILING DATE: 22-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 1749-114  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 881-3140  
; TELEFAX: (919) 881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-647-144-4  
  
Query Match 89.7%; Score 26; DB 2; Length 120;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYYIT 5  
|||:|  
Db 31 DYYMT 35

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,469  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/267,641  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: CGC 1750  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8615  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-765-469-6

Query Match 89.7%; Score 26; DB 3; Length 124;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYYIT 5  
Db 31 DYYMT 35

Search completed: June 28, 2001, 16:01:13  
Job time: 521 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 234.85 Seconds  
(without alignments)  
1.622 Million cell updates/sec

Title: US-09-724-406-4  
Perfect score: 29  
Sequence: 1 DYYIT 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	231	184422	cytochrome-c oxida
2	29	100.0	338	G71128	hypothetical prote
3	29	100.0	345	I48780	Stral/Eplg2 protei
4	29	100.0	345	I58406	LERK-2 - rat
5	29	100.0	346	S46993	elk ligand - human
6	29	100.0	358	H71088	hypothetical prote
7	29	100.0	360	T34510	hypothetical prote
8	29	100.0	365	D69092	conserved hypothet
9	29	100.0	369	ESBPC	3',5'-cyclic-nucle
10	29	100.0	473	D81322	outer membrane pro
11	29	100.0	527	A84050	acetate-CoA ligase
12	29	100.0	537	T50099	probable protein-t
13	29	100.0	736	C69307	conserved hypothet
14	29	100.0	1050	S54640	KCS1 protein - yea
15	29	100.0	1348	B23496	TyB protein - yea
16	29	100.0	1598	S69967	TyB protein - yea
17	29	100.0	1633	JC5056	polybromo 1 - chic
18	29	100.0	1770	S45842	TyB protein - yea
19	29	100.0	1770	S69953	TyB protein - yea
20	29	100.0	1770	S69948	TyB protein - yea
21	29	100.0	1770	S70233	TyB protein - yea
22	29	100.0	1770	S70230	TyB protein - yea
23	29	100.0	1770	S69966	TyB protein - yea
24	29	100.0	1770	S69950	TyB protein - yea
25	29	100.0	1770	S58651	TyB protein - yea
26	29	100.0	1771	S53592	TyB protein - yea
27	29	100.0	1810	S69973	TyB protein - yea
28	29	100.0	2338	T25810	hypothetical prote
29	29	100.0	3147	T18674	hypothetical prote

30	28	96.6	181	2	S75415	probable ribosomal
31	28	96.6	297	2	E71425	hypothetical prote
32	28	96.6	301	2	S52013	H+-transporting AT
33	28	96.6	328	2	C86351	hypothetical prote
34	28	96.6	367	2	B75597	first mannose tra
35	28	96.6	381	2	F64354	hypothetical prote
36	28	96.6	389	2	D64337	16S rRNA 5'-region
37	28	96.6	405	2	S42371	ATP-dependent Clp
38	28	96.6	467	2	E69601	hypothetical prote
39	28	96.6	536	2	H85176	probable epoxide h
40	28	96.6	594	2	T33686	hypothetical prote
41	28	96.6	699	2	H82030	cysteine-tRNA lig
42	28	96.6	755	2	T32971	hypothetical prote
43	28	96.6	818	2	T33689	hypothetical prote
44	28	96.6	818	2	T33687	hypothetical prote
45	28	96.6	998	1	Q0BBB1	B1 protein - black

ALIGNMENTS

RESULT 1

I84422  
cytochrome-c oxidase (EC 1.9.3.1) chain II - common woolly monkey mitochondrion  
C:Species: mitochondrion Lagotrix lagotricha (common woolly monkey)  
C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 07-Dec-1999  
C:Accession: I84422  
R:Adkins, R.M.; Honeycutt, R.L.  
J. Mol. Evol. 38, 215-231, 1994  
A:Title: Evolution of the primate cytochrome c oxidase subunit II gene.  
A:Reference number: I36906; MUID:94275866  
A:Accession: I84422  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-231 <ADK>  
A:Cross-references: GB:L22779; NID:g438681; PIDN:AAA20565.1; PID:g438682  
C:Genetics:  
A:Genome: mitochondrion  
A:Genetic code: SGC1  
C:Superfamily: cytochrome-c oxidase chain II; cytochrome-c oxidase chain II homology  
C:Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inn  
F:9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
F:161.196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
F:196.196,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
F:198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 100.0% Score 29; DB 2; Length 231;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5

Db 119 DYYIT 123

RESULT 2

G71128  
hypothetical protein PH0796 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 28-Jul-2000  
C:Accession: G71128  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Se  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil  
A:Reference number: A71000; MUID:98344137  
A:Accession: G71128  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-338 <KAW>  
A:Cross-references: GB:AF000003; NID:g3236130; PIDN:BAA29889.1; PID:g3257206  
A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C:Genetics:  
 A:Gene: PH0796  
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0973

Query Match 100.0%; Score 29; DB 2; Length 338;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 85 DYYIT 89

## RESULT 3

Stral/Eplg2 protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I48780; A5507; A55062; S52670  
 R:Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbauer, B.; Dolle, Dev. Biol. 170, 420-433, 1995  
 A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal carcinoma cells  
 A:Reference number: I48780; MUID:95377533  
 A:Accession: I48780  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-345 <RES>  
 R:Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; Genomics 24, 127-132, 1994  
 A:Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encoding a protein tyrosine kinase  
 A:Reference number: A5507; MUID:95203867  
 A:Accession: A5507  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-345 <FLE>  
 A:Cross-references: GB:U07598  
 R:Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M. J. Biol. Chem. 269, 26606-26609, 1994  
 A:Title: cDNA cloning and characterization of a ligand for the Cdk5 receptor protein-tyrosine kinase  
 A:Reference number: A55062; MUID:95014510  
 A:Accession: A55062  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-89, 91-345 <SUA>  
 A:Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929  
 C:Genetics:  
 A:Gene: EPLG2

Query Match 100.0%; Score 29; DB 2; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 131 DYYIT 135

## RESULT 4

LERK-2 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I58406  
 R:Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollin OncoGene 9, 3241-3248, 1994  
 A:Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved  
 A:Reference number: I58406; MUID:95022634  
 A:Accession: I58406  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
 A:Residues: 1-345 <RES>  
 A:Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119  
 C:Genetics:  
 A:Gene: Eplg2

Query Match 100.0%; Score 29; DB 2; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 131 DYYIT 135

## RESULT 5

S46993  
 elk ligand - human  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 28-May-1999  
 C:Accession: S46993  
 R:Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Ko EMO J. 13, 3757-3762, 1994  
 A:Title: Molecular characterization of a family of ligands for eph-related tyrosine kinase  
 A:Reference number: S46993; MUID:94349923  
 A:Accession: S46993  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-346 <BEC>  
 A:Cross-references: GB:U09304; NID:g538366; PIDN:AAA53093.1; PID:g538367

Query Match 100.0%; Score 29; DB 2; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 131 DYYIT 135

## RESULT 6

H71088  
 hypothetical protein PH0973 - Pyrococcus horikoshii  
 C:Species: Pyrococcus horikoshii  
 C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 28-Jul-2000  
 C:Accession: H71088  
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yanamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogo DNA Res. 5, 55-76, 1998  
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon  
 A:Reference number: A71000; MUID:98344137  
 A:Accession: H71088  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-358 <KAW>  
 A:Cross-references: GB:AP00004; NID:g3236131; PIDN:BAA30070.1; PID:g3257387  
 A:Experimental source: strain OT3  
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C:Genetics:  
 A:Gene: PH0973  
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0973

Query Match 100.0%; Score 29; DB 2; Length 358;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 85 DYYIT 89

## RESULT 7

T34510  
 hypothetical protein ZK1290.10 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jun-2000  
 R:Taich, A.  
 submitted to the EMBL Data Library, July 1995  
 A:Description: The sequence of C. elegans cosmid ZK1290.  
 A:Reference number: Z21535  
 A:Accession: T34510  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-360 <TAI>  
 A:Cross-references: EMBL:U21308; PIDN:AAB93316.1; GSPDB:GN00020; CESP:ZK1290.10  
 A:Experimental source: strain Bristol N2; clone ZK1290  
 C:Genetics:  
 A:Gene: CESP:ZK1290.10  
 A:Map position: 2  
 A:Introns: 23/1; 48/1; 158/3; 216/1; 264/1; 312/1; 331/3  
 C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1290.10

Query Match 100.0%; Score 29; DB 2; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 207 DYYIT 211

## RESULT 8

D69092  
 conserved hypothetical protein MTH1686 - Methanobacterium thermoautotrophicum (strain De  
 C:Species: Methanobacterium thermoautotrophicum  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
 Qiu, D.; Spadafora, R.; Vicalire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.  
 K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
 A:Reference number: A69000; MUID:98037514  
 A:Accession: D69092  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-365 <MTH>  
 A:Cross-references: GB:AE000926; GB:AE000666; NID:g2622806; PIDN:AAB86158.1; PID:g262280  
 A:Experimental source: strain Delta H  
 C:Genetics:  
 A:Gene: MTH1686  
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0759

Query Match 100.0%; Score 29; DB 2; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 44 DYYIT 48

## RESULT 9

ESBYPC  
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), low-affinity - yeast (Saccharom  
 N:Alternate names: protein G0574; protein NRB369; protein YGL248w  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 31-Mar-1991 #sequence\_revision 12-Apr-1996 #text\_change 16-Jun-2000  
 C:Accession: S61613; S05879; S64274  
 R:Colisac, E.; Maillier, E.; Robineau, S.; Netter, P.

submitted to the EMBL Data Library, December 1995  
 A:Reference number: S61598  
 A:Accession: S61613

A:Molecule type: DNA  
 A:Residues: 1-369 <COI>

A:Cross-references: EMBL:X94357; NID:g1150575; PIDN:CAA64139.1; PID:g1150591  
 R:Nikawa, J.; Sass, P.; Wigler, M.  
 Mol. Cell. Biol. 7, 3629-3636, 1987

A:Title: Cloning and characterization of the low-affinity cyclic AMP phosphodiesteras  
 A:Reference number: S05879; MUID:88065501  
 A:Accession: S05879

A:Molecule type: DNA  
 A:Residues: 1-93, 'F', 95-369 <NIK>

A:Cross-references: EMBL:M1781; NID:g172228; PIDN:AAA34896.1; PID:g172229

A:Experimental source: strain PSI-2  
 R:Colisac, E.; Maillier, E.; Netter, P.

submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64271  
 A:Accession: S64274

A:Molecule type: DNA  
 A:Residues: 1-369 <COV>

A:Cross-references: EMBL:Z72770; NID:g1322920; PIDN:CAA96968.1; PID:g1322921; GSPDB:G

A:Experimental source: strain S288C  
 C:Genetics:

A:Gene: SGD:PDE1; MIPS:YGL248w  
 A:Cross-references: SGD:S0003217; MIPS:YGL248w

A:Map position: 7L  
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase

C:Keywords: phosphoric diester hydrolase

Query Match 100.0%; Score 29; DB 1; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 123 DYYIT 127

## RESULT 10

D81322  
 outer membrane protein Cj1170c [imported] - Campylobacter jejuni (strain NCTC 11168)  
 C:Species: Campylobacter jejuni  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 20-Apr-2000  
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Ba  
 Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals  
 A:Reference number: AB1250; MUID:20150912  
 A:Accession: D81322  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-473 <PAR>  
 A:Cross-references: GB:AL135077; GB:AL111168; NID:g96968444; PIDN:CAB73424.1; PID:g9696  
 A:Experimental source: serotype O2, strain NCTC 11168  
 C:Genetics:  
 A:Gene: Cj1170c  
 C:Superfamily: Campylobacter jejuni outer membrane protein Cj1170c

Query Match 100.0%; Score 29; DB 2; Length 473;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 Db 170 DYYIT 174

## RESULT 11

AB4050

Fri Jun 29 08:05:14 2001

us-09-724-406-4.rpr

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
 A:Residues: 1-736 <MLE>  
 A:Cross-references: GB:AE000782; NID:g2689396; PIDN:AAB90778.1; PID:g265  
 C:Superfamily: Archaeoglobus conserved hypothetical protein AF0459

Query Match 100.0%; Score 29; DB 1; Length 736;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 DB 552 DYYIT 556

## RESULT 14

S54640  
 KCS1 protein - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: protein D328; protein PZF1050; protein YD9335.03c; protein YDR017  
 C:Species: *Saccharomyces cerevisiae*  
 C:Date: 08-Jul-1995 sequence revision 01-Sep-1995 #text\_change 21-Jul-2000  
 C:Accession: S54640; S63423; S67830; S60373; S72114  
 R:Dedman, K.; Brown, D.; Hamlyn, N.; Bowman, S.  
 submitted to the EMBL Data Library, May 1995  
 A:Reference number: S54638  
 A:Accession: S54640

A:Molecule type: DNA  
 A:Residues: 1-1050 <DED>  
 A:Cross-references: EMBL:Z49770; NID:g840867; PID:g840870

A:Experimental source: strain AB972  
 R:Eide, L.G.; Sander, C.; Prydz, H.  
 submitted to the EMBL Data Library, February 1996  
 A:Description: Sequencing and analysis of a 35.4 kb region on the left arm of chromos  
 A:Reference number: S63416  
 A:Accession: S63423  
 A:Molecule type: DNA  
 A:Residues: 1-1050 <EID>  
 A:Cross-references: EMBL:X5966; NID:g1216215; PID:g225526; PID:g1216223  
 R:Prydz, H.; Eide, L.G.  
 submitted to the Protein Sequence Database, July 1996

A:Reference number: S67822  
 A:Accession: S67830  
 A:Molecule type: DNA  
 A:Residues: 1-1050 <PRY>  
 A:Cross-references: EMBL:Z74313; NID:g1431441; PID:g253292; PID:g1431442; MIPS:YDR017  
 A:Experimental source: strain S288C  
 R:Huang, K.N.; Symington, L.S.  
 Genetics 141, 1275-1285, 1995  
 A:Title: Suppressors of a *Saccharomyces cerevisiae* pkc1 mutation identify alleles of

A:Reference number: S60373; MUID:96170769  
 A:Accession: S60373  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-688, 'M', 690-1050 <HUA>  
 R:Eide, L.G.; Sander, C.; Prydz, H.  
 Yeast 12, 1085-1090, 1996  
 A:Title: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome IV

A:Reference number: S72107; MUID:97051598  
 A:Accession: S72114  
 A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
 A:Residues: 1-1050 <ETW>  
 A:Cross-references: EMBL:X5966; NID:g1216215; PID:CAA65208.1; PID:g1216223  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
 C:Genetics:  
 A:Gene: SGD:KCS1  
 A:Cross-references: MIPS:YDR017c; SGD:S0002424  
 A:Map position: 4R

Query Match 100.0%; Score 29; DB 2; Length 1050;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;

acetate-CoA ligase BH3201 [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 31-Dec-2000  
 C:Accession: A84050

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
 A:Reference number: A83650; MUID:20263314

A:Accession: A84050  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-527 <STO>

A:Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA06920.1; GSPDB:GN00  
 A:Experimental source: strain C-125

C:Genetics:  
 A:Gene: BH3201

C:Superfamily: human SA protein; acetate--CoA ligase homology

Query Match 100.0%; Score 29; DB 2; Length 527;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 DB 396 DYYIT 400

## RESULT 12

T50099  
 probable protein-tyrosine phosphatase CDC14 homolog [imported] - fission yeast (*Schizos*  
 C:Species: *Schizosaccharomyces pombe*  
 C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jun-2000  
 C:Accession: T50099  
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.  
 submitted to the EMBL Data Library, February 2000

A:Reference number: Z25037  
 A:Accession: T50099  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-537 <WOO>  
 A:Cross-references: EMBL:AL158056; PIDN:CA876271.1; GSPDB:GN00066; SPDB:SPAC1782.09c

A:Gene: SPDB:SPAC1782.09c  
 A:Map position: 1  
 A:Introns: 17/1

Query Match 100.0%; Score 29; DB 2; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
 |||||  
 DB 141 DYYIT 145

## RESULT 13

C69307  
 conserved hypothetical protein AF0459 - *Archaeoglobus fulgidus*  
 C:Species: *Archaeoglobus fulgidus*  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997  
 A:Authors: Uffnerback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343

A:Accession: C69307

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5

|||||

Db 821 DYYIT 825

RESULT 15

B23496

TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty1-17  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 20-Aug-1987 #sequence\_revision 20-Aug-1987 #text\_change 25-Apr-1997  
 C:Accession: B23496  
 R:Warrington, J.R.; Waring, R.B.; Newlon, C.S.; Indge, K.J.; Oliver, S.G.  
 Nucleic Acids Res. 13, 6679-6693, 1985  
 A:Title: Nucleotide sequence characterization of Ty 1-17, a class II transposon from yeast  
 A:Reference number: A93591; MUID:86041864  
 A:Accession: B23496  
 A:Molecule type: DNA  
 A:Residues: 1-1348 <WAB>  
 A:Cross-references: EMBL:X03840; EMBL:J01333; EMBL:X00633; EMBL:X02991  
 C:Genetics:  
 A:Mobile element: retrotransposon Ty1-17  
 C:Superfamily: TyB protein

Query Match

Best Local Similarity 100.0%; Score 29; DB 2; Length 1348;

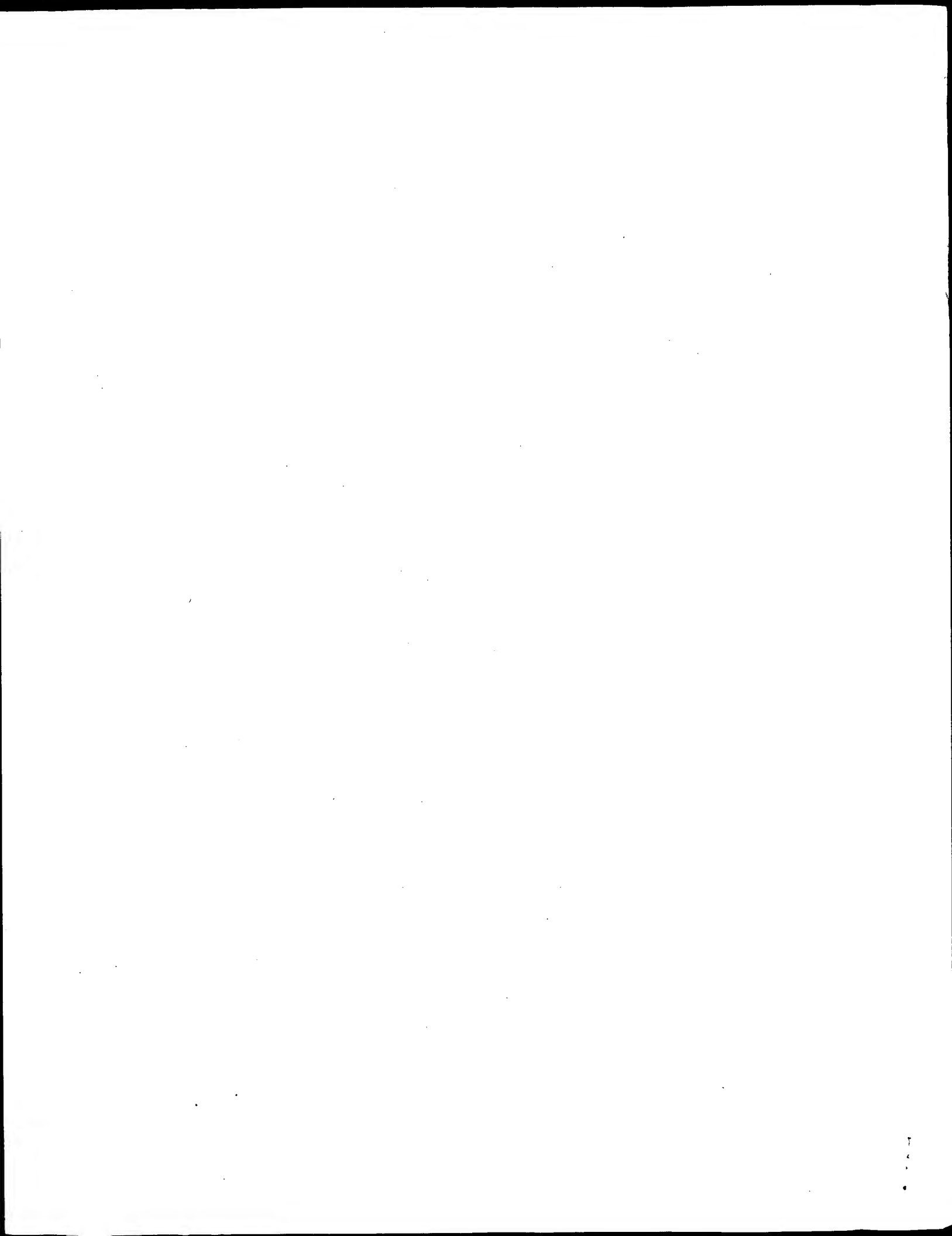
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5

|||||

Db 932 DYYIT 936

Search completed: June 28, 2001, 15:58:42  
 Job time: 370 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 105.36 seconds  
(without alignments)  
1.626 Million cell updates/sec

Title: US-09-724-406-4  
Perfect score: 29  
Sequence: 1 DYYIT 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	231	1	COX2_LAGLA
2	29	100.0	327	1	EFBI_XENIA
3	29	100.0	345	1	EFBI_MOUSE
4	29	100.0	345	1	EFBI_RAT
5	29	100.0	346	1	EFBI_HUMAN
6	29	100.0	360	1	YOFB_CAEEL
7	29	100.0	369	1	CNAI_YEAST
8	29	100.0	675	1	CIBA_PAEPP
9	29	100.0	695	1	CICB_PAEPP
10	29	100.0	706	1	CICB_PAEPP
11	29	100.0	1347	1	YCB9_YEAST
12	28	96.6	181	1	RS4_SULSO
13	28	96.6	381	1	Y438_METJA
14	28	96.6	389	1	Y299_METJA
15	28	96.6	405	1	YKX4_CAEEL
16	28	96.6	467	1	HSU4_BACSU
17	28	96.6	1444	1	RRPL_RDVF
18	28	96.6	1444	1	RRPL_RDVF
19	27	93.1	174	1	HDCH_LACS3
20	27	93.1	206	1	T2D8_YEAST
21	27	93.1	233	1	PIC1_AGRTU
22	27	93.1	861	1	RFCL_YEAST
23	27	93.1	1037	1	YHIV_ECOLI
24	27	93.1	1125	1	YHIV_ECOLI
25	27	93.1	1696	1	YHIV_ECOLI
26	26	89.7	371	1	YHIV_ECOLI
27	25	86.2	235	1	YHIV_ECOLI
28	25	86.2	235	1	YHIV_ECOLI
29	25	86.2	239	1	YHIV_ECOLI
30	25	86.2	331	1	YHIV_ECOLI
31	25	86.2	331	1	YHIV_ECOLI
32	25	86.2	353	1	YHIV_ECOLI
33	25	86.2	377	1	YHIV_ECOLI

34	25	86.2	377	1	PAT1_SOLTU	P15476 solanum tub
35	25	86.2	383	1	Y4GN_RHISN	P55470 rhizobium s
36	25	86.2	386	1	PAT0_SOLTU	P07745 solanum tub
37	25	86.2	386	1	PAT2_SOLTU	P15477 solanum tub
38	25	86.2	386	1	PAT3_SOLTU	P11768 solanum tub
39	25	86.2	429	1	CBPX_ORYSA	P52712 oryza sativ
40	25	86.2	432	1	AMIB_HAEIN	P44493 haemophilus
41	25	86.2	456	1	GLMU_ECOLI	P17114 escherichia
42	25	86.2	539	1	CBPX_ARATH	P32826 arabidopsis
43	25	86.2	553	1	IAGA_SALTI	P43016 salmoneilla
44	25	86.2	553	1	IAGA_SALTY	P43015 salmoneilla
45	25	86.2	567	1	ACHL_DROME	P09478 drosophila

## ALIGNMENTS

RESULT 1  
COX2\_LAGLA  
ID COX2\_LAGLA STANDARD; PRT; 231 AA.  
AC P98036;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1).  
GN MTCO2 OR COII.  
OS Lagotrix lagotricha (Common woolly monkey).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae;  
OC Lagotrix.  
OX NCBI\_TaxID=9519;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94275366; PubMed=8006990;  
RA Adkins R.M., Honeycutt R.L.;  
RT "Evolution of the primate cytochrome c oxidase subunit II gene."  
RL J. Mol. Evol. 38:215-231(1994).  
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-  
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2  
TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER  
A CENTER TO THE BINUCLEAR COPPER CENTER OF THE CATALYTIC SUBUNIT 1.  
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +  
4 FERRICYTOCHROME C.  
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  
INNER MEMBRANE.  
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.  
-----  
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-----  
EMBL; L22779; AAA20565.1; -  
HSP; P00404; IOCC.  
InterPro; IPR001505; -  
InterPro; IPR002429; -  
Pfam; PF00116; COX2; 1.  
PRINTS; PR01166; CYCOXIDASEII.  
PROSITE; PS00078; COX2; 1.  
Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
Electron transport; Respiratory chain.  
DOMAIN 1 26  
TRANSMEM 27 48  
FT DOMAIN 27 48  
FT DOMAIN 49 62  
FT TRANSMEM 63 82  
FT TRANSMEM 83 231  
FT DOMAIN 161 196  
FT METAL 196  
FT METAL 196

Fri Jun 29 08:05:14 2001

us-09-724-406-4.rsp

FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).  
 SQ SEQUENCE 231 AA; 26557 MW; 315E9B1B61CDED80 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 231;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYIIT 5

Db 119 DYIIT 123

RESULT 2

EFBL\_XENLA STANDARD; PRT; 327 AA.

AC 013097;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2)  
 DE (LERK-2) (ELK LIGAND) (ELK-L) (XLERK).  
 GN EFN1 OR EPLG2 OR LERK2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;

[1]

SEQUENCE FROM N.A.

RX MEDLINE-97316777; PubMed-9174051;  
 RA Jones T.L., Karavanova I., Chong L., Zhou R.P., Daar I.O.;  
 RT "Identification of Xlerk, an Eph family ligand regulated during  
 RT mesoderm induction and neurogenesis in Xenopus laevis."  
 RL Oncogene 14:2159-2166(1997).

CC -1- FUNCTION: MAY HAVE A ROLE IN THE DEVELOPING MESENCHYMAL AND  
 CC NERVOUS TISSUE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: IN THE ADULT, EXPRESSED AT LOW LEVELS IN MOST

CC ADULT TISSUES WITH INCREASED LEVELS OBSERVED IN THE KIDNEY,

CC OOCYTES, OVARY AND TESTIS.

CC -1- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE

CC CYTOPLASMIC DOMAIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; U31427; AAC35995.1;

CC DR InterPro: IPR001799;

CC DR Pfam: PF00812; Ephrin; 1.

CC DR PROSITE: PS01299; EPHRIN; 1.

CC KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;

CC FT SIGNAL; 1 20

CC FT CHAIN 21 327

CC FT DOMAIN 21 225

CC FT TRANSMEM 226 246

CC FT DOMAIN 247 327

CC FT DOMAIN 325 327

CC FT DOMAIN 131 131

CC FT CARBOHYD 202 202

CC SEQUENCE 327 AA; 36621 MW; 71230CE/F6BE5974 CRC64;

Query Match

Best Local Similarity

100.0%; Score 29; DB 1; Length 327;

100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYIIT 5  
 Db 123 DYIIT 127

RESULT 3

EFBL\_MOUSE STANDARD; PRT; 345 AA.

AC P32795;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2)

DE (LERK-2) (ELK LIGAND) (ELK-L) (STRA1 PROTEIN) (CEK5 RECEPTOR LIGAND)

DE (CEK5-L).

GN EFN1 OR EPLG2 OR LERK2 OR STRA1 OR EPL2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=129/SV;

RX MEDLINE-95203867; PubMed-7896266;

RA Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,

RA Jenkins N.A., Gilbert D.J., Copeland N.G., Davidson B.L.;

RA "Genomic organization and chromosomal localization of mouse Eplg2, a

RT gene encoding a binding protein for the receptor tyrosine kinase

RT elk."

RL Genomics 24:127-132(1994).

RN [2]

SEQUENCE FROM N.A.

RX MEDLINE-95377533; PubMed-7649373;

RA Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,

RA Schuhbaer B., Dollé P., Chambon P.;

RT "Efficient cloning of cDNAs of retinoic acid-responsive genes in P19

RT embryonal carcinoma cells and characterization of a novel mouse gene,

RT Stral (mouse LERK-2/Eplg2)."

RL Dev. Biol. 170:420-433(1995).

RN [3]

SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE-95014510; PubMed-7929389;

RA Shao H., Lou L., Pandey A., Pasquale E.B., Dixit V.M.;

RT "cDNA cloning and characterization of a ligand for the Cek5 receptor

RT protein-tyrosine kinase."

RL J. Biol. Chem. 269:26606-26609(1994).

RN [4]

FUNCTION

RX MEDLINE-20171264; PubMed-10704386;

RA Mondri R., Wideman C., Kaprielian Z.;

RT "Complementary expression of transmembrane ephrins and their receptors

RT in the mouse spinal cord: a possible role in constraining the

RT orientation of longitudinally projecting axons."

RL Development 127:1397-1410(2000).

CC -1- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL

CC AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE

CC ORIENTATION OF LONGITUDINALLY PROJECTING AXONS.

CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB1 AND EPHAL.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED ON LATERAL FLOOR PLATE CELLS.

CC SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH

CC THE FLOOR PLATE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL

CC LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISC.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLATE THROUGHOUT THE

CC PERIOD OF COMMISSURAL AXON PATHFINDING.

CC -1- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE

CC CYTOPLASMIC DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.

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EMBL; U21308; AAB93316.1; -  
WormPep; ZK1290.10; CR02080.  
Hypothetical protein; Signal.  
FT SIGNAL 1 21  
CHAIN 22 360  
SEQUENCE 360 AA; 39669 MW; 187516BC062D4F7 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 360;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
Db 207 DYYIT 211

RESULT 7

CNAL\_YEAST STANDARD; PRT; 369 AA.  
ID CNAL\_YEAST  
AC P22434;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE 3', 5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE 1 (EC 3.1.4.17) (PDEASE 1)  
DE (LOW-AFFINITY CAMP PHOSPHODIESTERASE) (3'; 5'-CNP).  
DE PDEI OR YGL248W OR NRB369.  
GN Saccharomyces cerevisiae (Baker's yeast).  
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;

[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=88065501; PubMed=2824992;  
RA Nikawa J.-I., Sass P., Wälgler M.;  
RT "Cloning and characterization of the low-affinity cyclic AMP  
phosphodiesterase gene of Saccharomyces cerevisiae.";  
RL Mol. Cell. Biol. 7:3629-3636(1987).  
RN [2]  
SEQUENCE FROM N.A.  
RP STRAIN=S28C / EV1679;  
RX MEDLINE=97127827; PubMed=8972578;  
RA Coissac E., Maillet E., Robineau S., Netter P.;  
RT "Sequence of a 39,411 bp DNA fragment covering the left end of  
chromosome VII of Saccharomyces cerevisiae.";  
RL Yeast 12:1555-1562(1996).  
CC -1- FUNCTION: CONTROLS THE LEVEL OF CAMP IN YEAST CELLS, TOGETHER WITH  
THE HIGH-AFFINITY CAMP PHOSPHODIESTERASE (PDE2).  
CC -1- CATALYTIC ACTIVITY: NUCLEOSIDE 3',5'-CYCLIC PHOSPHATE + H(2)O -  
NUCLEOSIDE 5'-PHOSPHATE.  
CC -1- SIMILARITY: BELONGS TO THE CAMP PHOSPHODIESTERASE CLASS-II FAMILY.

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EMBL; M17781; AAA34896.1; -  
EMBL; X94357; CAA64139.1; -  
EMBL; Z72770; CAA96968.1; -  
DR PIR; S05879; ESEVPC.  
DR SGD; S0003217; PDEL.  
DR InterPro; IPR000396;  
DR Pfam; PF02112; PDEASE-II; 1.  
DR PRINTS; PR00388; PDIESTERASE2.  
DR PROSITE; PS00607; PDEASE-II; 1.

-1- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY).  
-1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHE1 AND EPHE1. BINDS GRP1 AND GRP2.  
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
-1- TISSUE SPECIFICITY: HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS.  
-1- INDUCTION: BY TNF-ALPHA.  
-1- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE CYTOPLASMIC DOMAIN (BY SIMILARITY).  
-1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.

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EMBL; U09304; AAA53093.1; -  
EMBL; L37361; AAR52369.1; -  
EMBL; U09303; AAB41127.1; -  
EMBL; AL136092; CAB86409.1; -  
MIM; 300035; -  
InterPro; IPR001799; -  
Pfam; PF00812; Ephrin; 1.  
PROSITE; PS01299; Ephrin; 1.  
Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
Signal; Phosphorylation.  
FT SIGNAL 1 24  
FT CHAIN 25 346  
FT DOMAIN 25 237  
FT TRANSMEM 238 258  
FT DOMAIN 259 346  
FT DOMAIN 344 346  
FT CARBOHYD 139 139  
SEQUENCE 346 AA; 38006 MW; 473DD2F1A5BF89DE CRC64;

Query Match 100.0%; Score 29; DB 1; Length 346;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
Db 131 DYYIT 135

RESULT 6

YOFA\_CAEEL STANDARD; PRT; 360 AA.  
ID YOFA\_CAEEL  
AC Q09337;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HYPOTHETICAL 39.7 KDA PROTEIN ZK1290.10 IN CHROMOSOME II PRECURSOR.  
GN ZK1290.10.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Taich A.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

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KW Hydrolase; CAMP.  
FT CONFLICT 94  
SQ SEQUENCE 369 AA; 42016 MW; 47B752477E99BA88 CRC64;

L -> F (IN REF. 1).  
94

Query Match 100.0%; Score 29; DB 1; Length 369;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5  
|||||  
Db 123 DYVIT 127

## RESULT 8

ID CIBA\_PAEPP STANDARD; PRT; 675 AA.  
AC P57091;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DE PARASPORAL CRYSTAL PROTEIN CRV188A (PARASPORAL DELTA-ENDOTOXIN  
DE CRXVIIIB(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (76 KDA CRYSTAL  
PROTEIN).  
GN CRY188A OR CRXVIIIB(A).  
OS Paenibacillus popilliae (Bacillus popilliae).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Paenibacillus.  
OX NCBI\_TaxID=78057;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BP3;  
RA Patel R., Yousten A.A., Rippere K.;  
RT "Detection of two new cry genes in Paenibacillus popilliae.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB  
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE  
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
CC SPORE germination AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
CC OF THE SPORE COAT (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC -----  
DR EMBL; AF169250; AAF89667.1;  
KW Toxin; Sporulation.  
FT DOMAIN 101 104 POLY-LEU.  
FT DOMAIN 199 204 POLY-LEU.  
SQ SEQUENCE 675 AA; 75848 MW; 823B588B4AE81DF5 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 675;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5  
|||||  
Db 469 DYVIT 473

## RESULT 9

ID CIBA\_PAEPP STANDARD; PRT; 695 AA.  
AC P57092;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE PARASPORAL CRYSTAL PROTEIN CRV18CA (PARASPORAL DELTA-ENDOTOXIN  
DE CRXVIIIC(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (78 KDA CRYSTAL  
DE PROTEIN).  
GN CRY18CA OR CRXVIIIC(A).  
OS Paenibacillus popilliae (Bacillus popilliae).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Paenibacillus.  
OX NCBI\_TaxID=78057;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 14706;  
RA Patel R., Yousten A.A., Rippere K.;  
RT "Detection of two new cry genes in Paenibacillus popilliae.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB  
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE  
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
CC SPORE germination AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
CC OF THE SPORE COAT (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC -----  
DR EMBL; AF169251; AAF89668.1;  
KW Toxin; Sporulation.  
SQ SEQUENCE 695 AA; 78259 MW; 406AC9154D75E070 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 695;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5  
|||||  
Db 485 DYVIT 489

## RESULT 10

ID CIBA\_PAEPP STANDARD; PRT; 706 AA.  
AC Q45358;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DE PARASPORAL CRYSTAL PROTEIN CRV18AA (PARASPORAL DELTA-ENDOTOXIN  
DE CRXVIIIA(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (79 KDA CRYSTAL  
DE PROTEIN).  
GN CRY18AA OR CRXVIIIA(A) OR CRVBP1.  
OS Paenibacillus popilliae (Bacillus popilliae).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Paenibacillus.  
OX NCBI\_TaxID=78057;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN=H1 / SUBSP. MELOLONTHAE;  
RX MEDLINE=97352693; PubMed=9209052;  
RA Zhang J., Hodgman T.C., Krieger L., Schnetter W., Schairer H.U.;  
RT "Cloning and analysis of the first cry gene from Bacillus popilliae.";  
RL J. Bacteriol. 179:4336-4341(1997).  
CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB  
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE  
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH. ACTIVE ON  
CC M. MELOLONTHA.  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
CC SPORE germination AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC

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CC      OF THE SPORE COAT (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X99049; CAA67506.1; -
CC      InterPro: IPR001178; -
CC      Pfam: PF00555; endotoxin; 1.
CC      Toxin; Sporulation.
CC      FT CONFLICT 670 670 T -> F (IN AA SEQUENCE).
CC      SEQUENCE 706 AA; 79034 MW; 9172B949BE499C1D CRC64;
CC
CC      Query Match 100.0%; Score 29; DB 1; Length 706;
CC      Best Local Similarity 100.0%; Pred. No. 60;
CC      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 1 DYYIT 5
CC      Db 506 DYYIT 510
CC
CC      RESULT 11
CC      YCB9_YEAST STANDARD; PRT; 1347 AA.
CC      ID YCB9_YEAST
CC      AC P25384;
CC      DT 01-MAY-1992 (Rel. 22, Created)
CC      DT 01-MAY-1992 (Rel. 22, Last sequence update)
CC      DT 01-OCT-2000 (Rel. 40, Last annotation update)
CC      DE TRANSPOSIN TY1-17 PROTEIN B.
CC      GN TY1B OR YCLO19W OR YCLO19W.
CC      OS Saccharomyces cerevisiae (Baker's yeast).
CC      OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC      CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CC      OX NCBI_TaxID=4932;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.
CC      RX MEDLINE=86205247; PubMed=3010239;
CC      RA Warrington J.R., Anwar R., Newlon C.S., Waring R.B., Davies R.W.,
CC      RA Indge K.J., Oliver S.G.;
CC      RT "A 'hot-spot' for Ty transposition on the left arm of yeast
CC      RT chromosome III."
CC      RL Nucleic Acids Res. 14:3475-3485(1986).
CC      RN [2]
CC      RP SEQUENCE FROM N.A.
CC      RX MEDLINE=86041864; PubMed=2997719;
CC      RA Warrington J.R., Waring R.B., Newlon C.S., Indge K.J., Oliver S.G.;
CC      RA "Nucleotide sequence characterization of Ty 1-17, a class II
CC      RT transposon from yeast."
CC      RL Nucleic Acids Res. 13:6679-6693(1985).
CC      RN [3]
CC      RP SEQUENCE FROM N.A.
CC      RA Oliver S.G., Anwar R., Brown A., Gent M.E., Indge K.J., James C.M.,
CC      RA Staveva L.I.;
CC      RA Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
CC      RL -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A11.
CC      -----
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CC      -----
CC      EMBL; X03840; CAA27458.1; -
CC      EMBL; X59720; E264443; -

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DR PIR; B23496; B23496.
DR PIR; S19345; S19345.
DR MEROPS; A11.003; -
DR SGD; S000524; YCLO19W.
DR KW Transposable element; Hypothetical protein; Hydrolase;
DR FT NP_BIND 1223 1230 ATP (POTENTIAL).
DR SQ SEQUENCE 1347 AA; 154069 MW; AD3660C5E7B282FF CRC64;
CC
CC      Query Match 100.0%; Score 29; DB 1; Length 1347;
CC      Best Local Similarity 100.0%; Pred. No. 1.2e+02;
CC      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 1 DYYIT 5
CC      Db 931 DYYIT 935
CC
CC      RESULT 12
CC      RS4_SULSO STANDARD; PRT; 181 AA.
CC      ID RS4_SULSO
CC      AC P95987;
CC      DT 01-NOV-1997 (Rel. 35, Created)
CC      DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC      DT 01-OCT-2000 (Rel. 40, Last annotation update)
CC      DE 30S RIBOSOMAL PROTEIN S4P.
CC      GN RPS4P OR RPS4 OR C04049.
CC      OS Sulfolobus solfataricus.
CC      OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
CC      OX NCBI_TaxID=2287;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=DSM 1617 / P2;
CC      RX MEDLINE=97055432; PubMed=8899719;
CC      RA Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
CC      RA Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
CC      RA Doolittle W.F., Regan M.A., Charlebois R.L.;
CC      RT "Organizational characteristics and information content of an
CC      RT archaeal genome: 156 kb of sequence from Sulfolobus solfataricus
CC      RT P2."
CC      RL Mol. Microbiol. 22:175-191(1996).
CC      CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA
CC      (BY SIMILARITY).
CC      CC -1- SIMILARITY: CONTAINS 1 S4 RNA-BINDING DOMAIN.
CC      CC -1- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
CC      -----
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CC      -----
CC      EMBL; Y08257; CAA69529.1; -
CC      DR InterPro: IPR001912; -
CC      DR InterPro: IPR002942; -
CC      DR Pfam: PF01479; S4; 1.
CC      DR PROSITE; PS00632; RIBOSOMAL_S4; 1.
CC      KW Ribosomal protein; rRNA-binding.
CC      FT DOMAIN 104 151 RNA-BINDING (S4 TYPE).
CC      SQ SEQUENCE 181 AA; 20748 MW; E48B4C85CD98C522 CRC64;
CC
CC      Query Match 96.6%; Score 28; DB 1; Length 181;
CC      Best Local Similarity 80.0%; Pred. No. 22;
CC      Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 1 DYYIT 5
CC      Db 154 DYYIT 158

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RESULT 13
Y438_METJA
ID Y438_METJA STANDARD; PRT; 381 AA.
AC Q57880;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0438.
GN MJ0438.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: BELONGS TO THE UPF0020 FAMILY.
CC
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CC -----
CC EMBL; U67495; AAB98426.1; -
CC TIGR; MJ0438; -
CC InterPro; IPR000241; -
CC Pfam; PF01170; UPF0020; 1.
CC PROSITE; PS01261; UPF0020; 1.
CC PROSITE; PS00092; NC_MTASE; UNKNOWN_1.
CC Hypothetical protein.
CC SEQUENCE 381 AA; 43738 MW; 9BB972D94479444D CRC64;
DR EMBL; U67495; AAB98426.1; -
DR TIGR; MJ0438; -
DR InterPro; IPR000241; -
DR InterPro; IPR002052; -
DR Pfam; PF01170; UPF0020; 1.
DR PROSITE; PS01261; UPF0020; 1.
DR PROSITE; PS00092; NC_MTASE; UNKNOWN_1.
DR Hypothetical protein.
DR SEQUENCE 381 AA; 43738 MW; 9BB972D94479444D CRC64;

Query Match 96.6%; Score 28; DB 1; Length 381;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 2 DYYVT 6

RESULT 14
Y299_METJA
ID Y299_METJA STANDARD; PRT; 389 AA.
AC Q57747;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0299.
GN MJ0299.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Berks M., Smith A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE BESTROPHIN FAMILY.
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CC -----
CC EMBL; Z30423; CAA83005.1; -
CC PIR; S42371; S42371.
CC Wormpep; T20G5.4; CE00481.
CC InterPro; IPR000615; -
CC Pfam; PF01062; Worm_family_8; 1.

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RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC
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CC -----
CC EMBL; U67485; AAB98286.1; -
CC TIGR; MJ0299; -
CC InterPro; IPR002803; -
CC Pfam; PF01950; DUF100; 1.
CC Hypothetical protein.
CC SEQUENCE 389 AA; 43245 MW; 1B8D890F931CE73 CRC64;

Query Match 96.6%; Score 28; DB 1; Length 389;
Best Local Similarity 80.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 49 DYYVT 53

RESULT 15
YNX4_CAEEL
ID YNX4_CAEEL STANDARD; PRT; 405 AA.
AC P34577;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOTHETICAL 47.7 KDA PROTEIN T20G5.4 IN CHROMOSOME III.
GN T20G5.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Berks M., Smith A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE BESTROPHIN FAMILY.
CC
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CC -----
CC EMBL; Z30423; CAA83005.1; -
CC PIR; S42371; S42371.
CC Wormpep; T20G5.4; CE00481.
CC InterPro; IPR000615; -
CC Pfam; PF01062; Worm_family_8; 1.

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us-09-724-406-4.rsp

Fri Jun 29 08:05:14 2001

KW Hypothetical protein.  
SQ SEQUENCE 405 AA; 47718 MW; 0374DEF2334B0380 CRC64;  
  
Query Match 96.6%; Score 28; DB 1; Length 405;  
Best Local Similarity 80.0%; Pred. No. 53;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYYIT 5  
| | | |  
Db 204 DYYIT 208

Search completed: June 28, 2001, 15:54:34  
Job time: 122 sec

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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 411.58 Seconds  
(without alignments)  
1.607 Million cell updates/sec

Title: us-09-724-406-4  
Perfect score: 29  
Sequence: 1 DYYIT 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	104	14 Q9J583	Q9J583 fowlpox vir
2	29	100.0	208	8 O21565	O21565 sigmodon oc
3	29	100.0	338	1 O58526	O58526 pyrococcus
4	29	100.0	358	1 O58692	O58692 pyrococcus
5	29	100.0	365	1 O27721	O27721 methanobact
6	29	100.0	472	14 Q9EML2	Q9EML2 amsacta moo
7	29	100.0	473	2 Q9PNC5	Q9PNC5 campylobact
8	29	100.0	527	2 Q9K806	Q9K806 bacillus ha
9	29	100.0	537	3 Q9P7H1	Q9P7H1 schizosacch
10	29	100.0	613	5 Q9VBJ6	Q9VBJ6 drosophila
11	29	100.0	736	1 Q29790	Q29790 archaeoglob
12	29	100.0	767	3 Q12357	Q12357 saccharomyc
13	29	100.0	1050	3 Q12494	Q12494 saccharomyc
14	29	100.0	1285	3 Q03934	Q03934 saccharomyc
15	29	100.0	1346	3 Q04345	Q04345 saccharomyc
16	29	100.0	1346	3 Q05679	Q05679 saccharomyc
17	29	100.0	1346	3 Q05369	Q05369 saccharomyc
18	29	100.0	1347	3 Q03494	Q03494 saccharomyc
19	29	100.0	1633	13 Q90941	Q90941 gallus gall

20	29	100.0	1770	3 Q12113	Q12113 saccharomyc
21	29	100.0	1770	3 Q12501	Q12501 saccharomyc
22	29	100.0	1770	3 Q12503	Q12503 saccharomyc
23	29	100.0	1770	3 Q07791	Q07791 saccharomyc
24	29	100.0	1770	3 Q12472	Q12472 saccharomyc
25	29	100.0	1770	3 Q12491	Q12491 saccharomyc
26	29	100.0	1771	3 P87006	P87006 saccharomyc
27	29	100.0	1810	3 Q12022	Q12022 saccharomyc
28	29	100.0	2338	5 Q94269	Q94269 caenorhabdi
29	29	100.0	3147	5 Q17464	Q17464 caenorhabdi
30	28	96.6	107	3 Q9HEB0	Q9HEB0 neurospora
31	28	96.6	184	11 Q9JK38	Q9JK38 mus musculu
32	28	96.6	301	8 Q36376	Q36376 helianthus
33	28	96.6	328	10 Q9XI00	Q9XI00 arabidopsis
34	28	96.6	353	14 Q9PY20	Q9PY20 xestia c-ni
35	28	96.6	367	2 Q9RZB4	Q9RZB4 deinococcus
36	28	96.6	429	2 Q56212	Q56212 streptococc
37	28	96.6	443	5 Q9VLC1	Q9VLC1 drosophila
38	28	96.6	536	10 Q23444	Q23444 arabidopsis
39	28	96.6	586	10 Q9SNT3	Q9SNT3 oryza sativ
40	28	96.6	594	5 Q9TZ18	Q9TZ18 caenorhabdi
41	28	96.6	699	2 Q9JWJ3	Q9JWJ3 neisseria m
42	28	96.6	755	5 Q45093	Q45093 caenorhabdi
43	28	96.6	791	1 Q9HM29	Q9HM29 thermoplasm
44	28	96.6	818	5 Q9TZ17	Q9TZ17 caenorhabdi
45	28	96.6	818	5 Q9TW90	Q9TW90 caenorhabdi

ALIGNMENTS

RESULT 1

Q9J583 ID Q9J583 PRELIMINARY; PRT; 104 AA.

AC Q9J583;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE ORF FPV147 HT MOTIF GENE FAMILY PROTEIN.

GN FPV147.

OS Fowlpox virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Avipoxvirus.

OX NCBI\_Taxid=10361;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-20193820; PubMed-10729156;

RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;

RT "The genome of fowlpox virus."

RL J. Virol. 74:3815-3831(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF198100; AAF44491.1;

SQ SEQUENCE 104 AA; 12685 MW; AB7468F313419D94 CRC64;

Query Match 100.0%; Score 29; DB 14; Length 104;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
| | | | |  
Db 44 DYYIT 48

RESULT 2

O21565 ID O21565 PRELIMINARY; PRT; 208 AA.

AC O21565;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)



Fri Jun 29 08:05:15 2001

us-09-724-406-4.rspt

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01-MAR-2001 (TREMBlrel. 16, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 4 (FRAGMENT).
ND4.
Sigmodon ochronathus (yellow-nosed cotton rat).
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
Sigmodon.
NCBI_TaxID=56214;
[1]
SEQUENCE FROM N.A.
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
CHAINS.
EMBL: U83822; AA87243.1; -.
InterPro: IPR000260; -.
DR InterPro: IPR001750; -.
DR Pfam: PF00361; oxidored_q1; 1.
DR Pfam: PF01059; oxidored_q5_N; 1.
DR Mitochondrion; NAD; Oxidoreductase.
KW NON_TER 208 208
FT SEQUENCE 208 AA; 23878 MW; 6668C7DD713A7E24 CRC64;
SQ

Query Match 100.0%; Score 29; DB 8; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXYIT 5
Db 47 DXYIT 51

RESULT 3
ID O58526 PRELIMINARY; PRT; 338 AA.
AC O58526;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HYPOTHETICAL 39.4 KDA PROTEIN PH0796.
GN PH0796.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
[1]
SEQUENCE FROM N.A.
STRAIN=OT3;
MEDLINE=98344137; PubMed=9679194;
RX Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
EMBL: AP000003; BAA29889.1; -.
KW Hypothetical protein.
DR SEQUENCE 338 AA; 39420 MW; CCE5BC8D0998EBDD CRC64;
SQ

Query Match 100.0%; Score 29; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXYIT 5
Db 85 DXYIT 89

RESULT 3
ID O58526 PRELIMINARY; PRT; 338 AA.
AC O58526;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HYPOTHETICAL 39.4 KDA PROTEIN PH0796.
GN PH0796.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
[1]
SEQUENCE FROM N.A.
STRAIN=OT3;
MEDLINE=98344137; PubMed=9679194;
RX Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
EMBL: AP000003; BAA29889.1; -.
KW Hypothetical protein.
DR SEQUENCE 338 AA; 39420 MW; CCE5BC8D0998EBDD CRC64;
SQ

Query Match 100.0%; Score 29; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXYIT 5
Db 85 DXYIT 89

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RESULT 4
ID O58692 PRELIMINARY; PRT; 358 AA.
AC O58692;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HYPOTHETICAL 42.1 KDA PROTEIN PH0973.
GN PH0973.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
[1]
SEQUENCE FROM N.A.
STRAIN=OT3;
MEDLINE=98344137; PubMed=9679194;
RX Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
EMBL: AP000004; BAA30070.1; -.
KW Hypothetical protein.
DR SEQUENCE 358 AA; 42097 MW; C68121A692B61460 CRC64;
SQ

Query Match 100.0%; Score 29; DB 1; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXYIT 5
Db 85 DXYIT 89

RESULT 5
ID O27721 PRELIMINARY; PRT; 365 AA.
AC O27721;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CONSERVED PROTEIN.
GN MTH1686.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OX NCBI_TaxID=145262;
[1]
SEQUENCE FROM N.A.
STRAIN=DELTA H;
MEDLINE=98037514; PubMed=9371463;
RX Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL EMBL: AE000926; AAB86158.1; -.
DR InterPro: IPR002803; -.
DR Pfam: PF01950; DUF100; 1.
DR ProDom: PD014260; -.
DR SEQUENCE 365 AA; 40286 MW; 5890E6CB9ECEFED24 CRC64;
SQ

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Query Match 100.0%; Score 29; DB 1; Length 365;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
Db 44 DYYIT 48

RESULT 6  
Q9EML2  
ID Q9EML2 PRELIMINARY; PRT; 472 AA.  
AC Q9EML2;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE AMV194.  
GN AMV194.  
OS Amsacta moorei entomopoxvirus (AnEPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
OC Entomopoxvirus B.  
OX NCBI\_TaxID=28321;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20396580; PubMed=10936094;  
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,  
Moyer R.W.;  
RA "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:  
Analysis and Comparison with Other Poxviruses.";  
RL Virology 274:120-139(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,  
Moyer R.W.;  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF250284; AAG02900.1; -  
SQ SEQUENCE 472 AA; 57680 MW; 532DF441C6009AFE CRC64;

Query Match 100.0%; Score 29; DB 14; Length 472;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
Db 200 DYYIT 204

RESULT 7  
Q9PNC5  
ID Q9PNC5 PRELIMINARY; PRT; 473 AA.  
AC Q9PNC5;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN.  
GN CJ1170C.  
OS Campylobacter jejuni.  
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
OC Campylobacter.  
OX NCBI\_TaxID=197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCTC 111168;  
RX MEDLINE=20150912; PubMed=10688204;  
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,  
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,  
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,  
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,  
Whitehead S., Barrell B.G.;  
RA "The genome sequence of the food-borne pathogen Campylobacter jejuni  
reveals hypervariable sequences.";  
RT Nature 403:665-668(2000).  
RL

DR EMBL: AL139077; CAB73424.1; -  
SQ SEQUENCE 473 AA; 53339 MW; AE6597673B356785 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 473;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
Db 170 DYYIT 174

RESULT 8  
Q9K806  
ID Q9K806 PRELIMINARY; PRT; 527 AA.  
AC Q9K806;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE ACETATE-COA LIGASE.  
GN BH3201.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=86565;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RA Takami H., Nakasone K., Takaki Y.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AP001513; BAB06920.1; -  
DR InterPro; IPR000873; -  
DR Pfam; PF00501; AMP-binding; 1.  
DR PRINTS; PR00154; AMPBINDING.  
DR PROSITE; PS00455; AMP\_BINDING; 1.  
KW Ligase.  
SQ SEQUENCE 527 AA; 59359 MW; 6E67E1DCFBA45B8D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 527;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5  
Db 396 DYYIT 400

RESULT 9  
Q9P7H1  
ID Q9P7H1 PRELIMINARY; PRT; 537 AA.  
AC Q9P7H1;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE PROBABLE PROTEIN-TYROSINE PHOSPHATASE CDC14 HOMOLOG.  
GN SPAC1782.09C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972H-;  
RA Wood V., Rajandream M.A., Barrell B.G., Brown S., Harris D.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL158056; CAB76271.1; -  
DR InterPro; IPR000242; -  
DR InterPro; IPR000340; -  
DR InterPro; IPR00387; -  
DR Pfam; PF00782; DSPC; 1.  
DR

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DR PRINTS: PR00700: PRTYPHPTASE.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 537 AA; 60253 MW; F5E50A8C0924C7EA CRC64;

Query Match 100.0%; Score 29; DB 3; Length 537;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXYIT 5
DB 141 DXYIT 145

RESULT 10
Q9VBJ6 PRELIMINARY; PRT; 613 AA.
AC Q9VBJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG14540 PROTEIN.
GN CG14540.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weisscock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
EMBL; AE003754; AAF56538.1; -

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DR FlyBase; FBgn0039398; CG14540.
SQ SEQUENCE 613 AA; 68546 MW; FE292B004E8E82FC CRC64;

Query Match 100.0%; Score 29; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXYIT 5
DB 76 DXYIT 80

RESULT 11
O29790 PRELIMINARY; PRT; 736 AA.
ID O29790;
AC O29790;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN AF0459.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AE001073; AAB90778.1; -
DR TIGR; AF0459; -
DR InterPro; IPR000731; -
DR InterPro; IPR001395; -
DR PROSITE; PS00063; ALDO-KETO-REDUCTASE_3; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 736 AA; 81942 MW; 1234B6CCA1995011 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 736;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXYIT 5
DB 552 DXYIT 556

RESULT 12
Q12357 PRELIMINARY; PRT; 767 AA.
ID Q12357;
AC Q12357;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE FRAME-SHIFT IN TYB PROBABLY NOT FUNCTIONAL.
GN TY1B.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

```

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rieger M., Mueller-Auer S., Brueckner M., Schaefer M.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z72824; CAA97037.1; -;  
 DR EMBL; Z72823; CAA97029.1; -;  
 DR InterPro; IPR000194; -;  
 DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; UNKNOWN\_1.  
 SQ SEQUENCE 767 AA; 87951 MW; 5F69264A58605BA5 CRC64;

Query Match 100.0%; Score 29; DB 3; Length 767;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYIT 5  
 |||||  
 Db 351 DYYIT 355

## RESULT 13

Q12494 PRELIMINARY; PRT; 1050 AA.  
 AC Q12494; P89899;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE CHROMOSOME IV READING FRAME ORF YDR017C.  
 GN KCS1.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Prydz H., Eide L.G.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96170769; PubMed=8601473;  
 RA Huang K.N., Symington L.S.;  
 RT "Suppressors of a Saccharomyces cerevisiae pkl1 mutation identify  
 RT alleles of the phosphatase gene PTC1 and of a novel gene encoding a  
 RT putative basic leucine zipper protein.";  
 RL Genetics 141:1275-1285(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Eide L.G., Sander C., Prydz H.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB972;  
 RA Dedman K., Brown D., Hamlyn N., Bowman S.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB572;  
 RA Barrell B., Rajandream M.A.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z74313; CAA98837.1; -;  
 DR EMBL; S81651; AAB36234.1; -;  
 DR EMBL; X95966; CAA65208.1; -;  
 DR EMBL; Z49770; CAA98942.1; -;

DR EMBL; Z74314; CAA98839.1; -;  
 DR SGD; S0002424; KCS1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1050 AA; 119549 MW; 9C7507CA5F4B0FC7 CRC64;

Query Match 100.0%; Score 29; DB 3; Length 1050;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYIT 5  
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 Db 821 DYYIT 825

## RESULT 14

Q03934 PRELIMINARY; PRT; 1285 AA.  
 AC Q03934;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE HYPOTHETICAL PROTEIN (FRAGMENT).  
 GN TYB OR YDR261W-B.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB972;  
 RA Murphy L., Harris D.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB972;  
 RA Barrell B., Rajandream M.A., Walsh S.V.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY. THE PROTEASE BELONGS TO THE PEPTIDASE FAMILY A1; ALSO  
 CC KNOWN AS THE EUKARYOTIC ASPARTYL PROTEASES FAMILY.  
 DR EMBL; Z68329; CAA92721.1; -;  
 DR SGD; S0007397; YDR261W-B.  
 DR InterPro; IPR000194; -;  
 DR InterPro; IPR001584; -;  
 DR InterPro; IPR001969; -;  
 DR Pfam; PF00665; rve; 1.  
 DR PROSITE; PS00141; ASP\_PROTEASE; 1.  
 DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; UNKNOWN\_1.  
 KW Aspartyl protease; Hydrolase; Hypothetical protein.  
 FT NON\_TER 1285 1285  
 SQ SEQUENCE 1285 AA; 146556 MW; 7E29F748600E52D2 CRC64;

Query Match 100.0%; Score 29; DB 3; Length 1285;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYIT 5  
 |||||  
 Db 930 DYYIT 934

## RESULT 15

Q04345 PRELIMINARY; PRT; 1346 AA.  
 AC Q04345;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE HYPOTHETICAL 153.9 KDA PROTEIN.  
 GN TYB, YDR673.05C OR YDR034C-D.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB972;  
 RA Connor R., Churcher C.M.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB972;  
 RA Barrell B., Rajandream M.A., Walsh S.V.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO THE PEPTIDASE FAMILY A1; ALSO  
 CC -2- KNOWN AS THE EUKARYOTIC ASPARTYL PROTEASES FAMILY.  
 DR EMBL; Z68196; CAA92372.1; -.  
 DR SGD; S0007345; YDR034C-D.  
 DR InterPro; IPR001194; -.  
 DR InterPro; IPR001584; -.  
 DR InterPro; IPR001969; -.  
 DR Pfam; PF00665; rve; 1.  
 DR PROSITE; PS00141; ASP\_PROTEASE; 1.  
 DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; UNKNOWN\_1.  
 KW Aspartyl protease; Hydrolase; Hypothetical protein.  
 SQ SEQUENCE 1346 AA; 153889 MW; 53B74F9E55C03ADF CRC64;

Query Match 100.0%; Score 29; DB 3; Length 1346;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYYIT 5  
 Db 930 DYYIT 934  
 |||||

Search completed: June 28, 2001, 16:08:18  
 Job time: 946 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:33 ; Search time 362.28 Seconds  
(without alignments)  
2.845 Million cell updates/sec

Title: US-09-724-406-6  
Perfect score: 101  
Sequence: 1 WYPGSGNTKYNKFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*
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- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*
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- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*
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- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	93	92.1	117	9 AAP80148	Biosynthetic antib
2	93	92.1	117	9 AAP80149	Biosynthetic antib
3	93	92.1	249	9 AAP80154	Biosynthetic antib
4	92	91.1	116	16 AAR79241	Heavy chain variab
5	91	90.1	138	21 AAY56873	MAB CT-M-01 heavy
6	91	90.1	139	14 AAR33950	CTMO1 VH. Synthet
7	91	90.1	139	14 AAR33953	gH1 variable domai
8	91	90.1	139	18 AAR29750	Anti-HMFg MAB CTMO
9	91	90.1	139	18 AAR29753	CDR-grafted humani
10	91	90.1	139	21 AAY56877	gH1 variable domai
11	91	90.1	382	18 AAW26651	Chimeric receptor

12	91	90.1	403	18 AAW26648	Chimeric receptor
13	91	90.1	473	18 AAW26646	Chimeric receptor
14	91	90.1	514	18 AAW26647	Chimeric receptor
15	91	90.1	514	18 AAW26649	Chimeric receptor
16	91	90.1	692	18 AAW26650	Chimeric receptor
17	90	89.1	17	21 AAY78323	Anti-zeta-chain an
18	90	89.1	123	21 AAY78325	Monoclonal antibod
19	90	89.1	469	14 AAR40384	Bispecific anti-ze
20	90	89.1	532	21 AAY78328	Activating polypep
21	88	87.1	555	22 AAB19871	Activating polypep
22	88	87.1	565	22 AAB19873	Activating polypep
23	88	87.1	577	22 AAB19872	Activating polypep
24	88	87.1	704	22 AAB19888	MLV envelope glyco
25	86	85.1	15	20 AAY40700	A3 derivative #21,
26	86	85.1	15	21 AAB30039	Scaffold protein S
27	84	83.2	112	22 AAB74000	Anti-chrysantheic
28	83	82.2	121	18 AAW07437	Anti-DNA antibody
29	82.5	81.7	122	9 AAP81365	Heavy chain variab
30	82	81.2	116	17 AAW03742	Murine monoclonal
31	82	81.2	132	22 AAB62049	Mouse monoclonal a
32	82	81.2	274	14 AAR44228	Chimeric Ig superf
33	80	79.2	122	18 AAW01577	Lead binding MAb 1
34	79	78.2	119	19 AAW49813	Amino acid sequenc
35	79	78.2	119	19 AAW49814	Amino acid sequenc
36	79	78.2	138	14 AAR32656	Variable region of
37	79	78.2	138	19 AAW49810	Humanised C4G1 Ig
38	79	78.2	222	14 AAR39267	Fragment of humani
39	79	78.2	222	19 AAW49817	Humanised C4G1 Ig
40	79	78.2	235	14 AAR39268	Humanised C4G1 Ig
41	79	78.2	235	19 AAW49818	Amino acid sequenc
42	79	78.2	449	14 AAR43339	Completely humanis
43	79	78.2	449	19 AAW49816	Amino acid sequenc
44	78	77.2	17	18 AAW27348	CDR2 from murine a
45	78	77.2	118	16 AAR79159	Human IgE receptor

ALIGNMENTS

RESULT 1  
AAP80148  
ID AAP80148 standard; peptide; 117 AA.  
XX  
AC AAP80148;  
XX  
DT 13-OCT-1990 (first entry)  
XX  
DE Biosynthetic antibody binding site.  
XX  
KW Biosynthetic antibody binding site; complementarity determining region;  
KW framework region.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Region 28..38  
FT /label=CDR1  
FT Region 46..66  
FT /label=CDR2  
FT Region 98..104  
FT /label=CDR3  
XX  
PN W08809344-A.  
XX  
PD 01-DEC-1988.  
XX  
PF Heavy chain variab  
XX MAB CT-M-01 heavy  
XX CTMO1 VH. Synthet  
XX 19-MAY-1988; 88WO-US01737.  
XX 21-MAY-1987; 87US-0052800.  
XX (CREA-) CREATIVE BIOMOLECULES INC.  
XX Huston JS, Oppermann H;  
PI

```

XX DR WPI; 1988-353928/49.
XX
XX PT Recombinant multifunctional protein - having antibody binding site and a
XX PT sequence for biological activity, ion sequestering or binding to a solid
XX PT support.
XX PS
XX PS Disclosure; : 5pp; English.
XX
XX CC The biosynthetic antibody binding site forms part of a single chain
XX CC multi-functional biosynthetic protein. The protein also comprises
XX CC an effector molecule with biological activity (eg an enzyme, toxin,
XX CC receptor binding site, growth factor, lymphokine, cytokine or
XX CC antimetabolite), an amino acid sequence capable of sequestering an
XX CC ion (eg calmodulin or metallothionein), or an amino acid sequence
XX CC capable of selective binding to a solid support (eg streptavidin or
XX CC a fragment of protein A). The BABS contains at least one domain
XX CC homologous to part/all of the variable region of an immunoglobulin
XX CC capable of binding the preselected antigenic determinant. The protein
XX CC can be used for specific binding assays, affinity purification, biocatalysts,
XX CC drug targeting, imaging and immunological treatment of oncogenic and
XX CC infectious diseases. It offers fewer cleavage sites to circulating
XX CC proteolytic enzymes, and has improved stability. It reaches target
XX CC tissues rapidly and is quickly cleared from the body. It also has
XX CC reduced immunogenicity and its design facilitates binding to other
XX CC moieties in drug targeting and imaging applications. The BABS
XX CC is a 26-10/g-loop hybrid - it comprises framework region from 26-10 VH
XX CC and the CDRs from glp-4 VH.
XX
XX SQ Sequence 117 AA;

Query Match 92.1%; Score 93; DB 9; Length 117;
Best Local Similarity 88.2%; Pred. No. 2.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WYPGSGNTKYNEKFKG 17
Db 50 wyppgngntkynenfkf 66
||||:||||||| |||

RESULT 2
AAP80149
ID AAP80149 standard; protein; 117 AA.
AC AAP80149;
XX
XX DT 13-OCT-1990 (first entry)
XX
XX DE Biosynthetic antibody binding site.
XX
XX KW Biosynthetic antibody binding site; complementarity determining region;
XX KW framework region.
XX
XX OS Mus musculus/Homo sapiens.
XX
XX FH Location/Qualifiers
XX FT Region 10..27
XX FT /label=newm1 framework region
XX FT Region 28..38
XX FT /label=CDR
XX FT Region 39..45
XX FT /label=newm2 framework region
XX FT Region 46..66
XX FT /label=CDR
XX FT Region 67..97
XX FT /label=newm3 framework region
XX FT Region 98..104
XX FT /label=CDR
XX FT Region 105..117
XX FT /label=newm4 framework region
XX
XX PN WO8809344-A.

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XX PD 01-DEC-1988.
XX
XX PF 19-MAY-1988; 88WO-US01737.
XX
XX PR 21-MAY-1987; 87US-0052800.
XX
XX PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX PI Huston JS, Oppermann H;
XX
XX WPI; 1988-353928/49.
XX
XX PT Recombinant multifunctional protein - having antibody binding site and
XX PT sequence for biological activity, ion sequestering or binding to a solid
XX PT support.
XX PS
XX PS Disclosure; : 5pp; English.
XX
XX CC The biosynthetic antibody binding site forms part of a single chain
XX CC multi-functional biosynthetic protein. The protein also comprises
XX CC an effector molecule with biological activity (eg an enzyme, toxin,
XX CC receptor binding site, growth factor, lymphokine, cytokine or
XX CC antimetabolite), an amino acid sequence capable of sequestering an
XX CC ion (eg calmodulin or metallothionein), or an amino acid sequence
XX CC capable of selective binding to a solid support (eg streptavidin or
XX CC a fragment of protein A). The BABS contains at least one domain
XX CC homologous to part/all of the variable region of an immunoglobulin
XX CC capable of binding the preselected antigenic determinant. The protein
XX CC can be used for specific binding assays, affinity purification, biocatalysts,
XX CC drug targeting, imaging and immunological treatment of oncogenic and
XX CC infectious diseases. It offers fewer cleavage sites to circulating
XX CC proteolytic enzymes, and has improved stability. It reaches target
XX CC tissues rapidly and is quickly cleared from the body. It also has
XX CC reduced immunogenicity and its design facilitates binding to other
XX CC moieties in drug targeting and imaging applications. The BABS
XX CC is a newm/g-loop hybrid - it comprises framework regions from human
XX CC myeloma antibody NEWM VH and the complementarity determining regions
XX CC from glp-4 VH, ie illustrates a 'humanised' binding site having a
XX CC human framework but an affinity for lysozyme similar to murine glp-4.
XX
XX SQ Sequence 117 AA;

Query Match 92.1%; Score 93; DB 9; Length 117;
Best Local Similarity 88.2%; Pred. No. 2.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WYPGSGNTKYNEKFKG 17
Db 50 wyppgngntkynenfkf 66
||||:||||||| |||

RESULT 3
AAP80154
ID AAP80154 standard; protein; 249 AA.
AC AAP80154;
XX
XX DT 01-JAN-1980 (first entry)
XX
XX DE Biosynthetic antibody binding site.
XX
XX KW Biosynthetic antibody binding site; framework region; assay; imaging;
XX KW multifunctional protein.
XX
XX PN WO8809344-A.
XX
XX PD 01-DEC-1988.
XX
XX PF 19-MAY-1988; 88WO-US01737.
XX
XX PR 21-MAY-1987; 87US-0052800.

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XX PA (CREA-) CREATIVE BIOMOLECULES INC.  
 XX PI Huston JS, Oppermann H;  
 XX DR WPI; 1988-353928/49.  
 XX DR N-PSDB; AAN80180.  
 XX  
 XX Recombinant multifunctional protein - having antibody binding site and a  
 PT sequence for biological activity, ion sequestering or binding to a  
 PT solid support.  
 XX PS  
 XX Disclosure; : 15pp; English.  
 XX  
 XX The biosynthetic antibody binding site forms part of a recombinant  
 CC multifunctional protein which also comprises an effector protein, an AA  
 CC acid sequence capable of sequestering an ion, or a sequence capable of  
 CC binding to a solid support. The BABS comprises the framework region from  
 CC murine anti-digoxin monoclonal antibody 26-10 heavy chain variable region  
 CC and the complementarity determining region from G-loop-4 heavy chain  
 CC variable region and has lysozyme specificity. The effector protein is an  
 CC enzyme, toxin, receptor, binding site, growth factor, cytokine  
 CC or antimetabolite. The sequence capable of sequestering an ion is  
 CC calmodulin or metallothionein. The sequence capable of binding to solid  
 CC support is streptavidin or a protein A fragment. The protein may be used  
 CC for, eg specific binding assays, affinity purification, biocatalysts, drug  
 CC targeting, imaging and immunological treatment of oncogenic etc.  
 CC diseases. The protein offers fewer cleavage sites to circulating  
 CC proteolytic enzymes and have improved stability. They reach target organs  
 CC rapidly and are cleared quickly from the body. They also have reduced  
 CC immunogenicity.  
 XX SQ Sequence 249 AA;

Query Match 92.1%; Score 93; DB 9; Length 249;  
 Best Local Similarity 88.2%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPCSGNTRYNEKFKG 17  
 |||||:||||| |||  
 Db 52 wlypgngntkynenfkf 68

RESULT 4  
 AAR79241  
 ID AAR79241 standard; Protein; 116 AA.

XX AC AAR79241;  
 XX DT 21-DEC-1995 (first entry)  
 XX DE Heavy chain variable region for monoclonal antibody 4A10.  
 XX KW Monoclonal antibody; heavy metal; mercury; variable region;  
 XX KW heavy chain.  
 XX OS Synthetic.  
 XX PN W09520607-A.  
 XX PD 03-AUG-1995.  
 XX PF 27-JAN-1995; 95WO-US01199.  
 XX PR 27-JAN-1994; 94US-0187407.  
 XX PA (BION-) BIONEERASKA INC.  
 XX PI Lopez O, Wagner FW, Wylie DE;  
 XX DR WPI; 1995-275415/36.  
 XX DR N-PSDB; AAR79498.

XX PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals  
 XX PS  
 XX Claim 13; Page 54; 106pp; English.  
 XX  
 XX Hybridoma antibodies have been produced with the spleen cells of  
 CC BALB/c mouse that had received multiple injections of mercuric ions  
 CC reacted with glutathione to produce a mercuric ion coordinate  
 CC covalent compound which was covalently bound to keyhole limpet  
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,  
 CC 5B6 and 3E8) were producing MABs that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed  
 CC by M-MLV reverse transcriptase. The primers used for cDNA synthesis  
 CC were complementary to the 5' end of the CH1 domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' end of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in AAQ97311-097518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used  
 CC for PCR amplification of that variable region, in conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer AAQ97518  
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in AAQ97498-097510 and the deduced AA sequences in AAR79241-R79250 &  
 CC AAR79970-R79971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here.  
 XX SQ Sequence 116 AA;

Query Match 91.1%; Score 92; DB 16; Length 116;  
 Best Local Similarity 88.2%; Pred. No. 3.3e-07;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPCSGNTRYNEKFKG 17  
 |||||:||||| |||  
 Db 50 wlypgdgstkynefkf 66

RESULT 5  
 AAY56873  
 ID AAY56873 standard; Protein; 138 AA.

XX AC AAY56873;  
 XX DT 14-APR-2000 (first entry)  
 XX DE MAB CT-M-01 heavy chain VH domain.  
 XX KW Cytotoxic; drug conjugate; humanized; monoclonal antibody; CT-M-01;  
 XX KW human milk fat globule; growth inhibition.  
 XX OS Homo sapiens.  
 XX PN US6015562-A.  
 XX PD 18-JAN-2000.  
 XX PF 16-FEB-1996; 96US-0603024.  
 XX PR 31-OCT-1994; 94US-0332025.  
 XX PR 22-SEP-1992; 92US-0948277.  
 XX PR 06-OCT-1993; 93US-0132725.  
 XX PA (AMCY ) AMERICAN CYANAMID CO.  
 XX PI Hamann PR, Hinman LM;  
 XX DR

CC peptides was isolated by PCR using the primer sequences given in  
CC AAQ38879-80. Examination of these amino acid sequences revealed  
CC considerable homology with other characterised immunoglobulin genes.  
CC The murine monoclonal antibody (MAB), CTMO1, was confirmed to be an  
CC IgG-kappa antibody. CTMO1 was used in the production of a humanised  
CC antibody for in vivo diagnosis and therapy of carcinomas of ovary,  
CC breast, uterus and lung.

XX

SQ Sequence 139 AA;

Query Match 90.1%; Score 91; DB 14; Length 139;  
Best Local Similarity 94.1%; Pred. No. 5.8e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1 WIYPGSGNTKNEKFKG 17  
II | ||||| |||||  
Db 69 widpgsgntkynefkfg 85

RESULT 7  
AAR33953  
ID AAR33953 standard; Protein; 139 AA.  
XX AAR33953;  
AC AC  
XX XX  
DT DT  
DE DE  
DE gH1 variable domain.  
XX XX  
KW Heavy; light; chain; variable; domain; carcinoma; monoclonal; HAM;  
KW Immunoglobulin; murine; antibody; MAB; ovary; humanised; diagnosis;  
KW therapy; breast; uterus; lung; CDR-grafted; gH1; CTMO1.  
XX XX  
OS Synthetic.  
XX XX  
FH Key Location/Qualifiers  
FT Region 45..54 /label= CDR1  
FT FT  
FT Region 69..85 /label= CDR2  
FT FT  
FT Region 118..128 /label= CDR3  
FT FT  
XX XX EP534742-A.  
XX XX  
XX 31-MAR-1993.  
XX XX  
XX 24-SEP-1992; 92EP-0308680.  
XX XX  
XX 26-SEP-1991; 91GB-0020467.  
XX XX  
PA (CLLT ) CELLTECH LTD.  
XX XX  
PI Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;  
PI Menendez AT, Owens RJ;  
XX XX  
XX WPI; 1993-102837/13.  
XX XX  
XX N-PSDB; AAQ38882-89.  
XX XX  
XX Anti-human milk fat globule humanised antibodies - useful as  
XX conjugate for in-vivo diagnosis and therapy of e.g. ovarian or  
XX breast cancer  
XX XX  
PS Disclosure; Page 27; 57pp; English.  
XX XX  
XX This sequence represents the CDR-grafted heavy chain, gH1. This  
XX protein is encoded by the DNA constructed using the oligonucleotides  
XX given in AAQ38882-89. This heavy chain was used in conjunction with a  
XX light chain (see also AAR33954) in the production of a humanised  
XX antibody molecule (HAM). At least one of the complementarity  
XX determining regions (CDR's) of the variable domain is derived from  
XX the mouse monoclonal antibody (MAB) CTMO1 and the remaining immuno-



CC (especially methylthio antitumour agents) and used for diagnosis or therapy of human carcinomas, e.g. of the ovary, breast, uterus CC and lung.

AA	Sequence	139 AA;
SQ		

Query Match 90.1%; Score 91; DB 18; Length 139;  
Best Local Similarity 94.1%; Pred. No. 5.8e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels

```

QY      1 WIYPGSGNTKYNEKFKG 17
      || |||||
Db     69 widpasantkynefkq 85

```

## RESULT

RESOL 3  
AAW29753  
ID AAW29753 standard: 139 AA

AA  
AC AAW29753:

14-JAN-1998 (first entry)

XX  
DE CDR-grafted humanised antibody heavy chain variable region αH1.

Humanised antibody; CDR-grafted antibody; chimeric antibody; CTMOI; KX  
complementarity determining region; human milk fat globule; HMF; KX  
monoclonal antibody; Mab; mouse; cancer; breast cancer; KX  
ovary carcinoma; lung cancer; uterus cancer; diagnosis; therapy. KX

Chimeric Homo sapiens.

OS	Chimeric mus musculus.
OS	Chimeric synthetic.
XX	.

Key	Location/Qual
-----	---------------

FT	Region	45..54	/label= CDR1
FT			

ET

$$\frac{F_T}{\text{label}}$$

FT  
CT  
/note  
comprehensively determining region 2  
from CTMO1<sup>n</sup>

```
FT region
FT :120
FT /label= CDR3
```

FTL from CTMO1"

FT	Misc-difference 2	/note= "murine residue"
FT		

```
FT MISC-difference 37 /note= "murine residue"
```

FT Misc-difference 71

FT /note= "murine residue"

FT.		/note=	"murine residue"
FT	Misc-difference	94	
FT		/note=	"murine residue"

ET	MISC	REFERENCE	103	/note= "murine residue"
ET				

FT	Misc-difference	104	"murine residue"
FT	Misc-difference	105	"murine residue"
FT	Misc-difference	107	"murine residue"
XX			
PN	EP781845-A2.		
XX			
XX	02-JUL-1997.		
XX			
XX	24-SEP-1992;	92EP-0308680.	
PF			

24-SEP-1992; 92EP-0308680.

XX



CC This protein comprises a chimeric receptor consisting of an scFv  
 CC engineered from anti-CD3 human antibody CTM01 linked to an  
 CC

•

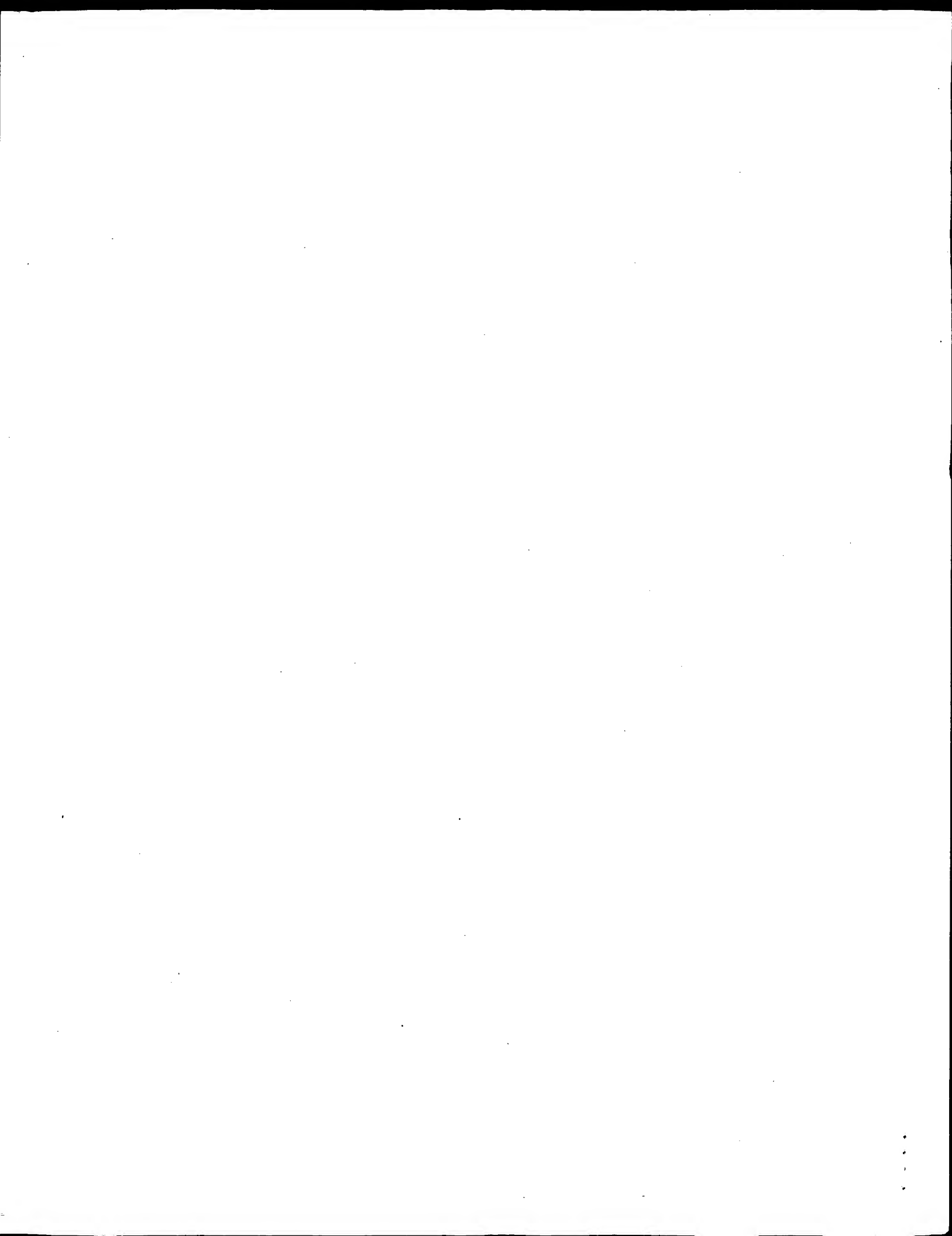
XX

44

PD 03-JUL-1997.  
XX  
PF 23-DEC-1996; 96WO-CB03209.  
XX  
PR 21-DEC-1995; 95GB-0026131.  
XX  
PA (CLLT ) CELLTech THERAPEUTICS LTD.  
XX  
PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;  
XX  
DR WPI; 1997-351052/32.  
DR N-PSDB; AAT90512.  
XX  
PT New DNA systems for activating cells - comprising DNA coding for a  
PT chimeric receptor comprising 2 or more different cytoplasmic  
PT signalling components.  
XX  
PS Disclosure; Fig 7; 90pp; English.  
XX  
CC This protein comprises a chimeric receptor consisting of an scfv  
CC engineered from anti-CD3 human antibody CTMO1 linked to an  
CC extracellular spacer comprising the human IgG1 hinge, CH2 and CH3,  
CC linked to transmembrane and intracellular regions of the human T  
CC cell receptor zeta chain. It can be expressed in host cells (e.g.  
CC Jurkat) using a chimeric receptor gene (see AAT90512) constructed  
CC from DNA cassettes encoding each receptor component. In a claimed  
CC cell activation process an effector cell is transformed with DNA  
CC encoding a chimeric receptor containing 2 or more different  
CC cytoplasmic signalling components. Also claimed is use of DNA  
CC encoding a recombinant chimeric receptor in a DNA delivery system.  
CC The DNA delivery systems can be used for the activation of cells to  
CC provide e.g. an increase in cell proliferation, expression of  
CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation  
CC of cytolytic activity, differentiation or other effector functions,  
CC antibody secretion, phagocytosis, tumour infiltration and/or  
CC increased adhesion. They can be used in the treatment of e.g.  
CC infectious disease, inflammatory disease, cancer, allergic/atopic  
CC disease, congenital disease, dermatologic disease, neurologic  
CC disease, transplant and metabolic/idiopathic disease (claimed).  
CC In particular, they can be used in the treatment of rheumatoid  
CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,  
CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple  
CC sclerosis, organ or tissue transplant rejection, graft-versus-host  
CC disease or diabetes (claimed).  
XX  
SQ Sequence 651 AA;

Query Match 90.1%; Score 91; DB 18; Length 651;  
Best Local Similarity 94.1%; Pred. No. 3.2e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WIYPGSGNTKYNEKFKG 17  
|||  
Db 209 widpgsgntkynefkfg 225

Search completed: June 28, 2001, 16:14:34  
Job time: 1322 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:13 ; Search time 138.34 Seconds  
(without alignments)  
2.475 Million cell updates/sec

Title: US-09-724-406-6  
Perfect score: 101  
Sequence: 1 WIYPGSGNTKYNEKFG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	91.1	116	2	US-08-888-366-2
2	91	90.1	138	3	US-08-603-024-2
3	91	90.1	139	1	US-08-253-877C-8
4	91	90.1	139	1	US-08-253-877C-19
5	91	90.1	139	2	US-08-452-164A-8
6	91	90.1	139	2	US-08-452-164A-19
7	91	90.1	139	3	US-08-603-024-18
8	83	82.2	98	3	US-08-881-037-64
9	80	79.2	122	4	US-08-767-128-4
10	79	78.2	119	1	US-08-458-516-10
11	79	78.2	119	1	US-08-458-516-11
12	79	78.2	138	1	US-08-458-516-7
13	79	78.2	222	1	US-08-458-516-22
14	79	78.2	235	1	US-08-458-516-23
15	79	78.2	449	1	US-08-458-516-13
16	76	75.2	355	3	US-08-875-811-57
17	75	74.3	113	3	US-08-881-037-18
18	75	74.3	121	3	US-08-881-037-65
19	74	73.3	140	1	US-08-476-275-6
20	74	73.3	249	2	US-08-797-689-18
21	72	71.3	17	1	US-08-318-970B-7
22	72	71.3	119	4	US-08-767-128-20
23	70	69.3	91	2	US-08-713-939A-70
24	70	69.3	91	2	US-08-713-939A-78
25	70	69.3	92	2	US-08-713-939A-79
26	70	69.3	92	2	US-08-713-939A-85
27	70	69.3	95	2	US-08-713-939A-86

28	70	69.3	101	2	US-08-713-939A-82
29	70	69.3	103	2	US-08-713-939A-84
30	70	69.3	108	2	US-08-713-939A-83
31	70	69.3	114	2	US-08-713-939A-68
32	70	69.3	114	2	US-08-713-939A-76
33	70	69.3	114	2	US-08-713-939A-77
34	70	69.3	119	4	US-08-767-128-10
35	69	68.3	17	4	US-07-987-264-2
36	69	68.3	117	2	US-08-822-028-2
37	69	68.3	117	4	US-08-479-285-2
38	69	68.3	118	2	US-08-428-257A-74
39	69	68.3	118	2	US-08-428-257A-78
40	69	68.3	118	4	US-09-199-149-2
41	69	68.3	118	4	US-09-199-149-5
42	69	68.3	118	4	US-07-987-264-14
43	69	68.3	118	4	US-07-987-264-60
44	69	68.3	119	2	US-08-561-521-10
45	69	68.3	119	2	US-08-561-521-12

## ALIGNMENTS

RESULT 1  
US-08-888-366-2  
; Sequence 2, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: US  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/888,366  
; FILING DATE: 03-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/187,407  
; FILING DATE: 27-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,542  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/493,299  
; FILING DATE: 14-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/324,392  
; FILING DATE: 14-MAR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.39USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-888-366-2

Query Match 91.1%; Score 92; DB 2; Length 116;  
Best Local Similarity 88.2%; Pred. No. 8.2e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIYPGSGNTKYNEKFKG 17  
|||||1:|||||||  
Db 50 WIYPGSGNTKYNEKFKG 66

## RESULT 2

US-08-603-024-2  
; Sequence 2, Application US/08603024  
; Patent No. 6015562  
; GENERAL INFORMATION:  
; APPLICANT: Hinman, Lois M.  
; APPLICANT: Menendez, Ana T.  
; APPLICANT: Hamann, Phillip R.  
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO  
; TITLE OF INVENTION: ANTITUMOR AGENTS  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Home Products Corporation  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07054

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/603,024  
FILING DATE: 16-FEB-1996

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 31,932-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-683-2158  
TELEFAX: 973-683-4117

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-603-024-2

Query Match 90.1%; Score 91; DB 3; Length 138;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIYPGSGNTKYNEKFKG 17  
|||||1:|||||||  
Db 69 WIDPGSGNTKYNEKFKG 85

## RESULT 3

US-08-253-877C-8  
; Sequence 8, Application US/08253877C  
; Patent No. 5773001  
; GENERAL INFORMATION:  
; APPLICANT: Hamann, Phillip R.  
; APPLICANT: Hinman, Lois  
; APPLICANT: Hollander, Irwin

; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tsou, Hwei-Ru  
; APPLICANT: Weiss, Martin J.  
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/253,877C  
FILING DATE: 03-JUN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-253-877C-8

Query Match 90.1%; Score 91; DB 1; Length 139;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIYPGSGNTKYNEKFKG 17  
|||||1:|||||||  
Db 69 WIDPGSGNTKYNEKFKG 85

## RESULT 4

US-08-253-877C-19  
; Sequence 19, Application US/08253877C  
; Patent No. 5773001  
; GENERAL INFORMATION:

; APPLICANT: Hamann, Phillip R.  
; APPLICANT: Hinman, Lois  
; APPLICANT: Hollander, Irwin  
; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tsou, Hwei-Ru  
; APPLICANT: Weiss, Martin J.

; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07470-8426

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/253,877C  
FILING DATE: 03-JUN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-3246  
TELEFAX: 201-683-3305  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-253-877C-19

Query Match 90.1%; Score 91; DB 1; Length 139;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNKFKG 17  
|| |||||  
DB 69 WIDPGSGNTKYNKFKG 85

## RESULT 5

US-08-452-164A-8  
Sequence 8, Application US/08452164A  
Patent No. 5877296

## GENERAL INFORMATION:

APPLICANT: Hamann, Philip R.  
APPLICANT: Hinman, Lois  
APPLICANT: Hollander, Irwin  
APPLICANT: Holcomb, Ryan  
APPLICANT: Hallett, William  
APPLICANT: Tsou, Hwei-Ru  
APPLICANT: Weiss, Martin J.  
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
Agents and Intermediates for Their Synthesis  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07054

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,164A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-4117  
TELEFAX: 201-683-2158  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-164A-8

Query Match 90.1%; Score 91; DB 2; Length 139;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNKFKG 17  
|| |||||  
DB 69 WIDPGSGNTKYNKFKG 85

## RESULT 6

US-08-452-164A-19  
Sequence 19, Application US/08452164A  
Patent No. 5877296

## GENERAL INFORMATION:

APPLICANT: Hamann, Philip R.  
APPLICANT: Hinman, Lois  
APPLICANT: Hollander, Irwin  
APPLICANT: Holcomb, Ryan  
APPLICANT: Hallett, William  
APPLICANT: Tsou, Hwei-Ru  
APPLICANT: Weiss, Martin J.  
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
Agents and Intermediates for Their Synthesis  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07054

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,164A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-164A-19

Query Match 90.1%; Score 91; DB 2; Length 139;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNKFKG 17  
|| |||||  
DB 69 WIDPGSGNTKYNKFKG 85

## RESULT 7

US-08-603-024-18  
; Sequence 18, Application US/08603024  
; Patent No. 6015562  
; GENERAL INFORMATION:  
; APPLICANT: Hinman, Lois M.  
; APPLICANT: Menendez, Ana T.  
; APPLICANT: Hamann, Philip R.  
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO  
; TITLE OF INVENTION: ANTITUMOR AGENTS  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Home Products Corporation  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/603,024  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,932-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 973-683-2158  
; TELEFAX: 973-683-4117  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 139 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-603-024-18

Query Match 90.1%; Score 91; DB 3; Length 139;  
Best Local Similarity 94.1%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 WIYPGSGNTKYNEKFG 17  
Db 69 WIDPGSGNTKYNEKFG 85

RESULT 8  
US-08-881-037-64  
; Sequence 64, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-64

Query Match 82.2%; Score 83; DB 3; Length 98;  
Best Local Similarity 93.8%; Pred. No. 1.5e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFG 17  
Db 51 IYPGSGNTKYNEKFG 66

RESULT 9  
US-08-767-128-4  
; Sequence 4, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GOEBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchants, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079west Center, 90 South Seventh St  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/767,128  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09258  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/541,373  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/462,798  
FILING DATE: 05-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.49USF1  
TELEPHONE: 612/371-5278  
TELEFAX: 612/332-9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-767-128-4

Query Match 79.2%; Score 80; DB 4; Length 122;  
Best Local Similarity 81.2%; Pred. No. 5.2e-05;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNEKFK 16  
| | | | |  
DB 50 WYPGSGSIKYNEKFK 65

RESULT 10  
US-08-458-516-10  
; Sequence 10, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal fragment  
US-08-458-516-10

Query Match 78.2%; Score 79; DB 1; Length 119;  
Best Local Similarity 87.5%; Pred. No. 7.1e-05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFKG 17  
| | | | |  
DB 51 IYPGSGGTNYNEKFKG 66

RESULT 11  
US-08-458-516-11  
; Sequence 11, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: N-terminal fragment  
; US-08-458-516-11

Query Match 78.2%; Score 79; DB 1; Length 119;  
Best Local Similarity 87.5%; Pred. No. 7.1e-05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFKG 17  
| | | | |  
DB 51 IYPGSGGTNYNEKFKG 66

RESULT 12  
US-08-458-516-7  
; Sequence 7, Application US/08458516

; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 138 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-458-516-7

Query Match 78.2%; Score 79; DB 1; Length 138;  
Best Local Similarity 87.5%; Pred. No. 8.3e-05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNKFKG 17  
||||| | |||||  
Db 70 IYPGSGGTNKNKFKG 85

RESULT 13  
US-08-458-516-22  
; Sequence 22, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 222 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-458-516-22

Query Match 78.2%; Score 79; DB 1; Length 222;  
Best Local Similarity 87.5%; Pred. No. 0.00014;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNKFKG 17  
||||| | |||||  
Db 51 IYPGSGGTNKNKFKG 66

RESULT 14  
US-08-458-516-23  
; Sequence 23, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid

Search completed: June 28, 2001, 16:01:13  
Job time: 521 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: June 28, 2001, 15:58:42 ; Search time 234.85 Seconds  
(without alignments)  
5.514 Million cell updates/sec

Title: US-09-724-406-6

Sequence: 1 WIYPGSGNTKYNEKFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: piri.\*  
2: piri2.\*  
3: piri3.\*  
4: piri4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	101	100.0	67	2 H28833	Ig kappa chain V r
2	101	100.0	107	2 PH0999	Ig heavy chain V r
3	101	100.0	109	2 PH0997	Ig heavy chain V r
4	101	100.0	111	2 PH0998	Ig heavy chain V r
5	101	100.0	246	2 S38950	Ig gamma chain - m
6	101	100.0	446	2 S40295	Ig gamma-2a chain
7	98	97.0	106	2 PH1002	Ig heavy chain V r
8	98	97.0	109	2 PH1001	Ig heavy chain V r
9	98	97.0	115	2 A54378	Ig heavy chain V r
10	92	91.1	104	2 S28466	Ig heavy chain V r
11	92	91.1	117	1 HVMSA1	Ig heavy chain V r
12	90	89.1	469	2 S37483	Ig gamma-2a chain
13	89	88.1	120	2 G28195	Ig heavy chain V r
14	89	88.1	138	2 S21810	Ig heavy chain V r
15	87	86.1	91	2 PH0242	Ig heavy chain V r
16	87	86.1	107	2 PH0240	Ig heavy chain V r
17	87	86.1	107	2 PH0243	Ig heavy chain V r
18	87	86.1	107	2 PH0241	Ig heavy chain V r
19	83	82.2	96	2 PH1165	Ig heavy chain V r
20	83	82.2	110	2 PH1000	Ig heavy chain V r
21	82	81.2	110	2 PH0244	Ig heavy chain V r
22	82	81.2	112	2 S26473	Ig heavy chain V r
23	82	81.2	112	2 PH0245	Ig heavy chain V r
24	82	81.2	120	2 F28195	Ig heavy chain V r
25	81	80.2	119	2 E30562	Ig heavy chain V r
26	79	78.2	112	2 PH0979	Ig heavy chain V r
27	77	76.2	115	2 PH0238	Ig heavy chain V r
28	75	74.3	94	2 G32513	Ig heavy chain V r
29	75	74.3	475	2 S01321	Ig gamma-2b chain

## ALIGNMENTS

### RESULT 1

H28833  
Ig kappa chain V region (HP22.202.16) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-May-1997  
C:Accession: H28833  
R:Corbet, S.; Hirn, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiff, C.  
J. Immunol. 141, 779-784, 1988  
A:Title: Allelic manipulation of the GAT idiotype cascade. Immunization of C57BL/6 mice with a monoclonal antibody against the GAT idiotype.  
A:Reference number: A92827; MUID:88285674  
A:Accession: H28833  
A:Molecule type: mRNA  
A:Residues: 1-67 <COR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 101; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 4.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
|||||  
Db 19 WIYPGSGNTKYNEKFKG 35

### RESULT 2

PH0999  
Ig heavy chain V region (clone 74-cl) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PH0999  
R:Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell development.  
A:Reference number: PH0971; MUID:92381444  
A:Accession: PH0999  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-107 <VIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMW>

Query Match 100.0%; Score 101; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 6.7e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
|||||

Db 49 WIYPGSGNTKYNEKFKG 65

RESULT 3

Ig heavy chain V region (clone 17s-c2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH0997

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0997

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-109 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 6.8e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 4

Ig heavy chain V region (clone 165.3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH0998

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0998

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 5

Ig gamma chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999

C:Accession: S38950

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha

A:Reference number: S38950; MUID:94128242

A:Accession: S38950

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-246 <KLE>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 246;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 6

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999

C:Accession: S40295

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

C:Genetics:

A:Map position: 12

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CH1>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F:360-427/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted

F:132/Disulfide bonds: interchain (to light chain) #status predicted

F:224,227,229/Disulfide bonds: interchain #status predicted

F:297/Binding site: carbohydrate (Asn) #status experimental

Query Match 100.0%; Score 101; DB 2; Length 446;

Best Local Similarity 100.0%; Pred. No. 2.9e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 7

Ig heavy chain V region (clone 165.45) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH1002

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1002

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

Db 49 WIYPGSGNTKYNEKFKG 65

RESULT 3

Ig heavy chain V region (clone 17s-c2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH0997

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0997

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-109 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 6.8e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 4

Ig heavy chain V region (clone 165.3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH0998

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0998

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 5

Ig gamma chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999

C:Accession: S38950

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha

A:Reference number: S38950; MUID:94128242

A:Accession: S38950

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-246 <KLE>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 246;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 6

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999

C:Accession: S40295

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

C:Genetics:

A:Map position: 12

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CH1>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F:360-427/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted

F:132/Disulfide bonds: interchain (to light chain) #status predicted

F:224,227,229/Disulfide bonds: interchain #status predicted

F:297/Binding site: carbohydrate (Asn) #status experimental

Query Match 100.0%; Score 101; DB 2; Length 446;

Best Local Similarity 100.0%; Pred. No. 2.9e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 7

Ig heavy chain V region (clone 165.45) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH1002

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1002

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology



C;Keywords: heterotetramer; immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 97.0%; Score 98; DB 2; Length 106;  
Best Local Similarity 94.1%; Pred. No. 2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
DB 49 WIYPGSGNTKYNDKFKG 65

## RESULT 8

PH1001  
Ig heavy chain V region (clone 111.68) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PH1001  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell  
A;Reference number: PH0971; MUID:92381444  
A;Accession: PH1001  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-109 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 97.0%; Score 98; DB 2; Length 109;  
Best Local Similarity 94.1%; Pred. No. 2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
DB 50 WIYPGSGNTKYNDKFKG 66

## RESULT 9

A54378  
Ig heavy chain V region anti-triplex DNA - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C;Accession: A54378  
R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.  
J. Biol. Chem. 269, 7019-7023, 1994  
A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence  
A;Reference number: A54378; MUID:94165109  
A;Accession: A54378  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-115 <AGA>  
A;Cross-references: GB:S68981; NID:g545744; PIDN:AB30095.1; PID:g545745  
A;Experimental source: spleen and myeloma cell line MOPC 315.43  
A;Note: sequence inconsistent with nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBIN:144172, NCBIIP:144173)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 97.0%; Score 98; DB 2; Length 115;  
Best Local Similarity 94.1%; Pred. No. 2.2e-08;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
DB 50 WIYPGSGNTKYNEKFKG 66

## RESULT 10

S26466  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S26466  
R;Kavaler, J.  
submitted to the EMBL Data Library, April 1991

A;Reference number: S26459  
A;Accession: S26466  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-104 <KAV>  
A;Cross-references: EMBL:X59116; NID:g51933; PIDN:CAA1842.1; PID:g51934  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:3-86/Domain: immunoglobulin homology <IMM>

Query Match 91.1%; Score 92; DB 2; Length 104;  
Best Local Similarity 88.2%; Pred. No. 1.7e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
DB 38 WIYPGSGNTKYNEKFKG 54

## RESULT 11

HVMSA1  
Ig heavy chain precursor V region (A1/A4) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 22-Jun-1999  
C;Accession: A02029  
R;Yancopoulos, G.D.; Alt, F.W.  
Cell 40, 271-281, 1985  
A;Title: Developmentally controlled and tissue-specific expression of unrearranged V-  
A;Reference number: A90860; MUID:85099340  
A;Accession: A02029  
A;Molecule type: DNA  
A;Residues: 1-117 <YAN>  
A;Cross-references: GB:M13787; NID:g196006; PIDN:AAA38499.1; PID:g466291  
A;Note: the sequence was determined from the germline gene  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <WAT>  
F:20-49/Region: framework 1  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:50-54/Region: complementarity-determining 1  
F:55-68/Region: framework 2  
F:69-85/Region: complementarity-determining 2  
F:86-117/Region: framework 3  
F:41-115/Disulfide bonds: #status predicted

Query Match 91.1%; Score 92; DB 1; Length 117;  
Best Local Similarity 88.2%; Pred. No. 2e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
DB 69 WIYPGSGNTKYNEKFKG 85

## RESULT 12

S37483  
Ig gamma-2a chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37483  
R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483  
A:Accession: S37483  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-469 <DUC>  
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 89.1%; Score 90; DB 2; Length 469;  
Best Local Similarity 88.2%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
||||| ||||||| |||  
DB 69 WIYPASGNTKYNEFKG 85

## RESULT 13

Ig heavy chain V region (anti-haloperidol antibody B) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 23-Jul-1999  
C:Accession: G28195  
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s  
A:Reference number: A28195; MUID:88153717  
A:Accession: G28195  
A:Molecule type: mRNA  
A:Residues: 1-120 <SHE>  
A:Cross-references: GB:M19772; NID:g195520; PIDN:AAA38340.1; PID:g195521  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 88.1%; Score 89; DB 2; Length 120;  
Best Local Similarity 88.2%; Pred. No. 6e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17  
||||| ||||||| |||  
DB 50 WIYPGNVNTKYNEKFKG 66

## RESULT 14

Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S21810  
R:Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.  
submitted to the EMBL Data Library, January 1991  
A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha  
A:Reference number: S21810  
A:Accession: S21810  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-138 <OST>  
A:Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164  
C:Genetics:  
A:introns: 15/3  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 88.1%; Score 89; DB 2; Length 138;  
Best Local Similarity 88.2%; Pred. No. 7e-07;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 WIYPGSGNTKYNEKFKG 17  
||||| ||||||| |||  
DB 69 WIYPGNVNTKYNEKFKG 85

## RESULT 15

Ig heavy chain V region (anti-DNA, S54VH) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
C:Accession: PL0242  
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein  
J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat  
A:Reference number: PL0231; MUID:90111618  
A:Accession: PL0242  
A:Molecule type: mRNA  
A:Residues: 1-91 <SHL>

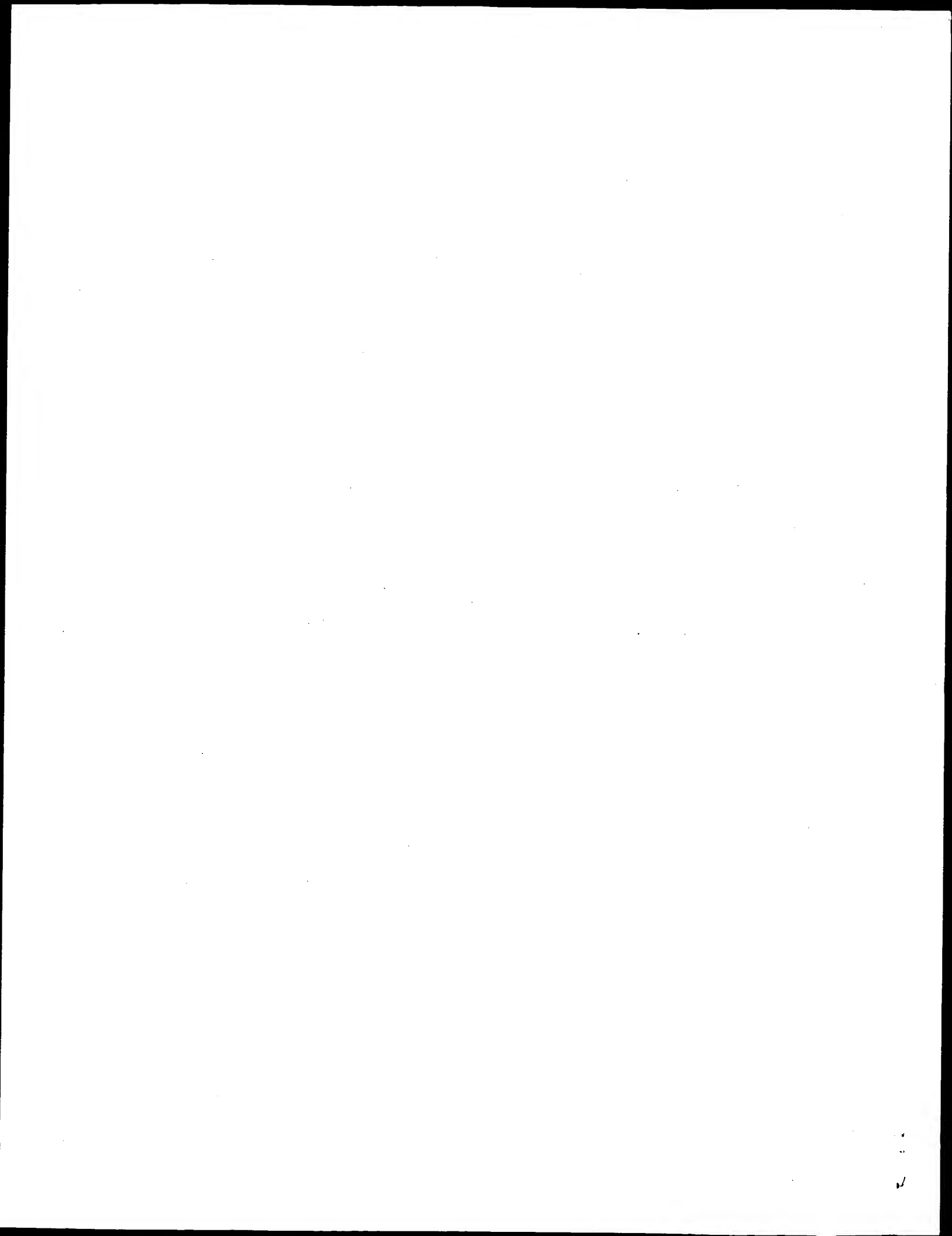
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-8/Region: framework 1  
F:9-13/Region: complementarity-determining 1  
F:14-27/Region: framework 2  
F:28-44/Region: complementarity-determining 2  
F:45-76/Region: framework 3  
F:77-87/Region: complementarity-determining 3  
F:88-91/Region: framework 4

Query Match 86.1%; Score 87; DB 2; Length 91;  
Best Local Similarity 93.8%; Pred. No. 9.4e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFK 16  
||| ||||||| |||  
DB 28 WIYSGSGNTKYNEKFK 43

Search completed: June 28, 2001, 15:58:42  
Job time: 370 sec





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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:34 ; Search time 105.36 Seconds  
(without alignments)  
5.527 Million cell updates/sec

Title: US-09-724-406-6

Perfect score: 101  
Sequence: 1 WIYPGSGNTRYNEKFKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	92	91.1	117	1 HV52_MOUSE	P06327 mus musculus
2	72	71.3	120	1 HV03_MOUSE	P01747 mus musculus
3	62	61.4	117	1 HV09_MOUSE	P01753 mus musculus
4	62	61.4	117	1 HV10_MOUSE	P01754 mus musculus
5	62	61.4	117	1 HV49_MOUSE	P06328 mus musculus
6	62	61.4	139	1 HV07_MOUSE	P01751 mus musculus
7	61	60.4	117	1 HV04_MOUSE	P01748 mus musculus
8	61	60.4	140	1 HV02_MOUSE	P01746 mus musculus
9	58	57.4	117	1 HV12_MOUSE	P01756 mus musculus
10	58	57.4	117	1 HV13_MOUSE	P01757 mus musculus
11	58	57.4	117	1 HV14_MOUSE	P01758 mus musculus
12	58	57.4	118	1 HV51_MOUSE	P06330 mus musculus
13	58	57.4	121	1 HV01_MOUSE	P01745 mus musculus
14	56	55.4	117	1 HV06_MOUSE	P01740 mus musculus
15	55	54.5	120	1 HV50_MOUSE	P01750 mus musculus
16	55	54.5	136	1 HV15_MOUSE	P06329 mus musculus
17	54	53.5	147	1 HV1C_HUMAN	P01759 mus musculus
18	53	52.5	117	1 HV05_MOUSE	P01744 homo sapien
19	50	49.5	138	1 HV48_MOUSE	P01749 mus musculus
20	49	48.5	117	1 HV1G_HUMAN	P03980 mus musculus
21	47	46.5	137	1 HV11_MOUSE	P23083 homo sapien
22	47	46.5	606	1 RP3A_MOUSE	P01755 mus musculus
23	47	46.5	684	1 RP3A_RAT	P47708 mus musculus
24	46.5	46.0	226	1 KAD3_BOVIN	P47709 rattus norv
25	46	45.5	117	1 HV1B_HUMAN	P08760 bos taurus
26	46	45.5	692	1 YK06_YEAST	P01743 homo sapien
27	45.5	45.0	819	1 EFG2_YEAST	P36062 saccharomyc
28	43.5	43.1	509	1 VP64_NPVOP	P39677 saccharomyc
29	43	42.6	566	1 HEMA_TAZIN	P13625 oryza pseu
30	43	42.6	596	1 NUOL_CAMJE	P26140 influenza a
31	42.5	42.1	116	1 HV61_MOUSE	Q9Pma7 campylobact
32	42.5	42.1	241	1 KADA_ORYSA	P18532 mus musculus
33	42.5	42.1	243	1 KADB_ORYSA	Q08479 oryza sativ
					Q08480 oryza sativ

34	42.5	42.1	246	1 KAD_ARATH	O82514 arabidopsis
35	42.5	42.1	509	1 VP67_NPVCF	P41717 choristoneu
36	42	41.6	183	1 RM32_YEAST	P25348 saccharomyc
37	42	41.6	376	1 ERG6_CANAL	O74198 candida alb
38	42	41.6	433	1 YBBY_ECOLI	P77328 escherichia
39	42	41.6	468	1 LIP2_RAT	P54318 rattus norv
40	42	41.6	496	1 GUN_PHAVU	P22503 phaseolus v
41	42	41.6	542	1 RESB_BACSU	P35161 bacillus su
42	42	41.6	566	1 HEMA_IJNZJ	P03455 influenza a
43	41	40.6	262	1 SPIB_HUMAN	O01892 homo sapien
44	41	40.6	304	1 STRL_STRGR	P29781 streptomyce
45	41	40.6	557	1 MAOX_ANAPL	P28227 anas platyr

## ALIGNMENTS

```

RESULT 1
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH58 A1/A4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VJ gene segments.";
RL Cell 40:271-28:(1985).
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CC -----
CC EMBL; M13787; AAA38499.1; -
CC PIR; A02029; HVMSA1.
CC InterPro; IPR003006; -
CC Pfam; PF00047; Ig_1.
CC Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19
FT DOMAIN 20 49 IG HEAVY CHAIN V REGION VH58 A1/A4.
FT DOMAIN 50 54 FRAMEWORK 1.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 65 85 FRAMEWORK 2.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING 2.
FT DISULFID 41 115 FRAMEWORK 3.
FT NON_TER 117 117 BY SIMILARITY.
SQ SEQUENCE 117 AA; 12971 MW; 880BC138856DFC9D CRC64;

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Query Match 91.1%; Score 92; DB 1; Length 117;  
Best Local Similarity 88.2%; Pred. No. 6.3e-08;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WIYPGSGNTRYNEKFKG 17

Db 69 WIYPGSGNTRYNEKFKG 85

RESULT 2  
HV03\_MOUSE

ID HV03\_MOUSE STANDARD; PRT; 120 AA.  
 AC P01747; 1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION 36-65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83131846; PubMed=6186498;  
 RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,  
 RA Marshak-Rothstein A.;  
 RT "The genetic basis of antibody production: the dominant anti-arsenate  
 RT idiotypic response of the strain A mouse."  
 RL Eur. J. Immunol. 12:1023-1032(1982).  
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE. THE AUTHORS  
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
 CC SEGMENT, JH2.  
 DR PIR: A02028; HVM5G7.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.  
 FT NON\_TER 120 120  
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;  
  
 Query Match 71.3%; Score 72; DB 1; Length 120;  
 Best Local Similarity 76.5%; Pred. No. 0.0001;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 1 WTYPGSGNTKYNEKFKG 17  
 Db : ||:| |||||  
 49 YINPGYTKYNEKFKG 65  
  
 RESULT 3  
 HV09\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01753; P11271;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the Npb family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region."  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
 DR PIR: B02034; HVM5L1.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 FRAMEWORK 3.  
 FT DOMAIN 86 117  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;  
  
 Query Match 61.4%; Score 62; DB 1; Length 117;  
 Best Local Similarity 80.0%; Pred. No. 0.004;  
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 2 IYPGSGNTKYNEKFK 16  
 Db : ||:| |||||  
 70 IDPNSGGTKYNEKFK 84  
  
 RESULT 5  
 HV49\_MOUSE

FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;  
  
 Query Match 61.4%; Score 62; DB 1; Length 117;  
 Best Local Similarity 80.0%; Pred. No. 0.004;  
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 2 IYPGSGNTKYNEKFK 16  
 Db : ||:| |||||  
 70 IDPNSGGTKYNEKFK 84

RESULT 4  
 HV10\_MOUSE STANDARD; PRT; 117 AA.  
 ID HV10\_MOUSE  
 AC P01754; P11270;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION 145 PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the Npb family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region."  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
 DR PIR: J00533; AAA38602.1; -.  
 DR PIR: C02034; HVMS45.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;  
  
 Query Match 61.4%; Score 62; DB 1; Length 117;  
 Best Local Similarity 80.0%; Pred. No. 0.004;  
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 2 IYPGSGNTKYNEKFK 16  
 Db : ||:| |||||  
 70 IDPNSGGTKYNEKFK 84  
  
 RESULT 5  
 HV49\_MOUSE



```

FT DOMAIN      86 117 FRAMEWORK 3.
FT DISULFID    41 115 BY SIMILARITY.
FT NON_TER     117 117
SQ SEQUENCE    117 AA; 12772 MW;  C530F829C906F69B CRC64;

Query Match      60.4%; Score 61; DB 1; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.0058;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFK 16
DB 70 INPGNGTYNEKFK 84

RESULT 8
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
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CC -----
DR EMBL; J00493; AAA38128.1;
DR PIR; A02028; HVM5G7
DR InterPro; IP003006;
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin v region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match      60.4%; Score 61; DB 1; Length 140;
Best Local Similarity 64.7%; Pred. No. 0.007;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFK 17
DB 69 YINPGNGYINYEKFK 85

RESULT 9
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -I- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR InterPro; IP003006;
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin v region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match      57.4%; Score 58; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.017;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFK 17
DB 51 INPNNGGTSYNQKFK 66

RESULT 10
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain v-region gene segments.";
RL Nature 283:35-40(1980).
CC -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR InterPro; IP003006;
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin v region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match      57.4%; Score 58; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.017;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFK 17
DB 51 INPNNGGTSYNQKFK 66

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QY	2	IYPGSGNTKYNEKFK	16
		:	
Db	51	INPSNGGTNYNEKFK	65





Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	69	68.3	110	11	Q9JL77	Q9JL77 mus musculus	
2	64	63.4	118	11	Q9Z1CA	Q9Z1CA mus musculus	
3	62	61.4	110	11	Q9JL83	Q9JL83 mus musculus	
4	58	57.4	109	11	Q9JL75	Q9JL75 mus musculus	
5	58	57.4	117	11	Q9QXF0	Q9QXF0 mus musculus	
6	58	57.4	117	11	Q9QXE9	Q9QXE9 mus musculus	
7	53	52.5	125	4	Q9JL95	Q9JL95 homo sapien	
8	53	52.5	498	2	Q9KQD9	Q9KQD9 bacillus ha	
9	52	51.5	119	4	Q9JL94	Q9JL94 homo sapien	
10	50.5	50.0	691	5	Q9VZE7	Q9VZE7 drosophila	
11	50	49.5	119	5	Q9GYZ2	Q9GYZ2 schistosoma	
12	49	48.5	172	5	Q9I799	Q9I799 caenorhabdi	
13	47	46.5	109	11	Q9JL85	Q9JL85 mus musculus	
14	47	46.5	143	10	Q9SMU5	Q9SMU5 arabidopsis	
15	46	45.5	89	11	Q9JL62	Q9JL62 mus musculus	
16	46	45.5	124	4	Q9JL92	Q9JL92 homo sapien	
17	46	45.5	305	11	Q9JHG9	Q9JHG9 mus musculus	
18	46	45.5	328	11	Q9JL65	Q9JL65 mus musculus	
19	45	44.6	218	2	Q9Z505	Q9Z505 streptomyce	

Q921C4	PRELIMINARY;	PRT;	118 AA.
ID Q921C4			
AC Q921C4;			





QY 1 WIYPGSGNTKYNEKFG 17  
 ||| | | | | | | | | |  
 Db 50 WINPNSWTNTYAKRFQ 66

RESULT 10  
 Q9VZE7 PRELIMINARY; PRT; 691 AA.  
 AC Q9VZE7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE CG1311 PROTEIN.  
 DE CG1311.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AF003480; AAF47876.1; -.  
 DR FlyBase; FBgn0035523; CG1311.  
 SQ SEQUENCE 691 AA; 76840 MW; 73309ED51C733208 CRC64;

Query Match 50.0%; Score 50.5; DB 5; Length 691;  
 Best Local Similarity 61.1%; Pred. No. 7.5;  
 Matches 11; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 3 YPGSGNT---KYNEKFG 17  
 ||| | | | | | | | | |  
 Db 59 YDSFGNTGKYNEKFG 76

RESULT 11  
 Q9GYZ2 PRELIMINARY; PRT; 119 AA.  
 AC Q9GYZ2;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;  
 OC Trematoda; Digenea; Strigeida; Schistosomatoidea; Schistosomatidae;  
 OX NCBI\_TaxID=6182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Song X.T., Feng Z.Q., Guan X.H.;  
 RT "Amplification, cloning and sequence analysis of the heavy chain  
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of  
 RT Schistosoma japonicum";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF282622; AAG01452.1; -.  
 FT NON\_TER 1 119  
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;  
 Query Match 49.5%; Score 50; DB 5; Length 119;  
 Best Local Similarity 56.2%; Pred. No. 1.2;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 WIYPGSGNTKYNEKPK 16  
 :| | | | | | | | | | | | | | | |  
 Db 50 YINPSRGYNTYKPK 65  
 RESULT 12  
 Q17999 PRELIMINARY; PRT; 172 AA.  
 AC Q17999;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DE R10E8.2 PROTEIN.  
 DE R10E8.2  
 GN R10E8.2  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ainscough R.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,  
 RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans."  
 RL Nature 368:32-38(1994).  
 DR EMBL; 281576; CAB04645.1; -.  
 DR InterPro; IPR002900; -.







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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:34 ; Search time 362.28 seconds  
(without alignments)  
1.339 Million cell updates/sec

Title: US-09-724-406-8  
Perfect score: 54  
Sequence: 1 YGNWYFAY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	92.6	140	AA12234	Mouse Mab 2G12 H c
2	50	92.6	141	AA12356	Heavy chain variab
3	44	81.5	369	AA12358	Anti-VHSV single c
4	43.5	80.6	116	AA12358	Heavy chain variab
5	43.5	80.6	116	AA12358	Heavy chain variab
6	43	79.6	122	AA12358	Lead binding Mab 1
7	43	79.6	129	AA12358	Heavy chain (VH) 9
8	42.5	78.7	248	AA12358	Human CD30 binding
9	42.5	78.7	273	AA12358	Single chain Fv an
10	41	75.9	119	AA12358	Lead binding Mab 1
11	37.5	69.4	116	AA12358	Anti-DNA antibody

12	37	68.5	17	AAW05038	Synthetic peptide
13	37	68.5	158	AA18127	Pinus radiata meth
14	37	68.5	210	AA18127	Pinus radiata meth
15	37	68.5	210	AA18127	Pinus radiata meth
16	36.5	67.6	234	AA122171	Drosophila Acp29AB
17	36.5	67.6	119	AAW49813	Amino acid sequenc
18	36.5	67.6	138	AAW49814	Amino acid sequenc
19	36.5	67.6	138	AAW49814	Amino acid sequenc
20	36.5	67.6	138	AAW49814	Amino acid sequenc
21	36.5	67.6	222	AAW49810	Mouse C4G1 Ig heav
22	36.5	67.6	222	AAW49810	Variable region of
23	36.5	67.6	222	AAW49810	Humanised C4G1 Ig
24	36.5	67.6	222	AAW49810	Fragment of human
25	36.5	67.6	222	AAW49810	Humanised C4G1 Ig
26	36.5	67.6	222	AAW49810	Amino acid sequenc
27	36	66.7	119	AAW49816	Completely humanis
28	36	66.7	119	AAW49816	Amino acid sequenc
29	36	66.7	119	AAW49816	Immunoglobulin hea
30	36	66.7	119	AAW49816	V region of H chai
31	36	66.7	270	AAW49816	Human HPD0V78 prot
32	36	66.7	270	AAW49816	TMV 30K movement p
33	36	66.7	272	AAW49816	Arabidopsis thalia
34	36	66.7	272	AAW49816	Arabidopsis thalia
35	36	66.7	470	AAW49816	Chimeric human-mou
36	36	66.7	470	AAW49816	Sequence of novel
37	36	66.7	573	AAW49816	Myeloidiophthora the
38	36	66.7	573	AAW49816	Myeloidiophthora the
39	36	66.7	573	AAW49816	Myeloidiophthora the
40	36	66.7	573	AAW49816	Myeloidiophthora the
41	36	66.7	573	AAW49816	Myeloidiophthora the
42	36	66.7	573	AAW49816	Myeloidiophthora the
43	36	66.7	573	AAW49816	Myeloidiophthora the
44	36	66.7	573	AAW49816	Myeloidiophthora the
45	36	66.7	616	AAW49816	Myeloidiophthora the

## ALIGNMENTS

RESULT 1	
AA12234	
ID AA12234 standard; Protein; 140 AA.	
XX	
AC AA12234;	
XX	
DT 19-AUG-1991 (first entry)	
XX	
DE Mouse Mab 2G12 H chain V region.	
XX	
KW HIV-1; chimera.	
XX	
OS Mus sp.	
XX	
PN WO9107494-A.	
XX	
PD 30-MAY-1991.	
XX	
PF 13-NOV-1990; 30WO-USO6627.	
XX	
PR 13-NOV-1989; 39US-0433703.	
XX	
PA (XOMA-) XOMA CORP.	
XX	
PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;	
XX	
DR WPI; 1991-178106/24.	
DR N-PSDB; AAQ12014.	
XX	
PT New chimeric mouse human antibodies - used in treatment, diagnosis	
XX	
PS Lead binding Mab 1	
XX	
PS Disclosure; Fig 7; 108pp; English.	

Fri Jun 29 08:05:21 2001

CC The mouse VH gene product may be used to produce chimeric mouse-  
 CC human Abs against HIV-1 comprising human Ig constant regions and  
 CC murine variable regions. These novel sequence are useful in  
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be  
 CC produced by a bacterial, yeast or mammalian expression system.  
 XX  
 SQ Sequence 140 AA;

Query Match 92.6%; Score 50; DB 12; Length 140;  
 Best Local Similarity 87.5%; Pred. No. 0.29;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGNWYFAY 8  
 DB 123 ygnwfay 130  
 III:IIII

RESULT 2  
 AAR12356  
 ID AAR12356 standard; Protein; 141 AA.  
 XX  
 AC AAR12356;  
 XX  
 DT 15-AUG-1991 (first entry)  
 XX  
 DE Heavy chain variable region of murine 2G12 immunoglobulin.  
 DE  
 KW Chimeric antibodies; immunocojugates; HIV; AIDS.  
 KW  
 XX Mus musculus.  
 OS  
 PN W09107493-A.  
 XX  
 PD 30-MAY-1991.  
 XX  
 PF 13-NOV-1990; 90WO-US06615.  
 XX  
 PR 13-NOV-1989; 89US-0433730.  
 XX  
 PA (XOMA-) XOMA CORP.  
 PA (GREG ) GREEN CROSS CORP.  
 XX  
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;  
 XX  
 DR WPI; 1991-178044/24.  
 DR N-PSDB; AAQ12058.  
 XX  
 PT New chimeric mouse-human antibodies - used to detect, kill and  
 PT remove HIV-1 antigen from sample  
 PT  
 PS Disclosure; fig 7; 107pp; English.  
 XX  
 CC This is the heavy-chain variable (V) region of a mouse monoclonal  
 CC antibody (MAB), 2G12, and is specific for an HIV-1 viral antigen.  
 CC It is used in the construction of a chimeric MAB comprising heavy  
 CC and light chains having murine V regions and human C regions.  
 CC The chimeric MABs are more effective than murine MAB 2G12 since  
 CC they have an increased compatibility in humans. The heavy and  
 CC light chain V-regions are joined by manipulating their respective  
 CC joining (J) regions, to generate restriction enzyme recognition  
 CC sites. The chimeric MABs can be used as immunocojugates, in  
 CC association with e.g. toxins for HIV treatment. They can also be  
 CC used in diagnosis of HIV.  
 CC See also AAQ12056-57 and AAQ12059-63.  
 SQ Sequence 141 AA;

Query Match 92.6%; Score 50; DB 12; Length 141;  
 Best Local Similarity 87.5%; Pred. No. 0.29;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGNWYFAY 8

DB 123 ygnwfay 130  
 III:IIII

RESULT 3  
 AAB73388  
 ID AAB73388 standard; Protein; 369 AA.  
 XX  
 AC AAB73388;  
 XX  
 DT 05-JUN-2001 (first entry)  
 XX  
 DE Anti-VHSV single chain antibody BUI.  
 DE  
 XX Anti-VHSV; single chain antibody BUI; SCAB; scFv;  
 KW monoclonal antibody 3F1H10; variable region; antiviral; anti-allergy;  
 KW human kappa light chain constant domain; vaccine; gene therapy;  
 KW rainbow trout TGF-beta signal peptide; transforming growth factor beta;  
 KW genetic prophylaxis.  
 XX  
 OS Chimeric - Oncorhynchus mykiss.  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 OS Synthetic.  
 XX  
 PN W0200121800-A1.  
 XX  
 PD 29-MAR-2001.  
 XX  
 PF 20-SEP-2000; 2000WO-GB03605.  
 XX  
 PR 20-SEP-1999; 99DK-0001329.  
 XX  
 PA (UVAB-) UNIV ABERDEEN.  
 PA (STAT-) STATENS VETERINAERE SERUMLABORATORIUM.  
 XX  
 PI Secombes CJ, Cunningham C, Lorenzen N;  
 XX  
 DR WPI; 2001-257991/26.  
 DR N-PSDB; AAF73388.  
 XX  
 PT New non-infectious nucleic acid construct encoding recombinant antibody  
 PT molecule, useful for conferring protective immunity to infectious  
 PT diseases, preventing allergic reactions or reactions caused by toxins  
 PT in animals -  
 XX  
 PS Example; Page -: 29pp; English.  
 XX  
 CC The invention relates to a non-infectious nucleic acid construct  
 CC encoding a recombinant (e.g., single chain) antibody molecule. The  
 CC nucleic acid construct is adapted for in vivo establishment of protective  
 CC immunity to an infectious disease in an animal, or is formulated for in  
 CC vivo prevention of an allergic reaction to an allergen or a reaction  
 CC caused by the presence of a toxic substance in an animal. Constructs of  
 CC the invention are thus useful for treating infectious disease caused by  
 CC viral haemorrhagic septicaemia virus (VHSV) (fish), infectious  
 CC haematopoietic necrosis virus (fish), bovine viral diarrhoea virus,  
 CC pseudorabies virus (pigs), plasmocytosis virus (mink), feline leukaemia  
 CC virus, human immunodeficiency virus, and hepatitis A virus (human).  
 CC Genetic prophylaxis methods using such constructs are useful for the  
 CC transient protection of individuals against exposure to pathogens or  
 CC toxins where no efficient vaccines are available, for inducing the  
 CC synthesis of antibodies of a desired specificity for use in  
 CC immunocompromised individuals, and for protecting an individual against  
 CC an allergic reaction. In contrast to DNA vaccines, including anti-  
 CC idotype vaccines, administration of plasmid-borne genes do not involve  
 CC specific activation of the immune system in the individual. Prophylaxis  
 CC against infectious diseases takes place without any side effects such as  
 CC the transfer of infectious diseases or induction of hypersensitivity  
 CC following repeated administration. The single chain antibodies will be  
 CC systemically distributed by the body fluids and protect the individual  
 CC if infection with the pathogen occurs. The present sequence represents a  
 CC portion of a construct of the invention which encodes a single chain

CC antibody, BUI. BUI is reactive to the fish pathogenic rhabdovirus, VHSV.  
 CC BUI is derived from the variable regions of the VHSV-reactive murine  
 CC monoclonal antibody 3FH10, and also contains the rainbow trout  
 CC transforming growth factor beta (TGF-beta) signal peptide at the N-  
 CC terminus (to ensure secretion of the single chain antibody) and the  
 CC human kappa light chain constant domain (used as a tag to facilitate  
 CC detection) at the C-terminus.  
 CC Note: The present sequence is not shown in the specification, but has  
 CC been decoded from the corresponding nucleic acid sequence (AAF76338).  
 XX  
 SQ Sequence 369 AA;

Query Match 81.5%; Score 44; DB 22; Length 369;  
 Best Local Similarity 87.5%; Pred. No. 7.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8  
 Db 123 ygndwfay 130  
 ||| ||||

RESULT 4  
 AAR79245  
 ID AAR79245 standard; Protein: 116 AA.  
 XX  
 AC AAR79245;

XX 21-DEC-1995 (first entry)

XX Heavy chain variable region for monoclonal antibody 2D5.  
 XX Monoclonal antibody; heavy metal; mercury; variable region;  
 KW heavy chain.  
 XX  
 OS Synthetic.

XX W09520607-A.

XX 03-AUG-1995.

XX 27-JAN-1995; 95WO-US01199.

XX 27-JAN-1994; 94US-0187407.

XX (BION-) BIONEBRASKA INC.

XX Lopez O, Wagner FW, Wylie DE;

XX WPI: 1995-275415/36.

XX N-PSDB; AAQ97502.

PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals

PS Claim 13; Page 59-60; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of  
 CC BALB/c mouse that had received multiple injections of mercuric ions  
 CC reacted with glutathione to produce a mercuric ion coordinate  
 CC covalent compound which was covalently bound to keyhole limpet  
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 2D5, 2D5,  
 CC 5B6 and 3B8) were producing MABs that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed  
 CC by MuLV reverse transcriptase. The primers used for cDNA synthesis  
 CC were complementary to the 5' end of the CHI domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' and of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in AAQ97511-097518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used

CC for PCR amplification of that variable region, in conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer AAQ97518  
 CC was used to amplify the MAB 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in AAQ97498-097510 and the deduced AA sequences in AAR79241-R79250 &  
 CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here.

XX SQ Sequence 116 AA;

Query Match 80.6%; Score 43.5; DB 16; Length 116;  
 Best Local Similarity 88.9%; Pred. No. 2.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 YGNYWFAY 8  
 Db 97 ygnywfay 105  
 |||| ||||

RESULT 5

AAR79246

ID AAR79246 standard; Protein: 116 AA.

XX AAR79246;

XX 21-DEC-1995 (first entry)

XX Heavy chain variable region for monoclonal antibody 5B6.

XX Monoclonal antibody; heavy metal; mercury; variable region;  
 KW heavy chain.

XX Synthetic.

XX W09520607-A.

XX 03-AUG-1995.

XX 27-JAN-1995; 95WO-US01199.

XX 27-JAN-1994; 94US-0187407.

XX (BION-) BIONEBRASKA INC.

XX Lopez O, Wagner FW, Wylie DE;

XX WPI: 1995-275415/36.

XX N-PSDB; AAQ97503.

PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals

PS Claim 13; Page 61; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of  
 CC BALB/c mouse that had received multiple injections of mercuric ions  
 CC reacted with glutathione to produce a mercuric ion coordinate  
 CC covalent compound which was covalently bound to keyhole limpet  
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 2D5, 2D5,  
 CC 5B6 and 3B8) were producing MABs that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed  
 CC by MuLV reverse transcriptase. The primers used for cDNA synthesis  
 CC were complementary to the 5' end of the CHI domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' and of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in AAQ97511-097518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used

CC for PCR amplification of that variable region, in conjunction with  
CC an appropriate V-region primer. In addition, the VH primer AAQ97518  
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences  
CC of the PCR amplified nucleotides were determined. These are given  
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &  
CC AAR79970-R79971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC sequence listings. The descriptions in the sequence listings are  
CC used here.

XX SQ Sequence 116 AA;

Query Match 80.6%; Score 43.5; DB 16; Length 116;  
Best Local Similarity 88.9%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 YGNY-WFAY 8  
|||||  
Db 97 ygnvewfay 105

RESULT 6  
AAW01577  
ID AAW01577 standard; Protein; 122 AA.  
XX AC AAW01577;  
XX DT 22-AUG-1997 (first entry)  
XX DE Lead binding MAB 1254 heavy chain variable region.  
XX KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;  
XX KW pharmaceutical; health care; skin treatment; pesticide; herbicide;  
XX KW heavy metal.  
XX OS Mus musculus.  
XX PN WO9639518-A1.  
XX PD 12-DEC-1996.  
XX PF 05-JUN-1996; 96WO-US09258.  
XX PR 10-OCT-1995; 95US-0541373.  
XX PR 05-JUN-1995; 95US-0462796.  
XX PA (BION-) BIONEERASKA INC.  
XX PI Lopez O, Murray PJ, Wylie DE;  
XX DR WPI; 1997-043140/04.  
XX DR N-PSDB; AAT58251.  
XX PT DNA encoding heavy metal binding polypeptide sequences - used for  
XX PT detecting, removing, adding or neutralising heavy metals, such as  
XX PT lead cations  
XX PS Claim 12; Page 58; 125pp; English.

The present sequence represents the heavy chain variable region for  
CC monoclonal antibody (Mab) 1254, which immunoreacts with a lead cation.  
CC The sequence was derived from RNA isolated from mouse hybridoma cells.  
CC The protein can be used for binding heavy metals, such as lead cations.  
CC It can be used for detecting, removing, adding or neutralising the  
CC heavy metals in biological and inanimate systems. It can be used in  
CC e.g. aqueous liquid systems, in biological or environmental systems or  
CC in such compositions as perfumes, cosmetics, pharmaceuticals, health  
CC care products, skin treatment products, pesticides, herbicides,  
CC solvents used in the production of semi-conductor and integrated  
CC circuit components and production materials for electronic components.  
CC The products can provide for applications involving minute amounts of  
CC specific heavy metals.

XX SQ Sequence 122 AA;

Query Match 79.6%; Score 43; DB 18; Length 122;  
Best Local Similarity 80.0%; Pred. No. 3.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 YGNY-WFAY 8  
|||||  
Db 102 ygnvawfay 111

RESULT 7  
AAV43866  
ID AAV43866 standard; Peptide; 129 AA.  
XX AC AAV43866;  
XX DT 11-FEB-2000 (first entry)  
XX DE Heavy chain (VH) gene sequence of Bacillus anthracis antibody 7-1.  
XX XX Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus;  
XX KW VH gene usage; anthrax.  
XX OS Mus sp.  
XX PN WO9955842-A1.  
XX PD 04-NOV-1999.  
XX PF 27-APR-1999; 99WO-US09122.  
XX PR 29-APR-1998; 98US-0069628.  
XX PA (UABR-) UAB RES FOUND.  
XX PI Kearney JF;  
XX DR WPI; 2000-013435/01.  
XX PT Monoclonal antibody specific for Bacillus spores, used to detect  
XX PT anthrax -  
XX PS Example 13; Page 53-54; 64pp; English.  
XX CC AAV43862-75 represent the amino acid sequences of the heavy chain  
CC (VH) gene sequences from antibodies against Bacillus anthracis  
CC spores. The antibodies are produced by different hybridomas. The  
CC specification describes monoclonal antibodies (especially IgG  
CC antibodies) which are highly specific and can discriminate between the  
CC spores of the Bacillus family. The antibodies are produced by exposing  
CC mice to Bacillus spores. The humoral immune response to Bacillus spore  
CC shows a conservation of VH gene usage which is distinct for each spore.  
CC Peptide fragments derived from the antibodies are also capable of  
CC binding spores. The monoclonal antibody, and peptide fragments of it, can  
CC be used to detect Bacillus spores in a field sample. It is particularly  
CC uses for detecting anthrax in a field sample.

XX SQ Sequence 129 AA;

Query Match 79.6%; Score 43; DB 21; Length 129;  
Best Local Similarity 80.0%; Pred. No. 3.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 YGNY-WFAY 8  
|||||  
Db 77 ygnvpawfay 86

RESULT 8

AAW58826  
 ID AAW58826 standard; Protein; 248 AA.  
 AC AAW58826;  
 XX  
 DT 18-AUG-1998 (first entry)  
 XX  
 DE Human CD30 binding protein.  
 XX  
 KW CD30 binding protein; human; suppressor; proliferation; metastasis;  
 KW tumour formation; CD30 antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE19640733-A1.  
 XX  
 PD 09-APR-1998.  
 XX  
 PF 02-OCT-1996; 96DE-1040733.  
 XX  
 PR 02-OCT-1996; 96DE-1040733.  
 XX  
 PA (ABKE/) ABKEN H.  
 XX  
 DR WPI; 1998-218120/20.  
 DR N-PSDB; AAV11399.  
 XX  
 XX Polypeptide than binds to CD30 without cell activation - for  
 PT inhibiting proliferation and metastasis of tumour cells, etc.  
 PT  
 PS Claim 3; Page 7-8; 8pp; German.  
 XX  
 CC This sequence represents a human CD30 binding protein which can be  
 CC used in a method for suppressing unchecked proliferation, tumour  
 CC formation and metastasis of cells expressing the CD30 antigen. This  
 CC protein specifically binds to CD30 without inducing cell activation by  
 CC CD30. The protein can also be used for probing, binding or enriching  
 CC CD30-expressing cells in vivo or in body fluids, cell suspensions or  
 CC tissues in vitro. A substance coupled to the protein accumulates in the  
 CC vicinity of CD30-expressing cells in vivo or in vitro.  
 XX  
 SQ Sequence 248 AA;

Query Match 78.7%; Score 42.5; DB 19; Length 248;  
 Best Local Similarity 72.7%; Pred. No. 8.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 1 YGNY---WFAV 8  
 DB 104 YGNYEYTWFAV 114

RESULT 9  
 AAB70763  
 ID AAB70763 standard; Protein; 273 AA.  
 AC AAB70763;  
 XX  
 DT 18-MAY-2001 (first entry)  
 XX  
 DE Single chain Fv antibody construct anti-CD30 VL domain protein.  
 XX  
 KW Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;  
 KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;  
 KW tumor cell; natural killer cell activation; Hodgkin's disease;  
 KW Reed-Sternberg disease.  
 XX  
 OS Synthetic.  
 XX  
 PN DE19937264-A1.  
 XX  
 PD 15-FEB-2001.

XX 06-AUG-1999; 99DE-1037264.  
 PF  
 XX 06-AUG-1999; 99DE-1037264.  
 PR  
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 PA  
 XX Arndt M, Little M, Kiprianov S, Krauss J, Pfreundschuh M;  
 PI WPI; 2001-184000/19.  
 DR  
 XX New Fv-antibody construct, useful for treating Hodgkin and  
 PT Reed-Sternberg diseases, has binding sites for CD16 receptor and CD30  
 PT surface protein  
 PT  
 XX Disclosure; Page 11; 18pp; German.  
 PS  
 XX This invention describes a novel Fv-antibody construct (I) having binding  
 CC sites for a CD16 receptor and a CD30 surface protein. The invention also  
 CC describes (1) expression vector encoding (I); (2) transformants  
 CC containing the vector of (1); (3) preparation of (I) by culturing cells  
 CC of (2); and (4) kit comprising (I) and/or the vector of (1), and  
 CC auxiliaries such as buffers, solvents, carriers, controls and labels, or  
 CC their replacements. The products of the invention have cytostatic  
 CC activity. (I) causes lysis of CD30+, specifically tumor, cells. It  
 CC activates natural killer cells, through the CD16 receptor, and directs  
 CC them to CD30-expressing cells. (I) are used to treat diseases in which  
 CC CD30+ cells are implicated, particularly tumors and specifically Hodgkin  
 CC or Reed-Sternberg diseases. (I) have a stronger lytic action than known  
 CC bispecific antibodies, can be produced on a large scale with high purity,  
 CC and contain no components that can induce unwanted immune responses.  
 XX  
 SQ Sequence 273 AA;

Query Match 78.7%; Score 42.5; DB 22; Length 273;  
 Best Local Similarity 72.7%; Pred. No. 9.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 1 YGNY---WFAV 8  
 DB 104 YGNYEYTWFAV 114

RESULT 10  
 AAW01585  
 ID AAW01585 standard; Protein; 119 AA.  
 XX  
 AC AAW01585;  
 XX  
 DT 22-AUG-1997 (first entry)  
 XX  
 DE Lead binding MAB 11D11 heavy chain variable region.  
 XX  
 KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;  
 KW pharmaceutical; health care; skin treatment; pesticide; herbicide;  
 KW heavy metal.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9639518-A1.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 05-JUN-1996; 96WO-US09258.  
 XX  
 PR 10-OCT-1995; 95US-0541373.  
 PR 05-JUN-1995; 95US-0462798.  
 XX  
 PA (BION-) BIONEERASKA INC.  
 XX  
 PI Lopez O, Murray PJ, Wylie DE;  
 XX

```

DR WPI; 1997-043140/04.
DR N-PSDB; AAT58259.
XX
XX DNA encoding heavy metal binding polypeptide sequences - used for
XX detecting, removing, adding or neutralising heavy metals, such as
XX lead cations
XX
XX Claim 12; Page 73; 125pp; English.
XX
XX The present sequence represents the heavy chain variable region for
XX monoclonal antibody (MAB) 10f4, which immunoreacts with a lead cation.
XX The sequence was derived from RNA isolated from mouse hybridoma cells.
XX The protein can be used for binding heavy metals, such as lead cations.
XX It can be used for detecting, removing, adding or neutralising the
XX heavy metals in biological and inanimate systems. It can be used in
XX e.g. aqueous liquid systems, in biological or environmental systems or
XX in such compositions as perfumes, cosmetics, pharmaceuticals, health
XX care products, skin treatment products, pesticides, herbicides,
XX solvents used in the production of semi-conductor and integrated
XX circuit components and production materials for electronic components.
XX The products can provide for applications involving minute amounts of
XX specific heavy metals.
XX
XX Sequence 119 AA;
SQ
Query Match 75.9%; Score 41; DB 18; Length 119;
Best Local Similarity 75.0%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YGNYWFAY 8
DB 101 yghlwfay 108
| | | | |
RESULT 11
AAW04592
ID AAW04592 standard; Protein; 116 AA.
XX
XX AAW04592;
XX
XX 11-AUG-1997 (first entry)
XX
XX Anti-DNA antibody 10f4 heavy chain variable region.
XX
XX Heavy chain; variable region; anti-DNA; monoclonal; antibody;
XX MAB 10f4; hairpin; diagnosis; inflammatory glomerulonephritis;
XX systemic lupus erythematosus; screening; treatment; prevention;
XX SLE; disease.
XX
XX Mus spp.
XX
XX Key Location/Qualifiers
FH Region 1..22 /label= framework_I
FT Region 23..27 /label= CDR_I
FT Region 28..41 /label= framework_II
FT Region 42..58 /label= CDR_II
FT Region 59..90 /label= framework_III
FT Region 91..105 /label= CDR_III
FT Region 106..116 /label= J_region
FT
FT W09636361-AL.
XX
XX 21-NOV-1996.
XX
XX 16-MAY-1996; 96WO-US07113.
XX
18-MAY-1995; 95US-0443540.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Glick GD, Swanson PC;
XX
XX WPI; 1997-011854/01.
XX N-PSDB; AAT43736.
XX
XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
XX develop prods. for diagnosis and treatment of disorders, e.g.
XX glomerulonephritis or systemic lupus erythematosus
XX
XX Example; Fig 7; 102pp; English.
XX
XX The present sequence is the heavy chain variable region of the
XX anti-DNA monoclonal antibody (MAB) 10f4, which has a high affinity
XX for single stranded DNA, low or no affinity for double stranded DNA
XX and specifically binds a DNA hairpin. The MAB can be used to diagnose
XX disorders associated with the pathological complexation of DNA,
XX e.g. inflammatory glomerulonephritis and systemic lupus
XX erythematosus. It can also be used to generate reagents to screen
XX for pharmaceutical agents, and treat and/or prevent an above
XX disorder.
XX
XX Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells
XX from which were then fused with Sp2/0 myeloma cells to give
XX hybridomas producing the anti-DNA MAB. 10f4 was found to react
XX strongly with single stranded DNA and poly(dT), moderately with
XX poly(dG) and weakly with poly(dI).
XX
XX Sequence 116 AA;
SQ
Query Match 69.4%; Score 37.5; DB 18; Length 116;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 YGNY-WFAY 8
DB 97 ysnypwfay 105
| | | | |
RESULT 12
AAW05038
ID AAW05038 standard; peptide; 17 AA.
XX
XX AAW05038;
XX
XX 29-MAY-1997 (first entry)
XX
XX Synthetic peptide for treating systemic lupus erythematosus.
XX
XX SLE; systemic lupus erythematosus; autoimmune disease; monoclonal;
XX anti-DNA antibody; CDR; complementarity determining region; 16/6 Id;
XX idiotype; nuclear antigen.
XX
XX Synthetic.
XX
XX W09630057-AL.
XX
XX 03-OCT-1996.
XX
XX 27-MAR-1996; 96WO-US04206.
XX
XX 28-MAR-1995; 95IL-0113159.
XX
XX {RYCU/} RYCUS A.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Mozes E, Waisman A;
XX
XX WPI; 1996-455014/45.
XX

```



XX New synthetic peptide(s) for treating systemic lupus erythematosus -  
PT based on complementarity determining region of pathogenic anti-DNA  
PT monoclonal antibody that induces SLE-like disease in mice  
XX  
PS Claim 8; Page 37; 51pp; English.  
XX  
CC AAW05029-W05038 are synthetic peptides based on the complementarity-  
CC determining region (CDR) of the heavy or light chain of a pathogenic  
CC 16/6 id anti-DNA monoclonal antibody (MAB), that induces a systemic  
CC lupus erythematosus (SLE)-like disease in mice. The peptides and their  
CC derivatives are used for treating SLE. The peptides inhibit or suppress  
CC specific antigen responses of SLE patients without affecting all other  
CC immune responses.  
XX  
XX Sequence 17 AA;

Query Match 68.5%; Score 37; DB 17; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YGNW 5  
Db 9 YGNW 13  
|||||

RESULT 13  
AAB18127  
ID AAB18127 standard; Protein; 158 AA.  
AC AAB18127;  
XX  
XX 08-NOV-2000 (first entry)  
XX  
XX Pinus radiata methyl sterol oxidase protein SEQ ID NO:288.  
XX  
KW Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;  
KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;  
KW genome mapping; physical mapping; positional cloning; forestry;  
KW agriculture; medicine; fermentation; plant development; pest resistance;  
KW pinene; myrcene; Monterey pine.  
XX  
OS Pinus radiata.  
XX  
XX WO200036081-A2.  
XX  
XX 22-JUN-2000.  
XX  
XX 16-DEC-1999; 99WO-NZ00219.  
XX  
XX 17-DEC-1998; 98US-0215504.  
XX  
XX 29-JUL-1999; 99US-0146441.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
XX Havukkala IJ;  
XX  
XX WPI: 2000-431575/37.  
XX  
XX N-PSDB; AAA69563.  
XX  
XX New plant polynucleotides encoding polypeptides involved in the  
PT production and modification of isoprenoids, useful in forestry and  
PT agriculture for manipulation of isoprenoid metabolism -  
XX  
XX Claim 26; Page 158; 164pp; English.  
XX  
XX The present invention describes plant polynucleotides encoding  
CC polypeptides involved in the production and modification of isoprenoids,  
CC such as terpenoid and steroid compounds. The polynucleotides are used  
CC in genome mapping, in physical mapping and in positional cloning of  
CC genes. The polynucleotides and polypeptides are useful in forestry and  
CC agriculture for manipulation of isoprenoid metabolism, in medicine for  
CC therapeutic effects, including direct application in diseased organisms

CC agriculture for manipulation of isoprenoid metabolism, in medicine for  
CC therapeutic effects, including direct application in diseased organisms  
CC or indirect application by transgenic organisms and in fermentation and  
CC chemical processing industries involving isoprenoids. In plant  
CC applications, manipulating isoprenoid pathways or isoprenoid composition  
CC may, for example, affect plant development, pest resistance, and the  
CC value of extractives (e.g. pinene and myrcene). The ubiquitous and  
CC varied roles of isoprenoids make the polynucleotides attractive targets  
CC for biotechnical applications in a variety of fields. AAG69527 to  
CC AAG69690 and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus  
CC radiata polynucleotides and proteins used in the exemplification of the  
CC present invention.  
XX  
XX Sequence 158 AA;

Query Match 68.5%; Score 37; DB 21; Length 158;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YGNW 5  
Db 45 YGNW 49  
|||||

RESULT 14  
AAB18064  
ID AAB18064 standard; Protein; 210 AA.  
XX  
XX AAB18064;  
XX  
XX 08-NOV-2000 (first entry)  
XX  
XX Pinus radiata methyl sterol oxidase protein SEQ ID NO:225.  
XX  
KW Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;  
KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;  
KW genome mapping; physical mapping; positional cloning; forestry;  
KW agriculture; medicine; fermentation; plant development; pest resistance;  
KW pinene; myrcene; Monterey pine.  
XX  
OS Pinus radiata.  
XX  
XX WO200036081-A2.  
XX  
XX 22-JUN-2000.  
XX  
XX 16-DEC-1999; 99WO-NZ00219.  
XX  
XX 17-DEC-1998; 98US-0215504.  
XX  
XX 29-JUL-1999; 99US-0146441.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
XX Havukkala IJ;  
XX  
XX WPI: 2000-431575/37.  
XX  
XX N-PSDB; AAA69664.  
XX  
XX New plant polynucleotides encoding polypeptides involved in the  
PT production and modification of isoprenoids, useful in forestry and  
PT agriculture for manipulation of isoprenoid metabolism -  
XX  
XX Claim 26; Page 129; 164pp; English.  
XX  
XX The present invention describes plant polynucleotides encoding  
CC polypeptides involved in the production and modification of isoprenoids,  
CC such as terpenoid and steroid compounds. The polynucleotides are used  
CC in genome mapping, in physical mapping and in positional cloning of  
CC genes. The polynucleotides and polypeptides are useful in forestry and  
CC agriculture for manipulation of isoprenoid metabolism, in medicine for  
CC therapeutic effects, including direct application in diseased organisms

Fri Jun 29 08:05:21 2001

us-09-724-406-8.rag

CC or indirect application by transgenic organisms and in fermentation and  
 CC chemical processing industries involving isoprenoids. In plant  
 CC applications, manipulating isoprenoid pathways or isoprenoid composition  
 CC may, for example, affect plant development, pest resistance, and the  
 CC value of extractives (e.g. pinene and myrcene). The ubiquitous and  
 CC varied roles of isoprenoids make the polynucleotides attractive targets  
 CC for biotechnical applications in a variety of fields. AA69527 to  
 CC AA69690 and AA618004 to AA618143 represent Eucalyptus grandis and Pinus  
 CC radiata polynucleotides and proteins used in the exemplification of the  
 CC present invention.

XX SQ Sequence 210 AA;

Query Match 68.5%; Score 37; DB 21; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNYW 5  
 Db 45 ygnyw 49  
 |||||

## RESULT 15

AA22171  
 ID . AA22171 standard; Protein; 234 AA.

XX AC AA22171;

XX DT 09-SEP-1999 (first entry)

XX DE Drosophila Acp29AB protein.

XX KW Accessory gland protein; Acp; toxin; insecticide; Drosophila; mating;  
 XX KX caterpillar; development inhibitor; insect pest; plant protection.

XX OS Drosophila melanogaster.

XX PN WO9932149-A1.

XX PD 01-JUL-1999.

XX PF 23-DEC-1998; 98WO-US27603.

XX PR 23-DEC-1997; 97US-0071315.

XX PA (CORR ) CORNELL RES FOUND INC.

XX PI Lung O, Tram K, Wolfner MF;

XX DR WPI: 1999-418871/35.

XX DR N-PSDB; AA84364.

XX PT Nucleic acid encoding accessory gland proteins of Drosophila

XX PS Claim 38; Page 20; 89pp; English.

XX CC This sequence is a Drosophila melanogaster accessory gland protein  
 CC (Acp) of the invention. A particular Acp, designated Acp62F, is toxic to  
 CC insects, particularly to Drosophila and caterpillars, and it (or vectors  
 CC that express it) can be used to kill or inhibit development of insect  
 CC pests, for plant protection. More generally detection of Acp's in a  
 CC female fruit fly is indicative of recent mating.

XX SQ Sequence 234 AA;

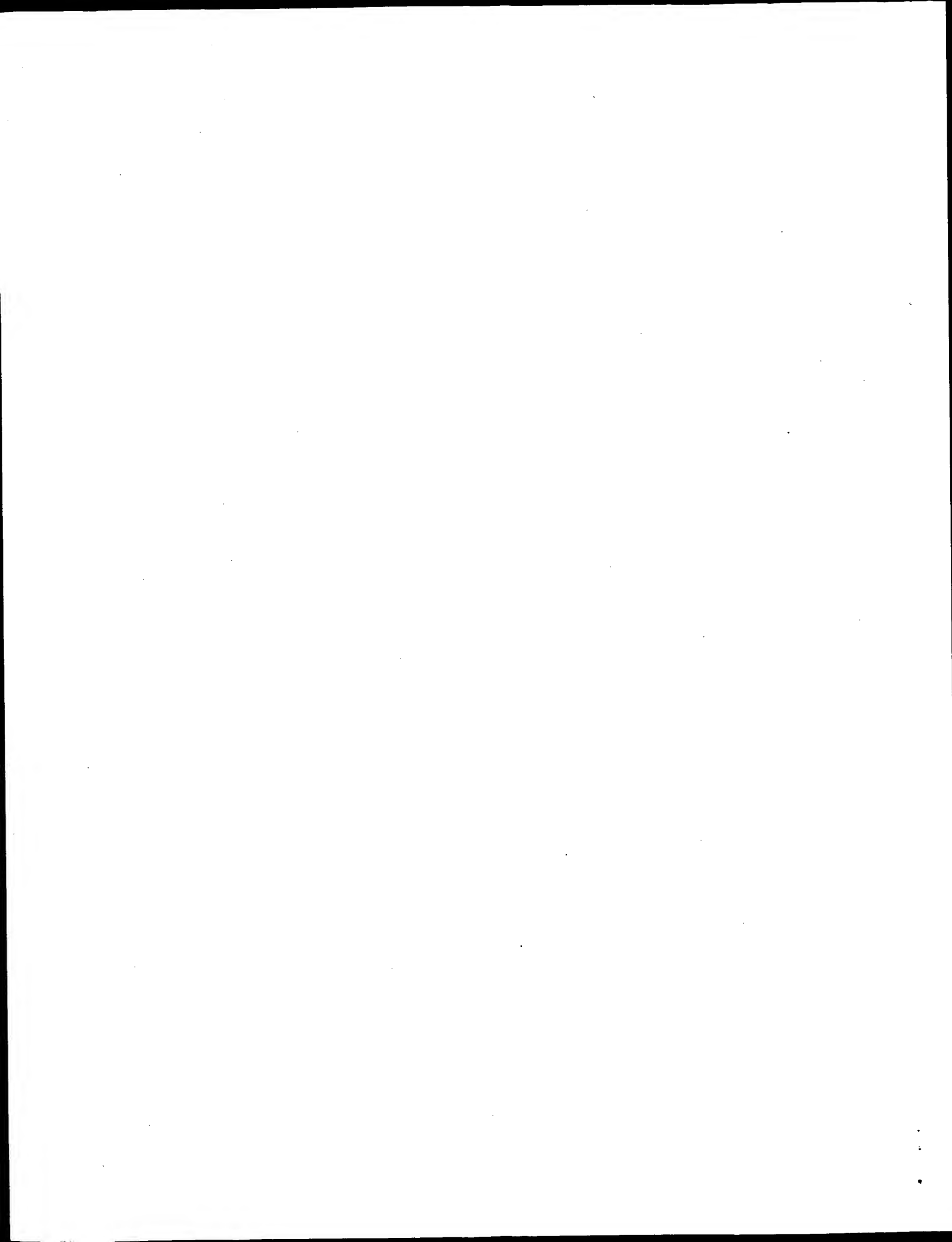
Query Match 68.5%; Score 37; DB 20; Length 234;  
 Best Local Similarity 83.3%; Pred. No. 64;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NYWFAY 8  
 |||||

Db 50 nywfty 55

Search completed: June 28, 2001, 16:14:34  
 Job time: 1322 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:13 ; Search time 138.34 Seconds  
(without alignments)  
1.165 Million cell updates/sec

Title: US-09-724-406-8  
Perfect score: 54  
Sequence: 1 YGNYWYAY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: /cgn2\_6/ptodata/2/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43.5	80.6	116	2	US-08-888-366-10
2	43.5	80.6	116	2	US-08-888-366-12
3	43	79.6	122	4	US-08-767-128-4
4	41	75.9	119	4	US-08-767-128-20
5	37.5	69.4	116	3	US-08-881-037-19
6	37	68.5	221	4	US-08-448-489-19
7	37	68.5	731	2	US-08-696-944-20
8	36.5	67.6	119	1	US-08-458-516-10
9	36.5	67.6	138	1	US-08-458-516-11
10	36.5	67.6	138	1	US-08-458-516-7
11	36.5	67.6	222	1	US-08-458-516-22
12	36.5	67.6	225	1	US-08-458-516-23
13	36.5	67.6	449	1	US-08-458-516-13
14	36	66.7	573	2	US-08-991-531-1
15	36	66.7	573	2	US-09-032-315-10
16	36	66.7	573	2	US-08-993-318A-10
17	36	66.7	573	3	US-09-028-887-1
18	36	66.7	573	4	US-09-399-886-10
19	36	66.7	573	4	US-09-396-260-10
20	36	66.7	573	4	US-09-518-901-1
21	36	66.7	616	1	US-08-149-100-2
22	36	66.7	616	1	US-08-749-882A-2
23	36	66.7	616	2	US-08-539-134-2
24	36	66.7	616	2	US-08-991-531-2
25	36	66.7	616	2	US-09-032-315-9
26	36	66.7	616	2	US-08-993-318A-9
27	36	66.7	616	3	US-09-028-887-2

28 36 66.7 616 4 US-09-399-886-9 Sequence 9, Appli  
29 36 66.7 616 4 US-09-396-260-9 Sequence 9, Appli  
30 36 66.7 616 4 US-09-518-901-2 Sequence 2, Appli  
31 36 66.7 616 5 PCT-US95-06816-2 Sequence 2, Appli  
32 36 66.7 620 1 US-08-706-037-27 Sequence 27, Appli  
33 36 66.7 620 1 US-08-940-661A-2 Sequence 2, Appli  
34 36 66.7 620 2 US-09-083-485-2 Sequence 2, Appli  
35 36 66.7 620 2 US-09-005-397-27 Sequence 2, Appli  
36 36 66.7 620 2 US-08-939-218A-2 Sequence 27, Appli  
37 36 66.7 620 5 PCT-US95-06815-2 Sequence 2, Appli  
38 36 66.7 989 2 US-08-070-301-14 Sequence 14, Appli  
39 35 64.8 437 4 US-08-961-083-70 Sequence 70, Appli  
40 34 63.0 401 2 US-08-846-762-9 Sequence 9, Appli  
41 34 63.0 401 2 US-08-820-521-2 Sequence 2, Appli  
42 34 63.0 401 4 US-09-248-715-2 Sequence 2, Appli  
43 34 63.0 430 1 US-08-601-435-2 Sequence 2, Appli  
44 34 63.0 430 2 US-08-931-047-2 Sequence 2, Appli  
45 34 63.0 430 2 US-08-783-202-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-888-366-10  
; Sequence 10, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/888,366  
; FILING DATE: 03-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/187,407  
; FILING DATE: 27-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,542  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/493,299  
; FILING DATE: 14-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/324,392  
; FILING DATE: 14-MAR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.39USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-888-366-10

Query Match 80.6%; Score 43.5; DB 2; Length 116;  
Best Local Similarity 88.9%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 YGNY-WFAY 8  
|||||  
Db 97 YGNYWVAF 105

RESULT 2

US-08-888-366-12  
; Sequence 12, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/888,366  
; FILING DATE: 03-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/187,407  
; FILING DATE: 27-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,542  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/493,299  
; FILING DATE: 14-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/324,392  
; FILING DATE: 14-MAR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.39USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-888-366-12

Query Match 80.6%; Score 43.5; DB 2; Length 116;  
Best Local Similarity 88.9%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 YGNY-WFAY 8  
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Db 97 YGNYWVAF 105

Db 97 YGNYWVAF 105

RESULT 3

US-08-767-128-4  
; Sequence 4, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GOEBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079west Center, 90 South Seventh St  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/767,128  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 04-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09258  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/541,373  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/462,798  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.49USF1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/371-5278  
; TELEFAX: 612/332-9081  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-08-767-128-4

Query Match 79.6%; Score 43; DB 4; Length 122;  
Best Local Similarity 80.0%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 YGNY-WFAY 8  
|||||  
Db 102 YGNYWVAF 111

RESULT 4  
US-08-767-128-20  
; Sequence 20, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GOEBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079west Center, 90 South Seventh St  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/767,128  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 04-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09258  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/541,373  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/462,798  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.49USF1  
; TELEPHONE: 612/371-5278  
; TELEFAX: 612/332-9081  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-767-128-20

Query Match 75.9%; Score 41; DB 4; Length 119;  
Best Local Similarity 75.0%; Pred. No. 4.3;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGNYWFAY 8  
||: |||||  
Db 101 YGHLWFAY 108

RESULT 5  
US-08-881-037-19  
; Sequence 19, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Konski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-19

Query Match 69.4%; Score 37.5; DB 3; Length 116;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 YGNY-WFAY 8  
||: |||||  
Db 97 YSNYPWFAY 105

RESULT 6  
US-08-448-489-19  
; Sequence 19, Application US/08448489  
; Patent No. 6184022  
; GENERAL INFORMATION:  
; APPLICANT: SEIKI, Motoharu  
; APPLICANT: SATO, Hiroshi  
; APPLICANT: SHINAGAWA, Akira  
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
; FILE REFERENCE: 55-290P  
; CURRENT APPLICATION NUMBER: US/08/448,489  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 231  
; TYPE: PRT

; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
 ; OTHER INFORMATION: Matrix Metalloproteinase Family  
 US-08-448-489-19

Query Match 68.5%; Score 37; DB 4; Length 231;  
 Best Local Similarity 62.5%; Pred. No. 36;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNWFWAY 8  
 :|||||  
 Db 190 FGNYWGGY 197

RESULT 7  
 US-08-696-944-20  
 ; Sequence 20, Application US/08696944  
 ; Patent No. 5981831  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sumant CHENGAPPA  
 ; APPLICANT: Susan A. HELLYER  
 ; APPLICANT: John S. REID  
 ; APPLICANT: Jacqueline DE SILVA  
 ; TITLE OF INVENTION: No. 5981831el Exo-(1-4)-Beta-D Galactanase  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: MS Word  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/696,944  
 ; FILING DATE: 23-AUG-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB95/00372  
 ; FILING DATE: 23-FEB-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9403423.8  
 ; FILING DATE: 23-FEB-1994  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 731 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-696-944-20

Query Match 68.5%; Score 37; DB 2; Length 731;  
 Best Local Similarity 62.5%; Pred. No. 11e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNWFWAY 8  
 :|||  
 Db 28 YGNVWYDY 35

RESULT 8  
 US-08-458-516-10  
 ; Sequence 10, Application US/08458516  
 ; Patent No. 5777085  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Co, Man Sung  
 ; APPLICANT: Tso, J. Yun

; TITLE OF INVENTION: Humanized Antibodies Reactive with  
 ; TITLE OF INVENTION: GPIIB/IIIA  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: William M. Smith  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/458,516  
 ; FILING DATE:

; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/059,159  
 ; FILING DATE: 03-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M.  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 11823-37-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-326-2400  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 119 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: N-terminal fragment  
 US-08-458-516-10

Query Match 67.6%; Score 36.5; DB 1; Length 119;  
 Best Local Similarity 87.5%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GNY-WFAY 8  
 :|||  
 Db 101 GNYGWFWAY 108

RESULT 9  
 US-08-458-516-11  
 ; Sequence 11, Application US/08458516  
 ; Patent No. 5777085  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Co, Man Sung  
 ; APPLICANT: Tso, J. Yun  
 ; TITLE OF INVENTION: Humanized Antibodies Reactive with  
 ; TITLE OF INVENTION: GPIIB/IIIA  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: William M. Smith  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/458,516  
 ; FILING DATE:



CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal fragment  
US-08-458-516-11

Query Match 67.6%; Score 36.5; DB 1; Length 119;  
Best Local Similarity 87.5%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GNY-WFAY 8  
111 1111  
DB 101 GNYGWFAF 108

RESULT 10  
US-08-458-516-7  
SEQUENCE 7, Application US/08458516  
Patent No. 5777085  
GENERAL INFORMATION:  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-7

Query Match 67.6%; Score 36.5; DB 1; Length 138;  
Best Local Similarity 87.5%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GNY-WFAY 8  
111 1111  
DB 120 GNYGWFAF 127

RESULT 11  
US-08-458-516-22  
SEQUENCE 22, Application US/08458516  
Patent No. 5777085  
GENERAL INFORMATION:  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 222 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-22

Query Match 67.6%; Score 36.5; DB 1; Length 222;  
Best Local Similarity 87.5%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GNY-WFAY 8  
111 1111  
DB 101 GNYGWFAF 108

RESULT 12  
US-08-458-516-23  
SEQUENCE 23, Application US/08458516  
Patent No. 5777085  
GENERAL INFORMATION:  
APPLICANT: Tso, J. Yun

```

; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-23

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Query Match 67.6%; Score 36.5; DB 1; Length 235;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 2 GNY-WFAY 8
Db 101 GNYGWFA 108

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RESULT 13
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:

```

```

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13

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```

Query Match 67.6%; Score 36.5; DB 1; Length 449;
Best Local Similarity 87.5%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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```

Qy 2 GNY-WFAY 8
Db 101 GNYGWFA 108

```

```

RESULT 14
US-08-991-531-1
; Sequence 1, Application US/08991531
; Patent No. 5925554
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: Myceliophthora And Scytalidium Laccase
; TITLE OF INVENTION: Variants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59255540 No. 5925554disk of No. 5925554th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,531
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5125.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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Fri Jun 29 08:05:23 2001

US-08-991-531-1

Query Match 66.7%; Score 36; DB 2; Length 573;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6  
|  
|  
|  
|  
Db 284 GNYWF 288

RESULT 15  
US-09-032-315-10  
; Sequence 10, Application US/09032315  
; Patent No. 5985818  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen; Allan  
; APPLICANT: Xu, Feng  
; TITLE OF INVENTION: LACCASE MUTANTS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5985818o No. 5985818disk of No. 5985818th America, Inc.  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,315  
; FILING DATE: 27-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rozek, Carol  
; REGISTRATION NUMBER: 36,993  
; REFERENCE/DOCKET NUMBER: 5200.200-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 573 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-032-315-10

Query Match 66.7%; Score 36; DB 2; Length 573;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6  
|  
|  
|  
|  
Db 284 GNYWF 288

Search completed: June 28, 2001, 16:01:13  
Job time: 521 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:42 ; Search time 234.85 Seconds  
(without alignments)  
2.595 Million cell updates/sec

Title: US-09-724-406-8  
Perfect score: 54  
Sequence: 1 YGNWTFAY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	88.9	142	2 C34903	Ig heavy chain pre
2	46	85.2	137	2 E29380	Ig heavy chain pre
3	43	79.6	528	2 S24344	glucose transport
4	40	74.1	112	2 S26327	Ig heavy chain v r
5	40	74.1	115	2 S13694	Ig heavy chain v r
6	40	74.1	116	2 S13691	Ig heavy chain v r
7	40	74.1	137	2 S03326	Ig heavy chain pre
8	39	72.2	115	2 B25387	hypothetical prote
9	39	72.2	117	2 S01822	Ig heavy chain v-D
10	39	72.2	520	2 T18124	probable capsid pr
11	38	70.4	109	2 PL0233	Ig heavy chain v r
12	38	70.4	112	2 PL0232	Ig heavy chain v r
13	38	70.4	151	2 I80310	sepo protein - Esc
14	38	70.4	151	2 B86047	hypothetical prote
15	38	70.4	246	2 T28166	hypothetical prote
16	38	70.4	398	2 B71193	hypothetical prote
17	38	70.4	491	1 ISECKR	ketol-acid reducto
18	38	70.4	491	2 E86063	ketol-acid reducto
19	38	70.4	552	2 T39121	amino-acid permeas
20	38	70.4	732	2 B84902	hypothetical prote
21	38	70.4	790	2 T47959	hypothetical prote
22	37	68.5	108	2 C65013	hypothetical prote
23	37	68.5	108	2 H85881	hypothetical prote
24	37	68.5	118	2 S18316	ribulose-bisphosph
25	37	68.5	137	2 S24267	Ig heavy chain v r
26	37	68.5	140	2 S09216	Ig heavy chain pre
27	37	68.5	247	2 S23474	rod-core linker po
28	37	68.5	247	2 JS0593	rod-core linker po
29	37	68.5	353	1 S56750	single stranded D

30	37	68.5	467	2 S38535	cytochrome P450 76
31	37	68.5	638	2 JC2139	phenylethylamine o
32	37	68.5	684	2 A56102	amine oxidase (cop
33	37	68.5	731	2 S16595	gene CARSR12 prote
34	36.5	67.6	382	2 T45851	hypothetical prote
35	36	66.7	128	2 PH0094	Ig heavy chain v r
36	36	66.7	128	2 PH0095	Ig kappa chain v r
37	36	66.7	225	2 T24226	hypothetical prote
38	36	66.7	279	2 H84361	proline dehydrogen
39	36	66.7	361	1 F69254	probable hexosyltr
40	36	66.7	400	1 F69142	probable hexosyltr
41	36	66.7	616	2 S50998	transporter protei
42	36	66.7	619	1 KSNCLT	laccase (EC 1.10.3
43	36	66.7	619	1 KSNCLT	laccase (EC 1.10.3
44	36	66.7	621	2 S72493	laccase (EC 1.10.3
45	36	66.7	972	1 URBOAP	peptidylglycine mo

## ALIGNMENTS

RESULT 1  
C34903  
Ig heavy chain precursor V region (5-27) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996  
C:Accession: C34903  
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A:Title: Active site structure and antigen binding properties of idiotypically cross-  
A:Reference number: A34903; MUID:90094387  
A:Accession: C34903  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-142 <BED>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 88.9%; Score 48; DB 2; Length 142;  
Best Local Similarity 87.5%; Pred. No. 0.35;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWTFAY 8  
|| |||||  
Db 124 YGGYWFAY 131

RESULT 2  
E29380  
Ig heavy chain precursor V region (AC-1001) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 23-Jul-1999  
C:Accession: E29380  
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
J. Biol. Chem. 262, 13579-13583, 1987  
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variab  
A:Reference number: A92612; MUID:88007582  
A:Accession: E29380  
A:Molecule type: mRNA  
A:Residues: 1-137 <CEE>  
A:Cross-references: GB:M17164; GB:J02815; NID:g195411; PIDN:AAA38295.1; PID:g195412  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 46; DB 2; Length 137;  
Best Local Similarity 87.5%; Pred. No. 0.73;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWTFAY 8

Db 119 YGNLWFAY 126  
|||||

## RESULT 3

S24344  
glucose transport protein Glut7 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 04-Sep-1998  
C:Accession: S24344  
R:Waddell, I.D.; Zomerschoe, A.G.; Voice, M.W.; Burchell, A.  
Biochem. J. 286, 173-177, 1992  
A:Title: Cloning and expression of a hepatic microsomal glucose transport protein. Comp  
A:Reference number: S24344; MUID:92392274  
A:Accession: S24344  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-528 <WAD>  
C:Cross-references: EMBL:X66031; NID:g56266; PID:g56267  
C:Superfamily: glucose transport protein  
C:Keywords: transmembrane protein

Query Match 79.6%; Score 43; DB 2; Length 528;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6  
|||||

Db 475 YGNYWF 480

## RESULT 4

S26327  
Ig heavy chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: S26327  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e  
A:Reference number: S26309; MUID:91341421  
A:Accession: S26327  
A:Molecule type: mRNA  
A:Residues: 1-112 <STA>  
C:Cross-references: EMBL:X59192  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-91/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 112;  
Best Local Similarity 83.3%; Pred. No. 5.9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6  
|||||

Db 93 YGNYWF 98

## RESULT 5

S13694  
Ig heavy chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S13694  
R:Pennell, C.A.; Mercollino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.  
Eur. J. Immunol. 19, 1289-1295, 1989  
A:Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl  
A:Reference number: S13685; MUID:89338557  
A:Accession: S13694  
A:Molecule type: mRNA  
A:Residues: 1-115 <PEN>

A:Cross-references: EMBL:X53347; NID:g55240; PIDN:CAA37433.1; PID:g930210  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 115;  
Best Local Similarity 83.3%; Pred. No. 6.1;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6  
|||||

Db 99 YGNYWF 104

## RESULT 6

S13691  
Ig heavy chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S13691  
R:Pennell, C.A.; Mercollino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.  
Eur. J. Immunol. 19, 1289-1295, 1989  
A:Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to  
A:Reference number: S13685; MUID:89338557  
A:Accession: S13691  
A:Molecule type: mRNA  
A:Residues: 1-116 <PEN>  
C:Cross-references: EMBL:X53344; NID:g55235; PIDN:CAA37430.1; PID:g930207  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 116;  
Best Local Similarity 83.3%; Pred. No. 6.1;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6  
|||||

Db 99 YGNYWF 104

## RESULT 7

S03326  
Ig heavy chain precursor V-D-J region (clone pCP12) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 23-Jul-1999  
C:Accession: S03326  
R:Reininger, L.; Kaushik, A.; Izui, S.; Jaton, J.C.  
Eur. J. Immunol. 18, 1521-1526, 1988  
A:Title: A member of a new V(H) gene family encodes antibromelinated mouse red blood  
A:Reference number: S03326; MUID:89052754  
A:Accession: S03326  
A:Molecule type: mRNA  
A:Residues: 1-137 <REI>

A:Cross-references: EMBL:Y00743; NID:g52483; PIDN:CAA68712.1; PID:g52484  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-117/Product: Ig heavy chain V region pCP12 #status predicted <WAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:118-120/Domain: D region #status predicted <DRE>  
F:121-137/Domain: J region #status predicted <JRE>

Query Match 74.1%; Score 40; DB 2; Length 137;  
Best Local Similarity 83.3%; Pred. No. 7.2;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6  
|||||

Db 118 YGNYWF 123

## RESULT 8

B25387  
hypothetical protein 2 - phage T5

C:Species: phage T5

A:Note: host Escherichia coli

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 24-Nov-1999

C:Accession: B25387

R:Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.; Bayev, A.A.

Eur. J. Biochem. 156, 285-289, 1986

A:Title: Nucleotide sequence of the bacteriophage T5 DNA fragment which contains the gene

A:Reference number: A91166; MUID:86192452

A:Accession: B25387

A:Molecule type: DNA

A:Residues: 1-115 <SHL>

A:Cross-references: GB:X03798; NID:g15472; PIDN:CAA27425.1; PID:g15474

C:Superfamily: phage T5 hypothetical protein 2

Query Match 72.2%; Score 39; DB 2; Length 115;

Best Local Similarity 85.7%; Pred. No. 8.9;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWFEA 7

||| |||

Db 67 YGNWFEA 73

## RESULT 9

S01822

Ig heavy chain V-D-J region (hybridoma 10B10S) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000

C:Accession: S01822

R:Forster, I.; Gu, H.; Rajewsky, K.

EMBO J. 7, 3693-3703, 1988

A:Title: Germ-line antibody V regions as determinants of clonal persistence and malignant

A:Reference number: S01822; MUID:89091115

A:Accession: S01822

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <FOE>

A:Cross-references: EMBL:X12388; NID:g51924; PIDN:CAA30945.1; PID:g930158

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 39; DB 2; Length 117;

Best Local Similarity 75.0%; Pred. No. 9;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWFEA 8

||| |||

Db 99 YGNWFEA 106

## RESULT 10

T18124

probable capsid protein A622L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T18124

R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: T18124

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-520 <GRA>

A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96953.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A:Note: A622L

C:Keywords: coat protein

Query Match 72.2%; Score 39; DB 2; Length 520;

Best Local Similarity 62.5%; Pred. No. 38;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNWFEA 8

||| |||

Db 107 YNNWWTY 114

## RESULT 11

PL0233

Ig heavy chain V region (anti-DNA, DP1IVH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C:Accession: PL0233

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618

A:Accession: PL0233

A:Molecule type: mRNA

A:Residues: 1-109 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-96/Region: framework 3

F:97-104/Region: complementarity-determining 3

F:105-109/Region: framework 4

Query Match 70.4%; Score 38; DB 2; Length 109;

Best Local Similarity 85.7%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNVWFAY 8

|| || |||

Db 98 GNVWFAY 104

## RESULT 12

PL0232

Ig heavy chain V region (anti-DNA, DP7VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C:Accession: PL0232

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618

A:Accession: PL0232

A:Molecule type: mRNA

A:Residues: 1-112 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-96/Region: framework 3

F:97-104/Region: complementarity-determining 3

F:105-112/Region: framework 4

```

Query Match      70.4%; Score 38; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNYWFAY 8
   || ||||
Db 98 GNRWFAY 104

RESULT 13
180310
sepD protein - Escherichia coli
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999
C:Accession: I80310; S57615
R:Jarvis, K.G.; Giron, J.A.; Jerse, A.E.; McDaniel, T.K.; Donnenberg, M.S.; Kaper, J.B.
Proc. Natl. Acad. Sci. U.S.A. 92, 7996-8000, 1995
A:Title: Enteropathogenic Escherichia coli contains a putative type III secretion system
A:Reference number: I59412; MUID:95372406
A:Accession: I80310
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-151 <RES>
A:Cross-references: EMBL:Z49972; NID:g886475; PIDN:CAA90273.1; PID:g886476
C:Genetics:
A:Gene: sepD
C:Superfamily: Escherichia coli sepD protein

Query Match      70.4%; Score 38; DB 2; Length 151;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
   :|||||
Db 45 FGNYWVLY 52

RESULT 14
B86047
hypothetical protein Z5125 [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: B86047
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A83480; MUID:21074935; PMID:11206551
A:Accession: B86047
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <STO>
A:Cross-references: GB:AE005174; NID:g12518465; PIDN:AAG58938.1; GSPDB:GN00145; UWGP:Z51
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z5125
C:Superfamily: Escherichia coli sepD protein

Query Match      70.4%; Score 38; DB 2; Length 151;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
   :|||||
Db 45 FGNYWVLY 52

RESULT 15
T28166
hypothetical protein ORF5 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon)
C:Species: Melanoplus sanguinipes entomopoxvirus

```

```

A:Variety: isolate Tuscon
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28166
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612
A:Accession: T28166
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-246 <AFO>
A:Cross-references: EMBL:AF083866; NID:g4049647; PIDN:AAC97860.1; PID:g4049900
A:Experimental source: isolate Tuscon
C:Genetics:
A:Note: MSV005

```

```

Query Match      70.4%; Score 38; DB 2; Length 246;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 YGNYWFAY 8
   || |||
Db 230 YGYWYIY 237

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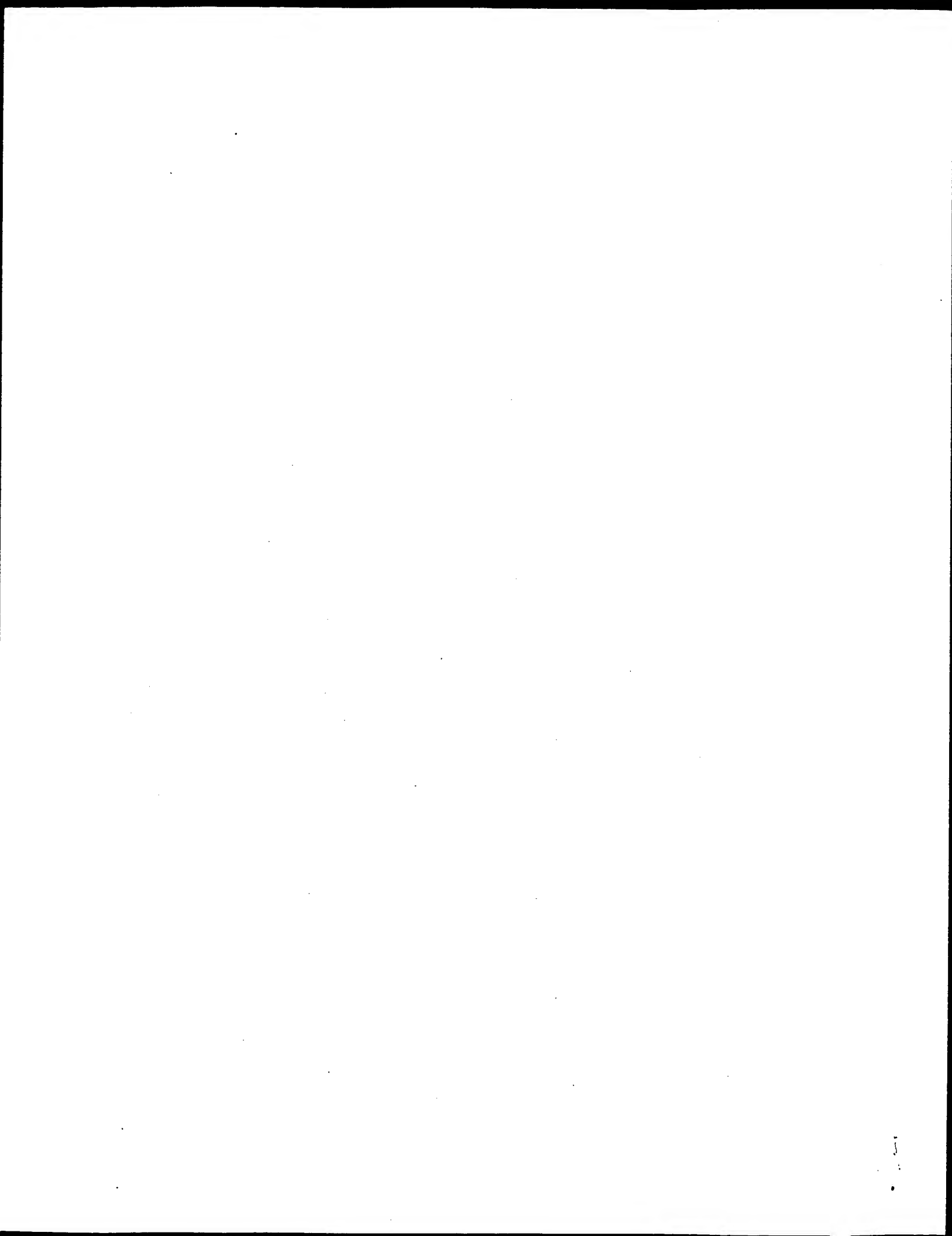
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Search completed: June 28, 2001, 15:58:43
Job time: 371 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:34 ; Search time 105.36 seconds  
(without alignments)  
2.601 Million cell updates/sec

Title: US-09-724-406-8  
Perfect score: 54  
Sequence: 1 YGNYWEAY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	70.4	490	1 ILVC_ECOLI	P05793 escherichia
2	37	68.5	108	1 YPEC_ECOLI	P76527 escherichia
3	37	68.5	118	1 RBS2_THIFE	Q07088 thiobacilli
4	37	68.5	234	1 A29B_DROME	O46197 drosophila
5	37	68.5	234	1 A29B_DROSI	Q9u568 drosophila
6	37	68.5	246	1 PYG2_ANASP	P29987 anabaena sp
7	37	68.5	247	1 PYG2_MASLA	P29732 mastigoclad
8	37	68.5	467	1 C761_SOLME	P37121 solanum mel
9	37	68.5	638	1 PAOX_ARTGO	P46881 arthroacte
10	37	68.5	683	1 AMOH_ARTGO	Q59118 arthroacte
11	37	68.5	731	1 BGAL_DIACA	Q00662 dianthus ca
12	36	66.7	619	1 LAC1_NEUCR	P06811 neurospora
13	36	66.7	619	1 LAC2_NEUCR	P10574 neurospora
14	36	66.7	621	1 LAC2_PODAN	P78722 podospora a
15	36	66.7	972	1 AMD_BOVIN	P10731 bos taurus
16	35	64.8	123	1 HV24_MOUSE	P01793 mus musculus
17	35	64.8	214	1 YQGE_BACST	P28754 bacillus st
18	35	64.8	387	1 O94A_DROME	Q9vcs9 drosophila
19	35	64.8	430	1 YQGE_BACSU	P54487 bacillus su
20	35	64.8	436	1 CYB_RHOCA	P08502 rhodobacter
21	35	64.8	440	1 CYB_PARDE	P05418 paracoccus
22	35	64.8	444	1 CYB_RHOSH	Q02761 rhodobacter
23	35	64.8	658	1 GUN3_FIBSU	P14250 fibrobacter
24	35	64.8	1500	1 SSP5_STRGN	P16952 streptococc
25	34	63.0	260	1 ERS1_YEAST	P17261 saccharomyc
26	34	63.0	346	1 GP41_HUMAN	O14843 homo sapien
27	34	63.0	346	1 GP42_HUMAN	O15529 homo sapien
28	34	63.0	459	1 MCRB_ECOLI	P15005 escherichia
29	34	63.0	599	1 VG9_BPRH2	P04331 bacterioph
30	34	63.0	599	1 VG9_BPPEZA	P07534 bacterioph
31	34	63.0	837	1 YP84_CAEEL	Q09225 caenorhabd
32	34	63.0	903	1 DPOL_BPR69	Q38087 bacterioph
33	33	61.1	108	1 VMEM_PVSP	P16651 potato viru

## RESULT 1

ID	ILVC_ECOLI	STANDARD;	PRT;	490 AA.
AC	P05793;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86) (ACETOHYDROXY-ACID			
DE	ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE).			
GN	ILVC.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG.855;			
RC	MEDLINE=92358234; PubMed=1379743;			
RA	Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;			
RT	"Analysis of the Escherichia coli genome: DNA sequence of the region			
RT	from 84.5 to 86.5 minutes.";			
RL	Science 257:771-778(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RC	MEDLINE=86111952; PubMed=3003115;			
RA	Wek R.C., Hatfield G.W.;			
RT	"Nucleotide sequence and in vivo expression of the ilvX and ilvC			
RT	genes in Escherichia coli K12. Transcription from divergent			
RT	overlapping promoters.";			
RL	J. Biol. Chem. 261:2441-2450(1986).			
RN	[3]			
RP	SEQUENCE OF 1-12.			
RC	STRAIN=K12 / BWG2;			
RC	MEDLINE=97443975; PubMed=92986466;			
RA	Link A.J., Robison K., Church G.M.;			
RT	"Comparing the predicted and observed properties of proteins encoded			
RT	in the genome of Escherichia coli K-12.";			
RL	Electrophoresis 18:1259-1313(1997).			
CC	-1- CATALYTIC ACTIVITY: (R)-2,3-DIHYDROXY-3-METHYLBUTANOATE + NADP(+)			
CC	= (S)-2-HYDROXY-2-METHYL-3-OXOBUTANOATE + NADPH.			
CC	-1- PATHWAY: SECOND STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.			
CC	-1- INDUCTION: IN THE PRESENCE OF ACETOHYDROXYBUTYRATE & ACETOLACTATE,			
CC	THE SUBSTRATES OF KETOL-ACID REDUCTOISOMERASE.			
CC	-1- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M87049; AAC67577.1; -.			
DR	EMBL; AB000454; AAC76779.1; -.			

P08732 escherichia  
O50165 borrelia bu  
P40218 saccharomyc  
Q95008 caenorhabd1  
O34504 bacillus su  
Q95000 brachyosio  
O88895 mus musculu  
P56520 gallus galli  
O15379 homo sapien  
Q9hy11 pseudomonas  
P19843 pseudomonas  
P20584 aspergillus

DR EMBL; M11689; AAA24029.1; -.  
 DR PIR; A26287; ISECKR.  
 DR PIR; S30672; S30672.  
 DR SWISS-2DPAGE; P05793; COLI.  
 DR EcoGene; EG10495; IIVC.  
 DR InterPro; IPR000506; -.  
 KW Pfam; PF01450; IIVC; 1.  
 KW Oxidoreductase; Branched-chain amino acid biosynthesis; NADP.  
 FT INIT\_MET 0  
 FT ACT\_SITE 131 131 POTENTIAL.  
 FT CONFLICT 250 250 E->K (IN REF. 2).  
 SQ SEQUENCE 490 AA; 53938 MW; 4587C397031B13A5 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 490;  
 Best Local Similarity 75.0%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGNWYFAY 8  
 |||||  
 Db 418 YGNVLFYS 425

RESULT 2  
 YPEC\_ECOLI  
 ID YPEC\_ECOLI STANDARD; PRT; 108 AA.  
 AC P76527;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE HYPOTHETICAL 13.3 KDA PROTEIN IN GLK-NUPC INTERGENIC REGION PRECURSOR.  
 GN YPEC.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 CC -1- SIMILARITY: TO E.COLI YAA.

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 CC -----

DR EMBL; AE000327; AAC75449.1; -.  
 DR EcoGene; EG14385; YPEC.  
 KW Hypothetical protein; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 108 HYPOTHETICAL PROTEIN YPEC.  
 SQ SEQUENCE 108 AA; 13263 MW; 7F418AE4140139B4 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNWY 5  
 |||||  
 Db 40 YGNWY 44

RESULT 3  
 RBS2\_THIFE  
 ID RES2\_THIFE STANDARD; PRT; 118 AA.  
 AC Q07088;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2 (EC 4.1.1.39) (RUBISCO  
 DE SMALL SUBUNIT 2).  
 DE GN CBS2 OR RECS2.  
 OS Thiobacillus ferrooxidans.  
 OC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.  
 OX NCBI\_TaxID=920;  
 RN [1]

SEQUENCE FROM N.A.  
 RX MEDLINE=92070528; PubMed=1959634;  
 RA Pulgar V., Gaete L., Allende J., Orellana O., Jordana X.,  
 RA Jedlicki E.;  
 RT "Isolation and nucleotide sequence of the Thiobacillus ferrooxidans  
 RT genes for the small and large subunits of ribulose 1,5-bisphosphate  
 RT carboxylase/oxygenase.";  
 RL FEBS Lett. 292:85-89(1991).

CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF  
 CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC  
 CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF  
 CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH  
 CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME  
 CC ACTIVE SITE.

CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =  
 CC 2 3-PHOSPHO-D-GLYCERATE.

CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =  
 CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.

CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.

CC -1- CAUTION: IN T.FERROXIDANS TWO SIMILAR SET OF GENES CODE FOR  
 CC RUBISCO LARGE AND SMALL CHAINS: THE RBCL1-RBCS1 AND THE RBCL2-  
 CC RBCS2 SETS.

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 CC -----

DR EMBL; X70355; CAA49815.1; -.  
 DR HSP; P00870; IAU5.  
 DR InterPro; IPR000894; -.  
 DR Pfam; PF00101; Rubisco\_small; 1.  
 KW Carbon dioxide fixation; Photorespiration; Lyase; Oxidoreductase;  
 KW Monooxygenase; Calvin cycle; Multigene family.  
 SQ SEQUENCE 118 AA; 13627 MW; 1B063498DECA6DD3 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 118;  
 Best Local Similarity 50.0%; Pred. No. 12;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGNWYFAY 8  
 :||||:  
 Db 58 FGNYWYMW 65

RESULT 4  
 A29B\_DROME  
 ID A29B\_DROME STANDARD; PRT; 234 AA.  
 AC A46197; Q9TVT3; Q9TW06; Q9TW07; Q9U976; Q9U977; Q9U978;  
 AC Q9U979; Q9V305;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE ACCESSORY GLAND PROTEIN ACP29AB PRECURSOR.



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DR FlyBase; FBgn0015583; Acp29AB.
DR InterPro; IPR001304; -.
DR Pfam; PF00059; lectin_c.1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Behavior; Signal; Polymorphism.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 234 ACCESSORY GLAND PROTEIN ACP29AB.
FT DOMAIN 137 228 C-TYPE LECTIN (LONG FORM).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 29 59 K -> R (IN STRAINS LA1, LA3, LA4, LA5, LA14, LA15, LA16, LA21, LA25, LA34, LA35, LA41, LA45, LA52B, M080B, MA5, MA8, MA13, MA18, MA20, MA21, MA45, MA48, MA52, MA67, ZIM26, ZIM29, ZIM30, ZIM56, WS6 AND WS19).
FT VARIANT 105 105 A -> S (IN STRAINS LA16 AND LA35).
FT VARIANT 113 113 R -> L (IN STRAINS LA14, LA14, LA16, LA35, M02B, M015B, M034A, M036A, M037A, M047A, M052B, M058B, M080B, MA5, MA7, MA13, MA18, MA20, MA21, MA45, MA48, MA50, MA52, MA67, WS1, WS6, WS9, WS12, WS16, WS26, WS47, WS56, ZIM2, ZIM26, ZIM29, ZIM30, ZIM32, ZIM37, ZIM42 AND ZIM56).
FT VARIANT 153 153 K -> M (IN STRAINS BERKELEY, LA13, LA14, LA15, LA16, M01B, M08B, M040B, M052B, MA5, MA21, MA45, MA52, MA67, ZIM29, ZIM30, ZIM42 AND ZIM56).
FT VARIANT 214 214 E -> D (IN STRAIN MA7).
SQ SEQUENCE 234 AA; 27173 MW; 8954CD3215480F3E CRC64;

Query Match 68.5%; Score 37; DB 1; Length 234;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NYWEAY 8
| | | | |
DB 50 NYWFTY 55

RESULT 5
ID A29B_DROSI STANDARD; PRT; 234 AA.
AC Q90968;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE ACCESSORY GLAND PROTEIN ACP29AB PRECURSOR.
GN ACP29AB.
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99282496; PubMed=10353898;
RA Aguade M.;
RT "Positive selection drives the evolution of the Acp29AB accessory gland protein in Drosophila.";
RL Genetics 152:543-551(1999).
CC -!- FUNCTION: RESPONSIBLE FOR PHYSIOLOGICAL AND BEHAVIORAL CHANGES IN MATED FEMALE FLIES.
CC -!- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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CC -----
DR EMBL; M80435; AAA22037.1; -.
DR PIR; JS0593; JS0593.

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CC -----
DR EMBL; AJ240552; CAB53227.1; -.
DR FlyBase; FBgn007777; Dsim\Acp29AB.
DR InterPro; IPR001304; -.
DR Pfam; PF00059; lectin_c.1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Behavior; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 234 ACCESSORY GLAND PROTEIN ACP29AB.
FT DOMAIN 137 228 C-TYPE LECTIN (LONG FORM).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26915 MW; EB9C556E02EFED98 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 234;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NYWEAY 8
| | | | |
DB 50 NYWFTY 55

RESULT 6
ID PYG2_ANASP STANDARD; PRT; 246 AA.
AC P29987;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG2 (L-RC 28.5).
DE PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG2 (L-RC 28.5).
GN CPCG2
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
RX MEDLINE=92077441; PubMed=1743523;
RA Bryant D.A., Stirewalt V.L., Glauser M., Frank G., Sidler W., Zuber H.;
RT "A small multigene family encodes the rod-core linker polypeptides of Anabaena sp. PCC7120 phycobilisomes.";
RL Gene 107:91-99(1991).
CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SURUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM THE CORE.
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
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CC -----
DR EMBL; M80435; AAA22037.1; -.
DR PIR; JS0593; JS0593.

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DR InterPro: IPR001297; -  
 DR Pfam: PF00427; PBS\_linker\_poly; 1.  
 KW Phycobilisome; Photosynthesis; Multigene family.  
 FT INIT\_MET 0  
 SQ SEQUENCE 246 AA; 28520 MW; 19461DAD372F2DCA CRC64;

Query Match 68.5%; Score 37; DB 1; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNW 5  
 |||||  
 Db 176 YGNW 180

RESULT 7  
 ID PYG2\_MASLA STANDARD; PRT; 247 AA.  
 AC P29732;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE PHCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG2 (L-RC 28.7).  
 GN CPCG2.  
 OS Mastigocladus laminosus (Fischerella sp.).  
 OC Bacteria; Cyanobacteria; Stigonematales; Fischerella.  
 OX NCBI\_TaxID=1191;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=PCC 7603;  
 RX MEDLINE=92249337; PubMed=1577010;  
 RA Glauser M., Stirewalt V.L., Bryant D.A., Sidler W., Zuber H.;  
 RT "Structure of the genes encoding the rod-core linker polypeptides of  
 RT Mastigocladus laminosus phycobilisomes and functional aspects of the  
 RT phycobilliprotein/linker-polypeptide interactions.";  
 RL Eur. J. Biochem. 205:927-937(1992).  
 CC -1- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF  
 CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCABILISOMES  
 CC -1- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION  
 CC AND THE LOCATION OF THE DISC-SHAPED PHYCABILIPROTEIN UNITS WITHIN  
 CC THE PHYCABILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN  
 CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.  
 CC -1- SUBUNIT: THE PHYCABILISOME IS A HEMIDISCAL STRUCTURE THAT IS  
 CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT  
 CC CONTAINS PHYCABILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM  
 CC THE CORE.  
 CC -1- SIMILARITY: TO OTHER PHYCABILISOME LINKER PROTEINS.

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 -----  
 EMBL; X59763; CAA2434.1; -  
 DR PIR; S16059; S16059.  
 DR PIR; S23474; S23474.  
 DR InterPro: IPR001297; -  
 DR Pfam; PF00427; PBS\_linker\_poly; 1.  
 KW Phycobilisome; Photosynthesis; Multigene family.  
 SQ SEQUENCE 247 AA; 28707 MW; 5E183B4F1C2C77B8 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNW 5  
 |||||  
 Db 177 YGNW 181

RESULT 8  
 ID C761\_SOLME STANDARD; PRT; 467 AA.  
 AC P37121;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE CYTOCHROME P450 76A1 (EC 1.14.-.-) (CYPLXXVIA1) (P-450EG8) (FRAGMENT).  
 GN CYP76A1 OR CYP638.  
 OS Solanum melongena (Eggplant) (Aubergine).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
 OC Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4111;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=CV. SINSADOHARANASU; TISSUE=Hypocotyl;  
 RX MEDLINE=94032483; PubMed=8218411;  
 RA Toquri T., Kobayashi O., Umamoto N.;  
 RT "The cloning of eggplant seedling cDNAs encoding proteins from a  
 RT novel cytochrome P-450 family (CYP76).";  
 RL Biochim. Biophys. Acta 1216:165-169(1993).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 CC -----  
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 CC -----  
 EMBL; X71638; CAA50649.1; -  
 DR PIR; S38535; S38535.  
 DR InterPro: IPR001128; -  
 DR Pfam; PF00067; P450; 1.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Oxidoreductase; Monooxygenase; Heme; Multigene family.  
 FT NON\_TER 1  
 FT BINDING 410 410 HEME (BY SIMILARITY).  
 SQ SEQUENCE 467 AA; 53287 MW; D9A9B38DB5BF2108 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNW 5  
 |||||  
 Db 81 YGNW 85

RESULT 9  
 ID PAOX\_ARTGO STANDARD; PRT; 638 AA.  
 AC P46831;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE PHENYLETHYLAMINE OXIDASE PRECURSOR (EC 1.4.3.6) (AMINE OXIDASE).  
 OS Arthrobacter globiformis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.  
 OX NCBI\_TaxID=1665;  
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RP STRAIN=IFO 12137 / ATCC 8010;  
 RX MEDLINE=94197650; PubMed=8147851;  
 RA Tanizawa K., Matsuzaki R., Shimizu E., Yorifuji T., Fukui T.;  
 RT "Cloning and sequencing of phenylethylamine oxidase from Arthrobacter  
 RT globiformis and implication of Tyr-382 as the precursor to its

covalently bound quinone cofactor.";  
 RL Biochem. Biophys. Res. Commun. 199:1096-1102(1994).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 9-628.  
 RX MEDLINE=98070236; PubMed=9405045;  
 RA Wilce M.C., Dooley D.M., Freeman H.C., Guss J.M., Matsunami H.,  
 McIntire W.S., Ruggiero C.E., Tanizawa K., Yamaguchi H.;  
 RT "Crystal structures of the copper-containing amine oxidase from  
 Arthrobacter globiformis in the holo and apo forms: implications for  
 the biogenesis of topaquinoxine.";  
 RL Biochemistry 36:16116-16133(1997).  
 CC -1- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) -> RCHO + NH(3) +  
 H(2)O(2).  
 CC -1- COFACTOR: COPPER AND TOPAQUINONE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- INDUCTION: BY PHENETHYLAMINE.  
 CC -1- PTM: THE TOPA QUINONE IS GENERATED BY COPPER-DEPENDENT  
 AUTOXIDATION OF A SPECIFIC TYROSYL RESIDUE.  
 CC -1- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U03517; AAA18114.1;  
 DR PDB: 1AVK; 18-MAR-98.  
 DR PDB: 1AVL; 18-MAR-98.  
 DR PDB: 1AV4; 25-MAR-98.  
 DR InterPro: IPR000269;  
 DR Pfam: PF01179; Cu\_amine\_oxid; 1.  
 DR PROSITE: PS01164; COPPER\_AMINE\_OXID\_1; 1.  
 DR PROSITE: PS01165; COPPER\_AMINE\_OXID\_2; 1.  
 KW Oxidoreductase; copper; TPQ; 3D-structure.  
 FT PROPEP 1 2  
 FT CHAIN 3 638 PHENYLETHYLAMINE OXIDASE.  
 FT BINDING 382 382 TOPAQUINONE.  
 FT METAL 431 431 COPPER.  
 FT METAL 433 433 COPPER.  
 FT METAL 592 592 COPPER.  
 FT DISULFID 317 343  
 FT MUTAGEN 382 382 Y->F: LOSS OF ACTIVITY.  
 SQ SEQUENCE 638 AA; 70646 MW; 1800396BA7A983F2 CRC64;  
 Y->F: LOSS OF ACTIVITY.  
 Query Match 68.5%; Score 37; DB 1; Length 638;  
 Best Local Similarity 62.5%; Pred. No. 57;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YGNYWEAY 8  
 Db 384 YGFYWLY 391  
 ||| |  
 RESULT 10  
 ID AMOH\_ARTGO STANDARD; PRT; 683 AA.  
 AC Q59118;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HISTAMINE OXIDASE (EC 1.4.3.6) (COPPER AMINE OXIDASE).  
 OS Arthrobacter globiformis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.  
 OX NCBI\_TaxID=1665;  
 RN [1]  
 RC SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RP STRAIN-IFO 12137 / ATCC 8010;  
 RX MEDLINE=9518149; PubMed=7876243;

Choi Y.-H., Matsuzaki R., Fukui T., Shimizu E., Yorifuji T., Sato H.,  
 Ozaki Y., Tanizawa K.;  
 "Copper/topa quinone-containing histamine oxidase from Arthrobacter  
 globiformis. Molecular cloning and sequencing, overproduction of  
 precursor enzyme, and generation of topa quinone cofactor.";  
 J. Biol. Chem. 270:4712-4720(1995).  
 CC -1- FUNCTION: OXIDIZE HISTAMINE. OTHER AMINES INCLUDING  
 PHENETHYLAMINE, TYRAMINE, TRYPTAMINE, PUTRESCINE, AND BENZYLAMINE  
 ALSO SERVE AS SUBSTRATE.  
 CC -1- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) ->  
 RCHO + NH(3) + H(2)O(2).  
 CC -1- COFACTOR: COPPER AND TOPAQUINONE.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- INDUCTION: BY HISTAMINE.  
 CC -1- PTM: THE TOPA QUINONE IS GENERATED BY COPPER-DEPENDENT  
 AUTOXIDATION OF A SPECIFIC TYROSYL RESIDUE.  
 CC -1- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D38508; BAA07517.1;  
 DR HSP: P46881; 1AVL.  
 DR InterPro: IPR000269;  
 DR Pfam: PF01179; Cu\_amine\_oxid; 1.  
 DR PROSITE: PS01164; COPPER\_AMINE\_OXID\_1; 1.  
 DR PROSITE: PS01165; COPPER\_AMINE\_OXID\_2; FALSE\_NEG.  
 KW Oxidoreductase; copper; TPQ.  
 FT INIT\_MET 0 0  
 FT BINDING 401 401 TOPAQUINONE.  
 FT METAL 450 450 COPPER (POTENTIAL).  
 FT METAL 452 452 COPPER (POTENTIAL).  
 FT METAL 611 611 COPPER (POTENTIAL).  
 SQ SEQUENCE 683 AA; 74979 MW; 233C46C017201AA0 CRC64;  
 Query Match 68.5%; Score 37; DB 1; Length 683;  
 Best Local Similarity 62.5%; Pred. No. 60;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YGNYWEAY 8  
 Db 403 YGFYWLY 410  
 ||| |  
 RESULT 11  
 ID BGAL\_DIACA STANDARD; PRT; 731 AA.  
 AC Q00662;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE PUTATIVE BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE)  
 DE (SR12 PROTEIN).  
 OS CARSR12.  
 OS Dianthus caryophyllus (Carnation) (Clove pink).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales;  
 OC Caryophyllaceae; Caryophyllaceae; Dianthus.  
 OX NCBI\_TaxID=3570;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. WHITE SIM; TISSUE=Petal;  
 RX MEDLINE=91329738; PubMed=1868223;  
 RA Raghothama K.G., Lawton K.A., Goldsbrough P.B., Woodson W.R.;  
 "Characterization of an ethylene-regulated flower senescence-related  
 gene from carnation.";  
 Plant Mol. Biol. 17:61-71(1991).



CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-  
 CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.  
 CC -1- TISSUE SPECIFICITY: SNEESCING FLOWER PETALS.  
 CC -1- INDUCTION: REGULATED BY THE PHYTHORMONE ETHYLENE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X57171; CAA40459.1; -;  
 CC DR EMBL; S16595; S16595.  
 CC DR InterPro; IPR001944; -;  
 CC DR Pfam; PF01301; Glyco\_hydro\_35; 1.  
 CC DR PRINTS; PR00742; GLHYDRLASE35.  
 CC DR PROSITE; PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
 CC KW Hydrolase; Glycosidase; Signal.  
 CC FT CHAIN 1 29 POTENTIAL.  
 CC FT ACT\_SITE 30 731 PUTATIVE BETA-GALACTOSIDASE.  
 CC FT ACT\_SITE 187 187 PROTON DONOR (POTENTIAL).  
 CC FT ACT\_SITE 257 257 NUCLEOPHILE (POTENTIAL).  
 CC SQ SEQUENCE 731 AA; 82864 MW; 83FA8B5A3779C051 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 731;  
 Best Local Similarity 62.5%; Pred. No. 64;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNWYFAY 8  
 ||| |:  
 Db 28 YGNWYDY 35

RESULT 12  
 LAC2\_NEUCR STANDARD; PRT; 619 AA.  
 AC P06811;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE LACCASE PRECURSOR (EC 1.10.3.2) (BENZENEDIOL-OXYGEN OXIDOREDUCTASE)  
 DE (URISHIOL OXIDASE) (ALLELE OR).  
 GN LACC.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RX MEDLINE=88087214; PubMed=2961749;  
 RA Hermann U.A., Mueller G., Hunziker P.E., Lerch K.;  
 RT "Characterization of two allelic forms of Neurospora crassa laccase.  
 RT Amino- and carboxyl-terminal processing of a precursor.";  
 RL J. Biol. Chem. 263:885-896(1988).  
 RN [2]  
 RX MEDLINE=87067412; PubMed=2947240;  
 RA Hermann U.A., Lerch K.;  
 RT "Isolation and partial nucleotide sequence of the laccase gene from  
 RT Neurospora crassa: amino acid sequence homology of the protein to  
 RT human ceruloplasmin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).  
 CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED  
 CC PRODUCTS (PROBABLE).  
 CC -1- CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE +  
 CC 2 H(2)O.  
 CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU  
 CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE  
 CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.  
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M14554; AAA33590.1; -;  
 CC DR EMBL; M18333; AAA33591.1; -;  
 CC DR PIR; A28523; KSNGLD.  
 CC DR PIR; A29762; A29762.  
 CC DR InterPro; IPR001117; -;  
 CC DR Pfam; PF00394; Cu-oxidase; 2.  
 CC DR PROSITE; PS00079; MULTICOPPER\_OXIDASE1; 1.  
 CC DR PROSITE; PS00080; MULTICOPPER\_OXIDASE2; 1.  
 CC KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;  
 CC Glycoprotein; Repeat.  
 CC FT SIGNAL 1 21 POTENTIAL.  
 CC FT PROPEP 22 49  
 CC FT CHAIN 50 606 LACCASE.  
 CC FT PROPEP 607 619  
 CC FT DOMAIN 84 207 PLASTOCYANIN-LIKE 1.  
 CC FT DOMAIN 216 373 PLASTOCYANIN-LIKE 2.  
 CC FT DOMAIN 431 566 PLASTOCYANIN-LIKE 3.  
 CC FT METAL 144 144 COPPER (TYPE 2) (PROBABLE).  
 CC FT METAL 146 146 COPPER (TYPE 3) (PROBABLE).  
 CC FT METAL 189 189 COPPER (TYPE 3) (PROBABLE).  
 CC FT METAL 191 191 COPPER (TYPE 1) (PROBABLE).  
 CC FT METAL 477 477 COPPER (TYPE 2) (PROBABLE).  
 CC FT METAL 480 480 COPPER (TYPE 3) (PROBABLE).  
 CC FT METAL 548 548 COPPER (TYPE 1) (PROBABLE).  
 CC FT METAL 549 549 COPPER (TYPE 3) (PROBABLE).  
 CC FT METAL 550 550 COPPER (TYPE 1) (PROBABLE).  
 CC FT METAL 554 554 COPPER (TYPE 1) (PROBABLE).  
 CC FT METAL 559 559 COPPER (TYPE 1) (PROBABLE).  
 CC FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SQ SEQUENCE 619 AA; 68198 MW; FDE6D78B65048E3 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 619;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6  
 |||||  
 Db 335 GNYWF 339

RESULT 13  
 LAC2\_NEUCR STANDARD; PRT; 619 AA.  
 AC P10574;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE LACCASE PRECURSOR (EC 1.10.3.2) (BENZENEDIOL-OXYGEN OXIDOREDUCTASE)  
 DE (URISHIOL OXIDASE) (ALLELE TS).  
 GN LACC.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Sordariaceae; Neurospora.

NCBI\_TaxID=5141;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=88087214; PubMed=2961749;  
Germann U.A., Mueller G., Hunziker P.E., Lerch K.;  
RA "Characterization of two allelic forms of Neurospora crassa laccase."  
RT Amino- and carboxyl-terminal processing of a precursor.";  
RL J. Biol. Chem. 263:885-896(1988).  
CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED  
CC PRODUCTS (PROBABLE).  
CC -!- CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE +  
CC 2 H(2)O.  
CC -!- COFACTOR: BINDS 4 CU-TONS PER MOLECULE. THREE DISTINCT CU  
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE  
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).  
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.  
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.  
-----  
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or send an email to license@isb-sib.ch).  
-----  
EMBL; M18334; AAA33592.1; -.  
PIR; B28523; KGNCLE.  
InterPro; IPR001117; -.  
DR InterPro; IPR002355; -.  
DR Pfam; PF00394; Cu-oxidase; 2.  
DR PROSITE; PS00079; MULTICOPPER\_OXIDASE1; 1.  
DR PROSITE; PS00080; MULTICOPPER\_OXIDASE2; 1.  
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;  
KW Glycoprotein; Repeat.  
FT SIGNAL 1 21 POTENTIAL.  
FT FT PROPEP 22 49  
FT FT CHAIN 50 606 LACCASE.  
FT FT PROPEP 607 619  
FT DOMAIN 84 207  
FT DOMAIN 216 373 PLASTOCYANIN-LIKE 1.  
FT DOMAIN 431 566 PLASTOCYANIN-LIKE 3.  
FT METAL 144 144 COPPER (TYPE 2) (PROBABLE).  
FT METAL 146 146 COPPER (TYPE 3) (PROBABLE).  
FT METAL 189 189 COPPER (TYPE 3) (PROBABLE).  
FT METAL 191 191 COPPER (TYPE 3) (PROBABLE).  
FT METAL 477 477 COPPER (TYPE 3) (PROBABLE).  
FT METAL 480 480 COPPER (TYPE 1) (PROBABLE).  
FT METAL 482 482 COPPER (TYPE 2) (PROBABLE).  
FT METAL 548 548 COPPER (TYPE 3) (PROBABLE).  
FT METAL 549 549 COPPER (TYPE 3) (PROBABLE).  
FT METAL 550 550 COPPER (TYPE 3) (PROBABLE).  
FT METAL 554 554 COPPER (TYPE 1) (PROBABLE).  
FT METAL 559 559 COPPER (TYPE 1) (PROBABLE).  
FT CARBOHYD 139 139 N-LINKED (GLCNAC .) (POTENTIAL).  
FT CARBOHYD 282 282 N-LINKED (GLCNAC .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC .) (POTENTIAL).  
FT CARBOHYD 340 340 N-LINKED (GLCNAC .) (POTENTIAL).  
FT CARBOHYD 422 422 N-LINKED (GLCNAC .) (POTENTIAL).  
FT CARBOHYD 444 444 N-LINKED (GLCNAC .) (POTENTIAL).  
SQ SEQUENCE 619 AA; 68120 MW; 0BB6CCDE18841145 CRC64;

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Query Match      66.7%; Score 36; DB 1; Length 619;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GNYWF 6
Db      335 GNYWF 339

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RESULT	ID	LAC2_PODAN	STANDARD;	PRT;	621 AA.
AC	P78722;				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	LACCASE II PRECURSOR (EC 1.10.3.2) (BENZENEDIOL:OXYGEN OXIDOREDUCTASE)				
DE	(IRISHTOL OXIDASE) (DIPHENOL OXIDASE) (LACCASE-C).				
GN	LAC2.				
OS	Podospora anserina.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Sordariales; Sordariaceae; Podospora.				
OX	NCBI_TaxID=5145;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 26003;				
RX	MEDLINE=97071669; PubMed=8914515;				
RA	Fernandez-Larrea J., Stahl U.;				
RT	"Isolation and characterization of a laccase gene from Podospora				
RT	anserina".;				
RL	Mol. Gen. Genet. 252:539-551(1996).				
CC	-1- FUNCTION: PROBABLY INVOLVED IN LIGNIN DEGRADATION AND IN THE				
CC	DETIFICATION OF LIGNIN-DERIVED PRODUCTS IN ITS NATURAL HABITAT				
CC	(HERBIVOROUS DUNG), WHICH IS RICH IN LIGNIN OF GRASSES AND STRAW.				
CC	PROBABLY INVOLVED IN MELANIN SYNTHESIS AND IN PERITHECIA				
CC	DEVELOPMENT.				
CC	-1- CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE +				
CC	2 H(2)O.				
CC	-1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU				
CC	CENTERS KNOWN AS TYPE I OR BLUE, TYPE 2 OR NORMAL, AND TYPE				
CC	3 OR COUPLED BINUCLEAR (BY SIMILARITY).				
CC	-1- SUBUNIT: MONOMER.				
CC	-1- SUBCELLULAR LOCATION: SECRETED.				
CC	-1- DEVELOPMENTAL STAGE: LOW BASIC LEVELS THROUGHOUT THE GROWTH PHASE;				
CC	INCREASES AT LEAST 20-FOLD AT THE BEGINNING OF THE AUTOLYTIC PHASE				
CC	AND DECREASES AGAIN THEREAFTER.				
CC	-1- INDUCTION: UNDER OXIDATIVE STRESS ON THE MYCELIUM BY AROMATIC				
CC	XENOBIOICS (GUAIACOL, HYDROQUINONE, BENZOQUINONE), AND BY COPPER				
CC	SALT AT A CONCENTRATION OF 1MM (GROWING MYCELIUM).				
CC	-1- PTM: LACCASE II IS PROCESSED AT BOTH ITS N-TERMINUS AND ITS C-				
CC	TERMINUS.				
CC	-1- MISCELLANEOUS: PODOSPORA ANSERINA CONTAINS AT LEAST 3 LACCASE				
CC	ISOZYMES NAMED I, II, AND III. THEY DIFFER IN THEIR SUBSTRATE				
CC	SPECIFICITY, NUMBER OF SUBUNITS, ISOELECTRONIC POINT AND HEAT				
CC	STABILITY.				
CC	-1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.				
CC	-1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.				
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CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL; Y08827; CAA70061.1; -				
DR	InterPro; IPR001117; -				
DR	InterPro; IPR002355; -				
DR	Pfam; PF00394; Cu-oxidase; 2.				
DR	PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.				
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.				
KW	Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;				
KW	Lignin degradation; Melanin biosynthesis; Multigene family.				
FT	SIGNAL 1 23 POTENTIAL.				
FT	PROPEP 24 48 POTENTIAL.				
FT	CHAIN 49 605 LACCASE II.				
FT	PROPEP 606 621 POTENTIAL.				
FT	DOMAIN 78 201 PLASTOCYANIN-LIKE 1.				
FT	DOMAIN 210 367 PLASTOCYANIN-LIKE 2.				
FT	DOMAIN 430 566 PLASTOCYANIN-LIKE 3.				
FT	DOMAIN 138 138 COPPER(TYPE 2) (BY SIMILARITY).				
FT	METAL				

```

CC EMBL; M18683; AAA30683.1; -
DR PIR; A40063; URBOAP.
DR InterPro; IPR000323; -
DR InterPro; IPR000720; -
DR InterPro; IPR001258; -
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF01436; NHL; 4.
DR PRINTS; PR00790; PAMONOXGNASE.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_2; 1.
DR PROSITE; PS00085; CU2_MONOOXYGENASE; 1.
KW Oxidoreductase; Monooxygenase; Copper; Vitamin C; Transmembrane;
KW Glycoprotein; Phosphorylation; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 30 POTENTIAL.
FT CHAIN 31 972 PEPTIDYL-GLYCINE-ALPHA-AMIDATING
MONOOXYGENASE.
FT DOMAIN 31 873 INTRAGRANULAR (POTENTIAL).
FT TRANSMEM 874 897 POTENTIAL.
FT DOMAIN 898 972 CYTOPLASMIC (POTENTIAL).
FT METAL 237 237 COPPER (POTENTIAL).
FT METAL 239 239 COPPER (POTENTIAL).
FT METAL 240 240 COPPER (POTENTIAL).
FT METAL 359 359 COPPER (POTENTIAL).
FT METAL 361 361 COPPER (POTENTIAL).
FT METAL 362 362 COPPER (POTENTIAL).
FT CARBOHYD 762 762 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 972 AA; 108176 MW; 8BD41F83E341BAF1 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 621;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6
DB 329 GNYWF 333

RESULT 15
AMD_BOVIN
ID AND_BOVIN STANDARD; PRT; 972 AA.
AC P10731;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR
DE (EC 1.14.17.3) (PAM).
GN PAM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Plutitary;
RX MEDLINE=91042563; PubMed=3153462;
RA Elpper B.A., Park L.P., Dickerson I.M., Keutmann H.T., Thiele E.A.,
RA Rodriguez H., Schofield P.R., Mains R.E.;
RT "Structure of the precursor to an enzyme mediating COOH-terminal
amidation in peptide biosynthesis."
RL Mol. Endocrinol. 1:777-790(1987).
CC -1- FUNCTION: C-TERMINAL ALPHA-AMIDATION OF PEPTIDES.
CC -1- CATALYTIC ACTIVITY: PEPTIDYLGLYCINE + ASCORBATE + O(2) =
PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)O.
CC (THE PRODUCT IS UNSTABLE AND DISMUTATES TO GLYOXYLATE AND THE
CORRESPONDING DESGLYCINE PEPTIDE AMIDE).
CC -1- COFACTOR: COPPER, AND ASCORBATE.
CC -1- SUBCELLULAR LOCATION: SECRETORY GRANULES.
CC -1- SIMILARITY: BELONGS TO THE COPPER TYPE II, ASCORBATE-DEPENDENT
MONOOXYGENASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC EMBL; M18683; AAA30683.1; -
DR PIR; A40063; URBOAP.
DR InterPro; IPR000323; -
DR InterPro; IPR000720; -
DR InterPro; IPR001258; -
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF01436; NHL; 4.
DR PRINTS; PR00790; PAMONOXGNASE.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_2; 1.
DR PROSITE; PS00085; CU2_MONOOXYGENASE; 1.
KW Oxidoreductase; Monooxygenase; Copper; Vitamin C; Transmembrane;
KW Glycoprotein; Phosphorylation; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 30 POTENTIAL.
FT CHAIN 31 972 PEPTIDYL-GLYCINE-ALPHA-AMIDATING
MONOOXYGENASE.
FT DOMAIN 31 873 INTRAGRANULAR (POTENTIAL).
FT TRANSMEM 874 897 POTENTIAL.
FT DOMAIN 898 972 CYTOPLASMIC (POTENTIAL).
FT METAL 237 237 COPPER (POTENTIAL).
FT METAL 239 239 COPPER (POTENTIAL).
FT METAL 240 240 COPPER (POTENTIAL).
FT METAL 359 359 COPPER (POTENTIAL).
FT METAL 361 361 COPPER (POTENTIAL).
FT METAL 362 362 COPPER (POTENTIAL).
FT CARBOHYD 762 762 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 972 AA; 108176 MW; 8BD41F83E341BAF1 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 972;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6
DB 116 GNYWF 120
```

Search completed: June 28, 2001, 15:54:35  
Job time: 123 sec

Fri Jun 29 08:05:24 2001

us-09-724-406-8.rsp

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Page 10

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:19 ; Search time 411.58 Seconds  
(without alignments)  
2.572 Million cell updates/sec

Title: US-09-724-406-8  
Perfect score: 54  
Sequence: 1 YGNVWFA 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16.\*  
1: sp.archaea.\*  
2: sp.bacteria.\*  
3: sp.fungi.\*  
4: sp.human.\*  
5: sp.invertebrate.\*  
6: sp.mammal.\*  
7: sp.mhc.\*  
8: sp.organelle.\*  
9: sp.phage.\*  
10: sp.plant.\*  
11: sp.rodent.\*  
12: sp.unclassified.\*  
13: sp.vertebrate.\*  
14: sp.virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	72.2	115	9 Q38444	Q38444 bacteriophage
2	39	72.2	519	2 Q9RG14	Q9RG14 bacterioides
3	39	72.2	520	14 Q41104	Q41104 parametrium
4	38	70.4	151	2 Q47630	Q47630 escherichia
5	38	70.4	151	2 Q85635	Q85635 escherichia
6	38	70.4	246	14 Q9YW87	Q9YW87 melanopius
7	38	70.4	398	1 Q59482	Q59482 pyrococcus
8	38	70.4	491	2 Q9L6S4	Q9L6S4 salmonella
9	38	70.4	552	3 Q9URZ3	Q9URZ3 schizosacch
10	38	70.4	732	10 Q9SKE1	Q9SKE1 arabidopsis
11	38	70.4	790	10 Q9M371	Q9M371 arabidopsis
12	37	68.5	115	8 Q9TE75	Q9TE75 echinococcus
13	37	68.5	229	5 Q9GPE5	Q9GPE5 drosophila
14	37	68.5	229	5 Q9GPE4	Q9GPE4 drosophila
15	37	68.5	229	5 Q9GNI1	Q9GNI1 drosophila
16	37	68.5	229	5 Q9GN93	Q9GN93 drosophila
17	37	68.5	229	5 Q9GN92	Q9GN92 drosophila
18	37	68.5	331	4 Q99729	Q99729 homo sapien
19	37	68.5	331	11 Q88311	Q88311 rattus norv

20	37	68.5	332	11 Q9QX81	Q9QX81 rattus norv
21	37	68.5	495	10 Q98183	Q98183 catharanta
22	37	68.5	499	10 Q9SWE3	Q9SWE3 nicotiana t
23	36.5	67.6	382	10 Q9SN20	Q9SN20 arabidopsis
24	36	66.7	225	5 Q90950	Q90950 caenorhabdi
25	36	66.7	267	10 Q9FYA1	Q9FYA1 arabidopsis
26	36	66.7	279	1 Q9HNGO	Q9HNGO halobacteri
27	36	66.7	361	1 Q30197	Q30197 archaeoglob
28	36	66.7	400	1 Q26432	Q26432 methanobact
29	36	66.7	592	4 Q9NP91	Q9NP91 homo sapien
30	36	66.7	616	11 Q64093	Q64093 rattus norv
31	36	66.7	635	11 Q88575	Q88575 mus musculu
32	35	64.8	101	2 P95154	P95154 mycobacteri
33	35	64.8	119	9 Q80057	Q80057 bacterioph
34	35	64.8	238	10 Q81922	Q81922 capsicum an
35	35	64.8	289	2 Q9JIV2	Q9JIV2 neisseria m
36	35	64.8	289	2 Q9JIV2	Q9JIV2 neisseria m
37	35	64.8	302	2 Q32179	Q32179 bacillus su
38	35	64.8	310	2 Q9RW55	Q9RW55 deinococcus
39	35	64.8	310	2 Q9EXF1	Q9EXF1 listeria mo
40	35	64.8	319	2 Q9KB18	Q9KB18 bacillus ha
41	35	64.8	376	10 Q9FVH5	Q9FVH5 prunus arme
42	35	64.8	407	2 Q9KIV1	Q9KIV1 streptomyce
43	35	64.8	437	3 Q99036	Q99036 trichoderma
44	35	64.8	453	2 Q9ZDV3	Q9ZDV3 rickettsia
45	35	64.8	496	9 Q9MBP0	Q9MBP0 staphylococ

## ALIGNMENTS

RESULT 1  
Q38444 PRELIMINARY; PRT; 115 AA.  
ID Q38444;  
AC Q38444;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE ORF2.  
OS Bacteriophage T5.  
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.  
OX NCBI\_TaxID=10726;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86192453; PubMed=3516691;  
RA Shlyapnikov M.G.; Ksenzenko V.N.; Kryukov V.M.; Bayev A.A.;  
RT "Nucleotide sequence of the bacteriophage T5 DNA fragment which contains the gene for trNA<sup>asp</sup>.";  
RL Eur. J. Biochem. 156:285-289(1986).  
DR EMBL; X03798; CAA27425.1; -.  
SQ SEQUENCE 115 AA; 13375 MW; AF2864283F53BC11 CRC64;

Query Match 72.2%; Score 39; DB 9; Length 115;  
Best Local Similarity 85.7%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGNVWFA 7  
Db 67 YGNVWFA 73

RESULT 2  
Q9RG14 PRELIMINARY; PRT; 519 AA.  
ID Q9RG14;  
AC Q9RG14;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 61.2 KDA PROTEIN.  
OS Bacterioides fragilis.  
OC Bacteria; CFB group; Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=817;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-638R;  
 RX MEDLINE-99429872; PubMed=10498737;  
 RA Comstock L.E., Coyne M.J., Tzianabos A.O., Kasper D.L.;  
 RT "Interstrain variation of the polysaccharide B biosynthesis locus of  
 RT Bacteroides fragilis: Characterization of the region from strain  
 RT 638R.";  
 RL J. Bacteriol. 181:6192-6196(1999).  
 DR EMBL; AF125164; AAD56750.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 519 AA; 61151 MW; CFF7FC629006A741 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 519;  
 Best Local Similarity 83.3%; Pred. No. 79;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6  
 Db 289 FGNYWF 294  
 :|||||

RESULT 3  
 O41104 PRELIMINARY; PRT; 520 AA.  
 ID O41104;  
 AC O41104;  
 DT 01-JAN-1998 (TRENBLrel. 05, Created)  
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
 DE A622L PROTEIN.  
 GN A622L.  
 OS Parametrium bursaria chlorella virus 1 (PBCV-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.  
 OX NCBI\_TaxID=10506;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98022962; PubMed=9356347;  
 RA Li Y., Lu Z., Sun L., Ropp S., Kutish G.F., Rock D.L., Van Etten J.L.;  
 RT "Analysis of 74 kb of DNA located at the right end of the 330-kb  
 RT chlorella virus PBCV-1 genome.";  
 RL Virology 237:360-377(1997).  
 DR EMBL; U42580; AAC96953.1; -;  
 SQ SEQUENCE 520 AA; 58097 MW; OCC143D64C1640D7 CRC64;

Query Match 72.2%; Score 39; DB 14; Length 520;  
 Best Local Similarity 62.5%; Pred. No. 79;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWF 8  
 Db 107 YNNYWTY 114  
 :|||||

RESULT 4  
 Q47630 PRELIMINARY; PRT; 151 AA.  
 ID Q47630;  
 AC Q47630;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
 DE SEPD.  
 GN SEPD.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-E2348/69, (ENTEROPATHOGENIC E. COLI, LEE);  
 RX MEDLINE-95372406; PubMed=7644527;  
 RA Jarvis K.G., Giron J.A., Jerse A.E., McDaniel T.K., Sonnenberg M.S.,

RA Kaper J.B.;  
 RT "Enteropathogenic Escherichia coli contains a putative type III  
 RT secretion system necessary for the export of proteins involved in  
 RT attaching and effacing lesion formation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7996-8000(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Elliott S.J., Wainwright L.A., McDaniel T.K., Jarvis K.G., Deng Y.K.,  
 RA Lai L.C., McNamara B.P., Sonnenberg M.S., Kaper J.B.;  
 RL Mol. Microbiol. 0:0-0(1998).  
 DR EMBL; Z49972; CAA90273.1; -;  
 DR EMBL; AF022336; AAC38378.1; -;  
 SQ SEQUENCE 151 AA; 17563 MW; A100D54677FDF89B CRC64;

Query Match 70.4%; Score 38; DB 2; Length 151;  
 Best Local Similarity 62.5%; Pred. No. 31;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWF 8  
 Db 45 FGNYWVLY 52  
 :|||||

RESULT 5  
 O85635 PRELIMINARY; PRT; 151 AA.  
 ID O85635;  
 AC O85635;  
 DT 01-NOV-1998 (TRENBLrel. 08, Created)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
 DE L0040.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-EDL933.  
 RX MEDLINE-98339885; PubMed=9673266;  
 RA Perna N.T., Mayhew G.F., Posfai G., Elliott S., Sonnenberg M.S.,  
 RA Kaper J.B., Blattner F.R.;  
 RT "Molecular evolution of a pathogenicity island from enterohemorrhagic  
 RT Escherichia coli O157:H7.";  
 RL Infect. Immun. 66:3810-3817(1998).  
 DR EMBL; AF071034; AAC31519.1; -;  
 SQ SEQUENCE 151 AA; 17561 MW; A11A6F09942B6774 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 151;  
 Best Local Similarity 62.5%; Pred. No. 31;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWF 8  
 Db 45 FGNYWVLY 52  
 :|||||

RESULT 6  
 Q9YW87 PRELIMINARY; PRT; 246 AA.  
 ID Q9YW87;  
 AC Q9YW87;  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE ORF MSV005 HYPOTHETICAL PROTEIN.  
 GN MSV005.  
 OS Melanoplus sanguinipes entomopoxvirus (MsePV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
 OC Entomopoxvirus B.  
 OX NCBI\_TaxID=83191;  
 RN [1]  
 RP SEQUENCE FROM N.A.

Fri Jun 29 08:05:25 2001

us-09-724-406-8.rspt

RC STRAIN-TUCSON;  
RA MEDLINE-99102612; PubMed-9847359;  
RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;  
RT "The genome of Melanoplus sanguinipes entomopoxvirus";  
RL J. Virol. 73:533-552(1999).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP  
RC STRAIN-TUCSON;  
RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF063866; AAC97860.1; -  
SQ SEQUENCE 246 AA; 30090 MW; 098823A3E5D28ACB CRC64;

Query Match 70.4%; Score 38; DB 14; Length 246;  
Best Local Similarity 62.5%; Pred. No. 52;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8  
||| |||  
Db 230 YGYWYIY 237

RESULT 7  
ID O59482 PRELIMINARY; PRT; 398 AA.  
AC O59482;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE HYPOTHETICAL 44.8 KDA PROTEIN PH1818.  
GN PH1818.  
OS Pyrococcus horikoshii.  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
OX NCBI\_TaxID=53953;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN-OT3;  
RC MEDLINE-98341137; PubMed-9679194;  
RA Kawarabayashi Y., Savada M., Horikawa H., Haikawa Y., Hino Y.,  
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
RA Masuchi Y., Shizuya H., Kikuchi H.;  
RT "Complete sequence and gene organization of the genome of a hyper-  
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
RL DNA Res. 5:55-76(1998).  
DR EMBL; AP000007; BAA30937.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 398 AA; 44808 MW; 7A33583CCE449AA2 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 398;  
Best Local Similarity 83.3%; Pred. No. 87;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6  
|||||  
Db 365 YGNYWVI 370

RESULT 8  
ID Q9L6S4 PRELIMINARY; PRT; 491 AA.  
AC Q9L6S4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE S. TYPHIMURIUM KETOL-ACID REDUCTOISOMERASE (ILVC) (SP:P05989),  
CONTAINS SIMILARITY TO PFAM FAMILY PF01450 (ACETOHYDROXY ACID  
ISOMEROREDUCTASE), SCORE=628.8, E=3.1E-185, N=1.  
GN ILVC.

OS Salmonella typhimurium LT2.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
OX NCBI\_TaxID=99287;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN-SGSC1412;  
RC  
RA Washu;  
RT "The Salmonella typhimurium Genome Sequencing Project";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN-SGSC1412;  
RC  
RA Waterston R.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF233324; AAF33476.1; -  
DR InterPro; IPR000506; -  
DR Pfam; PF01450; ILVC; 1.  
KW Isomerase.  
SQ SEQUENCE 491 AA; 53941 MW; 4080B60E1B9658F0 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 491;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8  
||||| |||  
Db 419 YGNLYFSY 426

RESULT 9  
ID Q9URZ3 PRELIMINARY; PRT; 552 AA.  
AC Q9URZ3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE AMINO-ACID PERMEASE.  
GN SPAC69.10C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=972H-;  
RC Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL132779; CAB60020.1; -  
DR InterPro; IPR003027; -  
DR InterPro; IPR003293; -  
DR Pfam; PF003324; aa\_permeases; 1.  
DR PROSITE; PS00213; AMINO-ACID-PERMEASE; 1.  
SQ SEQUENCE 552 AA; 61119 MW; BF067D5A8172E1A5 CRC64;

Query Match 70.4%; Score 38; DB 3; Length 552;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NYWFAY 8  
|||: |||  
Db 127 NYWYAY 132

RESULT 10  
ID Q9SKE1 PRELIMINARY; PRT; 732 AA.  
AC Q9SKE1;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE AT2G46380 PROTEIN.  
 GN AT2G46380.  
 OS Arabidopsis thaliana (Mouse-ear cross).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhagen G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,  
 RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana.";  
 RL Nature 402:761-768(1999).  
 DR EMBL; AC006526; RAD23041.1; -.  
 SQ SEQUENCE 732 AA; 81362 MW; B8DEFCE759A00C9 CRC64;

Query Match 70.4%; Score 38; DB 10; Length 732;  
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNYWFAY 8  
 : : : :  
 Db 634 GNYWDY 640

RESULT 11  
 Q9M371 ID Q9M371 PRELIMINARY; PRT; 790 AA.  
 AC Q9M371;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HYPOTHETICAL 87.4 KDA PROTEIN.  
 GN F15G16.60.  
 OS Arabidopsis thaliana (Mouse-ear cross).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X., Quetier F., Salanoubat M.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; ALI32959; CAB71097.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 790 AA; 87375 MW; B222724B75690F30 CRC64;

Query Match 70.4%; Score 38; DB 10; Length 790;  
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNYWFAY 8  
 : : : :  
 Db 675 GNYWDY 681

RESULT 12  
 Q9TE75 ID Q9TE75 PRELIMINARY; PRT; 229 AA.

ID Q9TE75 PRELIMINARY; PRT; 115 AA.  
 AC Q9TE75;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE NADH DEHYDROGENASE SUBUNIT 3.  
 GN ND3.  
 OS Echinococcus multilocularis.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;  
 OC Cestoda; Eucestoda; Cyclophyllidae; Taeniidae; Echinococcus.  
 OX NCBI\_TaxID=6211;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fukunaga M.;  
 RT "Echinococcus multilocularis mitochondrial DNA sequence.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB018440; BAA84934.2; -.  
 DR InterPro: IPR000440; -.  
 DR Pfam: PF00507; oxidored\_q4; 1.  
 KW Mitochondrion.  
 SQ SEQUENCE 115 AA; 13770 MW; 6FFDE02CB8BE9C02 CRC64;

Query Match 68.5%; Score 37; DB 8; Length 115;  
 Best Local Similarity 50.0%; Pred. No. 33;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8  
 : : : :  
 Db 85 FGNEWYY 92

RESULT 13  
 Q9GPE5 ID Q9GPE5 PRELIMINARY; PRT; 229 AA.  
 AC Q9GPE5;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE ACP29 (FRAGMENT).  
 GN ACP29.  
 OS Drosophila simulans (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7240;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SIM7;  
 RA Begun D., Whitely P., Todd B., Waldrup H., Clark A.;  
 RT "Molecular population genetics of male accessory gland proteins in  
 RT Drosophila.";  
 RL Genetics 0:0-0(2001).  
 DR EMBL; AY010653; AAG37405.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 229 229  
 SQ SEQUENCE 229 AA; 26335 MW; 199E3332ADC21997 CRC64;

Query Match 68.5%; Score 37; DB 5; Length 229;  
 Best Local Similarity 83.3%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NYWFAY 8  
 : : : :  
 Db 45 NYWFTY 50

RESULT 14  
 Q9GPE4 ID Q9GPE4 PRELIMINARY; PRT; 229 AA.  
 AC Q9GPE4;



us-09-724-406-8.rspt

Fri Jun 29 08:05:25 2001

01-MAR-2001 (TREMBlrel. 16, Created)  
 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 ACP29 (FRAGMENT).  
 ACP29.  
 Drosophila simulans (Fruit fly).  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7240;  
 RN [1]  
 SEQUENCE FROM N.A.  
 STRAIN-SIM8;  
 RA Begun D., Whitley P., Todd B., Waldrip H., Clark A.;  
 RT "Molecular population genetics of male accessory gland proteins in  
 Drosophila."  
 RL Genetics 0:0-0(2001).  
 DR EMBL; AY010654; AAG37406.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 229  
 SQ SEQUENCE 229 AA; 26320 MW; 2E824E1B4A5C6858 CRC64;

Query Match 68.5%; Score 37; DB 5; Length 229;  
 Best Local Similarity 83.3%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 NYWFAY 8  
 Db 45 NYWFY 50

RESULT 15  
 Q9GNI1 PRELIMINARY; PRT; 229 AA.  
 AC Q9GNI1; 2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE ACP29 (FRAGMENT).  
 GN ACP29.  
 OS Drosophila simulans (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7240;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SIM8, AND SIM4;  
 RA Begun D., Whitley P., Todd B., Waldrip H., Clark A.;  
 RT "Molecular population genetics of male accessory gland proteins in  
 Drosophila."  
 RL Genetics 0:0-0(2001).  
 DR EMBL; AY010652; AAG37404.1; -.  
 DR EMBL; AY010650; AAG37402.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 229  
 SQ SEQUENCE 229 AA; 26333 MW; 199E333C33BFF097 CRC64;

Query Match 68.5%; Score 37; DB 5; Length 229;  
 Best Local Similarity 83.3%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 NYWFAY 8  
 Db 45 NYWFY 50

Search completed: June 28, 2001, 16:08:20  
 Job time: 948 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:35 ; Search time 362.28 Seconds  
(\*without alignments)  
2.510 Million cell updates/sec

Title: US-09-724-406-12  
Perfect score: 78  
Sequence: 1 KASQSVDFDGSYMN 15

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 50623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	96.2	15	AA70195	MAB 3B9 light chain
2	75	96.2	15	AA70195	Anti-Fas MAB HFE7A
3	75	96.2	15	AA70195	CDR of the light chain
4	75	96.2	15	AA70195	Mouse anti-Fas ant
5	75	96.2	15	AA70195	Murine anti-Fas ant
6	75	96.2	15	AA70195	Antibody 4H5 L cha
7	75	96.2	15	AA70195	Murine CD4/CD34 re
8	75	96.2	15	AA70195	Antibody 4H5 L cha
9	75	96.2	15	AA70195	Murine derived pro
10	75	96.2	103	AA70195	
11	75	96.2	103	AA70195	

12	75	96.2	106	AA70195	MaE15 light chain.
13	75	96.2	106	AA70195	Light chain amino
14	75	96.2	111	AA70195	Immunoglobulin L c
15	75	96.2	111	AA70195	MaE11 light chain.
16	75	96.2	111	AA70195	Mouse anti-HIV mu5
17	75	96.2	111	AA70195	Mouse-human chimera
18	75	96.2	111	AA70195	Anti HIV antibody
19	75	96.2	111	AA70195	Chimeric anti HIV
20	75	96.2	111	AA70195	Light chain variab
21	75	96.2	111	AA70195	Light chain sequen
22	75	96.2	111	AA70195	Mus musculus anti-
23	75	96.2	111	AA70195	Light chain amino
24	75	96.2	111	AA70195	Antibody 4H5 L cha
25	75	96.2	111	AA70195	Murine derived pro
26	75	96.2	111	AA70195	Murine derived pro
27	75	96.2	111	AA70195	Variable light cha
28	75	96.2	112	AA70195	Human x mouse modi
29	75	96.2	112	AA70195	Monoclonal antibod
30	75	96.2	113	AA70195	Anti-Leu 3a light
31	75	96.2	115	AA70195	Sequence of the mo
32	75	96.2	120	AA70195	Amino acids sequen
33	75	96.2	131	AA70195	Anti-Leu 3a light
34	75	96.2	131	AA70195	Humanized antibody
35	75	96.2	131	AA70195	Humanized antibody
36	75	96.2	131	AA70195	Light chain variab
37	75	96.2	131	AA70195	Light chain variab
38	75	96.2	131	AA70195	Light chain sequen
39	75	96.2	131	AA70195	Light chain sequen
40	75	96.2	132	AA70195	Mouse MAB 3B9 ligh
41	75	96.2	132	AA70195	Light chain variab
42	75	96.2	132	AA70195	Light chain sequen
43	75	96.2	218	AA70195	Humanized anti-L-s
44	75	96.2	222	AA70195	Mu1 monoclonal ant
45	75	96.2	238	AA70195	Anti-Fas humanised

## ALIGNMENTS

RESULT 1  
ID AAR70195 standard; Protein; 15 AA.  
AC AAR70195;  
XX  
DT 20-SEP-1995 (first entry)  
DE MAB 3B9 light chain CDR.  
DE  
DE  
DE  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;  
KW complementarity determining region.  
XX  
XX Mus sp.  
XX  
XX WO9507301-A.  
XX  
XX 16-MAR-1995.  
XX  
XX 07-SEP-1994; 94WO-US10308.  
XX  
XX 07-SEP-1993; 93US-0117366.  
XX 14-OCT-1993; 93US-0136783.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX Gross MS, Holmes SD, Sylvester DR;  
XX WPI; 1995-123387/16.  
XX  
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
XX from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Page 54; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare  
XX hybridomas, which were screened for anti-IL-4 MAb secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pCEM7f+ and transformed into E. coli  
CC DH5-alpha. A light chain cDNA clone was sequenced (AAQ83490) that  
CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were  
CC identified.

XX Sequence 15 AA:

Query Match 96.2%; Score 75; DB 16; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.8e-06;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KASQSVDFDGDSDSYMN 15

|||||||:|||||||

Db 1 kasqsvdygdsgymn 15

RESULT 2

AAW83027  
ID AAW83027 standard; Peptide; 15 AA.

XX AAW83027;

XX 15-MAR-1999 (first entry)

XX Anti-Fas MAb HFE7A light chain CDR-LL.

XX HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;  
XX apoptosis; autoimmune disease; Hashimoto's disease;  
XX systemic lupus erythematosus; graft versus host disease;  
XX Sjogren syndrome; pernicious anaemia; Addison's disease;  
XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
XX rheumatoid arthritis; autoimmune haemolytic anaemia;  
XX myasthenia gravis; multiple sclerosis; Basedow's disease;  
XX thrombopenia purpura; insulin-dependent diabetes; allergy;  
XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
XX transplant rejection; therapy; complementarity determining region;  
XX CDR.

XX Mus musculus.

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY ) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

XX New antibodies and proteins bind conserved epitope of Fas antigen -  
PT used to evaluate drugs in animal models and to treat Fas-associated  
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
PT myocarditis, hepatitis and AIDS

XX Claim 9; Page 184; 292pp; English.

XX

CC This is the amino acid of complementarity determining region 1  
CC (CDR-LL) of the light chain (see AAW83042) of murine anti-human Fas  
CC monoclonal antibody HFE7A. The invention relates to antibodies,  
CC especially humanised antibodies (see AAW83031-37), recognising the  
CC Fas antigen. Such antibodies preferably comprise a heavy chain and  
CC a light chain including CDRs (see AAW83024-29) from the heavy and  
CC light chains of HFE7A. Humanised antibodies are produced by CDR  
CC grafting. The antibodies are capable of inducing apoptosis in  
CC abnormal cells expressing Fas, and of inhibiting Fas-induced  
CC apoptosis in normal cells. They are used to evaluate, in animal  
CC models, treatments of diseases that involve Fas/Fas ligand  
CC interactions, and also to treat such diseases, including autoimmune  
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,  
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's  
CC disease, thrombopenia purpura and insulin-dependent diabetes),  
CC allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
CC glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and  
CC transplant rejection (all claimed).

XX Sequence 15 AA;

Query Match 96.2%; Score 75; DB 19; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.8e-06;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KASQSVDFDGDSDSYMN 15

|||||||:|||||||

Db 1 kasqsvdygdsgymn 15

RESULT 3

AAW23772  
ID AAY23772 standard; Peptide; 15 AA.

XX AAY23772;

XX 13-SEP-1999 (first entry)

XX CDR of the light chain variable region of antibody 3B9.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;  
XX chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
XX immunoglobulin E-mediated allergic reaction; allergic rhinitis;  
XX conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
XX rheumatoid arthritis; host-versus-graft disease; renal disease;  
XX allergy; complementarity determining region.

XX Mus sp.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85889.

XX New DNA molecules encoding recombinant antibodies useful for

PT treating IL4-mediated conditions  
 XX Example 3; Column 43-44; 50pp; English.  
 XX The present sequence represents a complementarity determining region  
 CC (CDR) of the light chain variable region of murine interleukin-4  
 CC (IL-4) antibody 3B9. The specification describes chimeric and  
 CC humanised IL-4 monoclonal antibodies. The antibodies of the  
 CC invention are used in therapeutic and pharmaceutical compositions  
 CC for treating IL-4 mediated and immunoglobulin E-mediated allergic  
 CC reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis,  
 CC atopic asthma, anaphylactic shock, rheumatoid arthritis,  
 CC host-versus-graft disease and renal disease. They are also useful  
 CC in the diagnosis of an allergy or condition associated with excess  
 CC IL-4 production through the measurement e.g. by ELISA of circulating  
 CC endogenous IL-4 levels in humans.  
 XX  
 SQ Sequence 15 AA;

Query Match 96.2%; Score 75; DB 20; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGDSDYNN 15  
 | | | | | : | | | | |  
 Db 1 kasqsvdydgdsgynn 15

RESULT 4  
 AAY18114  
 ID AAY18114 standard; peptide; 15 AA.  
 AC AAY18114;

DT 11-AUG-1999 (first entry)  
 DE Light chain CDR for hIL-4 specific antibody.

XX Antibody: interleukin-4; IL4; immunoglobulin E; IgE mediated disease;  
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;  
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;  
 KW autoimmune disease; graft versus host disease;  
 KW complementarity determining region; CDR.

XX Synthetic.

XX US5914110-A.

XX 22-JUN-1999.

XX 07-JUN-1995; 95US-0483636.

XX 07-JUN-1995; 95US-0483636.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI: 1999-370482/31.

XX N-PSDB; AAX79513.

XX Recombinant IL4 antibodies

XX Claim 7; Column 43; 50pp; English.

XX This sequence represents a light chain complementarity determining region  
 CC (CDR) from an antibody of the invention. The antibody is a chimeric or  
 CC humanised interleukin-4 (IL4)-monoclonal antibody for the treatment of

CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for  
 CC the treatment of allergic disorders such as allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.  
 CC The antibodies are also useful for regulating B and T cell proliferation  
 CC and as such are useful in the treatment of autoimmune diseases and graft  
 CC versus host disease.  
 XX  
 SQ Sequence 15 AA;

Query Match 96.2%; Score 75; DB 20; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGDSDYNN 15  
 | | | | | : | | | | |  
 Db 1 kasqsvdydgdsgynn 15

RESULT 5  
 AAB14744  
 ID AAB14744 standard; peptide; 15 AA.  
 XX  
 AC AAB14744;

DT 24-NOV-2000 (first entry)  
 DE Mouse anti-Fas antibody HFE7A light chain CDR1.

XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; complementarity determining region; CDR; human Fas;  
 KW Fas ligand; complementarity determining region; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; light chain.

XX Mus musculus.

XX JP2000169393-A.

XX 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.

XX 30-SEP-1998; 98JP-0276883.

XX (SANY ) SANKYO CO LTD.

XX WPI: 2000-485645/43.

XX Preventive or treating agent for the diseases caused by an abnormality  
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 anti-Fas antibody -

XX Claim 10; Page 65; 139pp; Japanese.

XX The invention relates to compositions for the prevention or treatment  
 of diseases caused by an abnormality in the Fas/Fas ligand system  
 containing an anti-Fas antibody as the active component. The anti-Fas  
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 or a humanised version of HFE7A containing identical CDRs  
 (complementarity determining regions) to antibody HFE7A. Via its  
 interaction with Fas, the antibody of the invention acts as a modulator  
 of apoptosis. The compositions of the invention may therefore be used in  
 the treatment or prevention of conditions such as autoimmune diseases,  
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3  
 CC of the light chain of the murine anti-human Fas monoclonal antibody  
 CC HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).

XX Sequence 15 AA;

Query Match 96.2%; Score 75; DB 21; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFGDSYMN 15  
 Db 1 kasqsvdygdsgymn 15

RESULT 6  
 ID AAW90894 standard; peptide; 15 AA.  
 AC AAW90894;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Murine anti-Fas antibody peptide fragment #4.  
 XX  
 KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Mus musculus.  
 XX  
 PN EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI; 2000-258930/23.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 PS Disclosure; Page 98; 263pp; English.  
 XX  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a murine anti-Fas antibody peptide fragment described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 15 AA;

Query Match 96.2%; Score 75; DB 21; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFGDSYMN 15  
 Db 1 kasqsvdygdsgymn 15

RESULT 7  
 AAY59259  
 ID AAY59259 standard; peptide; 15 AA.  
 XX  
 AC AAY59259;  
 XX  
 DT 17-APR-2000 (first entry)  
 XX  
 DE Antibody 4H5 L chain variable region CDR1 fragment.  
 XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug; CDR;  
 KW complementarity determining region.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 DR WPI; 2000-091351/08.  
 XX  
 PT An antibody and the nucleic acid coding the antibody -  
 PS Claim 2; Page 14; 25pp; Japanese.

CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. Sequences  
 CC AAY59259-61 represent the complementarity determining region (CDR)-1,  
 CC CDR-2 and CDR-3 fragments in the L chain variable region of the  
 CC antibody 4H5 respectively.  
 XX  
 SQ Sequence 15 AA;

Query Match 96.2%; Score 75; DB 21; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFGDSYMN 15  
 Db 1 kasqsvdygdsgymn 15

RESULT 8

AA51136  
ID AAY51136 standard; Protein; 15 AA.  
XX  
AC AAY51136;  
XX  
DT 31-MAR-2000 (first entry)  
XX  
DE Murine CD4/CD34 recognizing antibody light chain CDR-1 region #1.  
XX  
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; complementarity determining region;  
KW CDR-1; light chain; murine.  
XX  
OS Mus sp.  
XX  
PN WO9961629-A1.  
XX  
PD 02-DEC-1999.  
XX  
PF 24-MAY-1999; 99WO-JP02711.  
XX  
PR 25-MAY-1998; 98JP-0159957.  
PR 26-MAY-1998; 98JP-0163023.  
XX  
PA (ASAH ) ASahi Kasei Kogyo KK.  
PA (ASAH ) ASahi Medical CO LTD.  
PI Ono M, Soka T, Morimoto I, Miyamura K;  
XX  
DR WPI; 2000-086720/07.  
XX  
PT Devices containing antibodies recognising CD4 or CD34 and their use for  
PT the separation of CD4 or CD34 positive cells -  
XX  
PS Claim 3; Page 76; 11pp; Japanese.  
XX  
CC This invention describes a novel device (I) for separating cluster  
CC differentiation (CD)-positive cells using a recombinant (chimeric or  
CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
CC for the separation of CD4 or CD34 positive cells, which is useful for  
CC the collection of hematopoietic undifferentiated cells, elimination of  
CC lymphocytes from cells to be used in bone marrow transplantation, the  
CC detection of leukemic cells and the production of medicinal  
CC compositions for the treatment of HIV infection and autoimmune diseases.  
CC This sequence represents a murine derived complementarity determining  
CC region CDR-1 protein fragment which is used to illustrate the method of  
CC the invention.  
XX  
SQ Sequence 15 AA;  
  
Query Match 96.2%; Score 75; DB 21; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.8e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KASQSVDFDGSYNN 15  
Db 1 kasqsvdydgsynn 15  
| | | | | : | | | | |  
  
RESULT 9  
AAR66143  
ID AAR66143 standard; peptide; 19 AA.  
XX  
AC AAR66143;  
XX  
DT 12-JUL-1995 (first entry)  
XX  
DE CD-4 antibody variable region complementary peptide.  
XX  
KW CD-4 antibody variable region; complementary peptide;  
KW extra-corporeal blood circulation; cell filter material.

XX Synthetic.  
OS  
PN JP06269663-A.  
XX  
PD 27-SEP-1994.  
XX  
PF 17-MAR-1993; 93JP-0057206.  
XX  
PR 17-MAR-1993; 93JP-0057206.  
XX  
PA (TOYM ) TOYOBO KK.  
XX  
DR WPI; 1994-346316/43.  
XX  
PT Material for collecting cells positive for CD-4 antibody -  
PT comprises nonwoven fabric having keto-alkyl halide functional gp  
XX  
PS Example 1; Page 6; 9pp; Japanese.  
XX  
CC AAR66140-B66146 are peptides complementary to the variable region  
CC of the CD-4 antibody, these peptides are fixed onto a claimed  
CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with  
CC keto-alkyl halide functional groups. This material can be used  
CC as a filter for CD-4 positive cells in a medical treatment  
CC involving the extra-corporeal circulation of blood.  
XX  
SQ Sequence 19 AA;  
  
Query Match 96.2%; Score 75; DB 15; Length 19;  
Best Local Similarity 93.3%; Pred. No. 2.3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KASQSVDFDGSYNN 15  
Db 5 kasqsvdydgsynn 19  
| | | | | : | | | | |  
  
RESULT 10  
AAY59263  
ID AAY59263 standard; protein; 103 AA.  
XX  
AC AAY59263;  
XX  
DT 17-APR-2000 (first entry)  
XX  
DE Antibody 4H5 L chain variable region.  
XX  
KW CD4 antigen; anti-human; antibody; 4H5; drug.  
XX  
OS Mus sp.  
XX  
PN JP11332563-A.  
XX  
PD 07-DEC-1999.  
XX  
PF 26-MAY-1998; 98JP-0163034.  
XX  
PR 26-MAY-1998; 98JP-0163034.  
XX  
PA (ASAH ) ASahi Kasei Kogyo KK.  
XX  
DR WPI; 2000-091351/08.  
XX  
N-PSDB; AAZ58662.  
XX  
PT An antibody and the nucleic acid coding the antibody -  
XX  
PS Claim 5; Page 15-16; 25pp; Japanese.  
XX  
CC The invention provides an antibody having affinity to CD4 antigen. The  
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC application for drugs. It is highly safe in human dose. The present

CC sequence represents the L chain variable region of the antibody 4H5.

SQ Sequence 103 AA;

Query Match 96.2%; Score 75; DB 21; Length 103;  
Best Local Similarity 93.3%; Pred. No. 1.5e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGD SYNN 15  
| | | | | : | | | | |  
Db 16 kasqsvdydgdsynn 30

RESULT 11

AA51140  
ID AAY51140 standard; Protein; 103 AA.

XX AC AAY51140;

XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #2.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; murine.

OS Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH ) ASAH KASEI KOGYO KK.

XX (ASAH ) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX N-PSDB; AA244204.

XX Devices containing antibodies recognising CD4 or CD34 and their use for

XX the separation of CD4 or CD34 positive cells

XX Claim 22; Page 79; 111pp; Japanese.

XX This invention describes a novel device (1) for separating cluster  
CC differentiation (CD)-positive cells using a recombinant (chimeric or  
CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
CC for the separation of CD4 or CD34 positive cells, which is useful for  
CC the collection of hematopoietic undifferentiated cells, elimination of  
CC lymphocytes from cells to be used in bone marrow transplantation, the  
CC detection of leukemic cells and the production of medicinal  
CC compositions for the treatment of HIV infection and autoimmune diseases.  
CC This sequence represents a murine derived protein fragment which is used  
CC to illustrate the method of the invention.

XX Sequence 103 AA;

Query Match 96.2%; Score 75; DB 21; Length 103;  
Best Local Similarity 93.3%; Pred. No. 1.5e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGD SYNN 15  
| | | | | : | | | | |  
Db 16 kasqsvdydgdsynn 30

RESULT 12

AA33309

ID AAR33309 standard; Protein; 106 AA.

XX AC AAR33309;

XX 05-JUL-1993 (first entry)

XX MAE15 light chain.

XX Antibody; high affinity; FCEH; low affinity; FCEL;  
KW IgE receptor; histamine; mast cell; basophil; Kabat;  
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.

XX Synthetic.

XX WO9304173-A.

XX 04-MAR-1993.

XX 14-AUG-1992; 92WO-US06860.

XX 14-AUG-1991; 91US-0744768.

XX 07-MAY-1992; 92US-0879495.

XX (GETH ) GENENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 1993-094004/11.

XX Polypeptide(s) binding to specific Fc epsilon receptors - act as  
PT IgE antagonists; useful for treating and preventing IgE-mediated  
PT disorders e.g. allergies

XX Disclosure; Fig 2; 113pp; English.

XX Antibodies capable of binding FCEL-bound IgE but which are  
CC substantially incapable of binding FCEH-bound IgE or inducing  
CC histamine release from mast cells or basophils, comprise a human  
CC Kabat CDR domain into which has been substituted a positionally  
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE  
CC antibodies MAE11, MAE13, MAE15 or MAE17.

XX Sequence 106 AA;

Query Match 96.2%; Score 75; DB 14; Length 106;  
Best Local Similarity 93.3%; Pred. No. 1.5e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGD SYNN 15  
| | | | | : | | | | |  
Db 24 kasqsvdydgdsynn 38

RESULT 13

AA5197

ID AAY85197 standard; protein; 106 AA.

XX AC AAY85197;

XX 29-JUN-2000 (first entry)

XX Light chain amino acid sequence of mouse antibody MAE15.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH;  
KW low affinity binding receptor; high affinity binding receptor; allergy;  
KW diagnosis; treatment; histamine release; prevent; light chain.

XX Mus sp.



US6037453-A.  
 14-MAR-2000.  
 06-JUN-1995; 95US-0466151.  
 15-MAR-1995; 95US-0405617.  
 14-AUG-1992; 92WO-US06860.  
 26-JAN-1994; 94US-0185899.  
 (GETH ) GENENTECH INC.  
 Presta LG, Jardieu PM;  
 WPI; 2000-269913/23.  
 New bispecific antibodies, useful for treating immunoglobulin  
 E-mediated disease, binds to IgE, but only when on the low affinity  
 receptor, and to an antigen other than IgE -  
 Claim 1; Fig 2; 48pp; English.  
 This sequence represents the light chain amino acid sequence of a mouse  
 anti-human immunoglobulin E (IgE) antibody. The invention relates to a  
 bispecific antibody that binds specifically to IgE when IgE is bound to  
 its low affinity receptor (FcεR), but does not bind to IgE, when IgE is  
 bound to its high affinity receptor (FcγR). The bispecific antibody  
 comprises an IgE-binding arm with human framework residues of a recipient  
 human antibody and donor murine CDR (complementarity determining region)  
 residues, but with at least one human CDR residue replacing the analogous  
 murine residue. The antibody also comprises an Fv that is specific for a  
 predetermined antigen other than IgE. The antibodies work by displacing  
 bound IgE from its receptor, or via competitive inhibition of its  
 binding. The bispecific antibodies are used for diagnosis, treatment and  
 prevention of allergy and other IgE-mediated diseases, also, when  
 immobilised, for the isolation of FcεR from cells (for research or  
 therapy). The bispecific antibodies of the invention do not cause  
 granulation or release of histamine from mast cells.

Query Match 96.2%; Score 75; DB 21; Length 106;  
 Best Local Similarity 93.3%; Pred. No. 1.5e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDSDYMN 15  
 DB 24 kasqsvdygdsgymn 38  
 RESULT 14  
 AAP90541  
 ID AAP90541 standard; protein; 111 AA.  
 XX  
 AC AAP90541;  
 XX  
 DT 20-OCT-1989 (first entry)  
 XX  
 DE Immunoglobulin L chain variable region.  
 XX  
 KW Immunoglobulin; L chain variable region; HIV.  
 XX  
 OS Mus musculus.  
 XX  
 PN EP327000-A.  
 XX  
 PD 09-AUG-1989.  
 XX  
 PF 30-JAN-1989; 89EP-0101583.  
 XX  
 PR 30-JAN-1988; 88JP-0020255.

08-JUL-1988; 88JP-0171385.  
 (KAGA ) THE CHEMO-SERO-THERAPEUTIC RESEARCH INSTITUTE.  
 Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T;  
 Takatsuki K;  
 WPI; 1989-229050/32.  
 N-PSDB; AAN90491, AAN90492, AAN90493.  
 Chimeric anti-human immune virus antibodies - contg. mouse variable  
 regions and human constant regions for diagnosis, treatment and  
 prevention of AIDS  
 XX Claim 5; page 15; 33pp; English.  
 XX The sequence is an L chain variable region from an immunoglobulin with  
 CC anti-HIV neutralising activity. See AAN90491-3, and AAN90495.  
 XX Sequence 111 AA;  
 SQ

Query Match 96.2%; Score 75; DB 10; Length 111;  
 Best Local Similarity 93.3%; Pred. No. 1.6e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDSDYMN 15  
 DB 24 kasqsvdygdsgymn 38  
 RESULT 15  
 AAR33305  
 ID AAR33305 standard; protein; 111 AA.  
 XX  
 AC AAR33305;  
 XX  
 DT 05-JUL-1993 (first entry)  
 XX  
 DE MAE11 light chain.  
 XX  
 KW Antibody; high affinity; FcεH; low affinity; FcεL;  
 KW IgE receptor; histamine; mast cell; basophil; Kabat;  
 KW CDR; murine; MAE11; MAE15; MAE17.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9304173-A.  
 XX  
 PD 04-MAR-1993.  
 XX  
 PF 14-AUG-1992; 92WO-US06860.  
 XX  
 PR 14-AUG-1991; 91US-0744768.  
 PR 07-MAY-1992; 92US-0879495.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Jardieu PM, Presta LG;  
 XX  
 DR WPI; 1993-094004/11.  
 XX  
 PT Polypeptide(s) binding to specific Fc epsilon receptors - act as  
 PT IgE antagonists; useful for treating and preventing IgE-mediated  
 PT disorders e.g. allergies  
 XX  
 PS Disclosure; Fig 2; 113pp; English.  
 XX  
 CC Antibodies capable of binding FcεL-bound IgE but which are  
 CC substantially incapable of binding FcεH-bound IgE or inducing  
 CC histamine release from mast cells or basophils, comprise a human  
 CC Kabat CDR domain into which has been substituted a positionally  
 CC analogous residue from a Kabat CDR domain of the murine anti-huIgE

CC antibodies MAE11, MAE13, MAE15 or MAE17.

XX  
SQ Sequence 111 AA;

Query Match 96.2%; Score 75; DB 14; Length 111;  
Best Local Similarity 93.3%; Pred. NO. 1.6e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15  
|||||||:|||||||  
Db 24 kasqsvdydgd symn 38

Search completed: June 28, 2001, 16:14:35  
Job time: 1323 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:13 ; Search time 138.34 Seconds  
(without alignments)  
2.184 Million cell updates/sec

Title: US-09-724-406-12

Perfect score: 78

Sequence: 1 KASQSVDFDGDYSYM 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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5: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	96.2	15	2	US-08-483-636-16
2	75	96.2	15	2	US-08-483-632-16
3	75	96.2	106	3	US-08-466-151-6
4	75	96.2	111	1	US-08-491-845-8
5	75	96.2	111	1	US-08-491-845-16
6	75	96.2	111	2	US-08-483-636-73
7	75	96.2	111	2	US-08-483-632-73
8	75	96.2	111	2	US-08-887-352B-5
9	75	96.2	111	3	US-08-466-151-2
10	75	96.2	111	4	US-09-109-207C-5
11	75	96.2	115	4	US-08-513-968-51
12	75	96.2	120	1	US-08-111-080-24
13	75	96.2	120	1	US-08-211-980-24
14	75	96.2	120	5	PCT-US93-07967-24
15	75	96.2	131	2	US-08-483-636-14
16	75	96.2	131	2	US-08-483-636-58
17	75	96.2	131	2	US-08-483-632-14
18	75	96.2	131	2	US-08-483-632-58
19	75	96.2	131	4	US-08-579-378A-18
20	75	96.2	131	4	US-08-579-378A-14
21	75	96.2	132	2	US-08-483-636-2
22	75	96.2	132	2	US-08-483-632-2
23	75	96.2	218	5	PCT-US96-13152-2
24	72	92.3	111	2	US-08-887-352B-6
25	72	92.3	111	4	US-09-109-207C-10
26	72	92.3	114	2	US-08-887-352B-10
27	72	92.3	114	4	US-09-109-207C-10

28	72	92.3	218	2	US-08-887-352B-13	Sequence 13, Appl
29	72	92.3	218	3	US-08-466-151-9	Sequence 9, Appl
30	72	92.3	218	4	US-09-109-207C-13	Sequence 13, Appl
31	69	88.5	41	3	US-08-984-277-5	Sequence 5, Appl
32	69	88.5	239	2	US-08-553-497A-18	Sequence 18, Appl
33	68	87.2	114	4	US-08-887-352B-9	Sequence 9, Appl
34	65	83.3	114	2	US-09-109-207C-9	Sequence 9, Appl
35	53	67.3	114	2	US-08-887-352B-8	Sequence 8, Appl
36	53	67.3	218	4	US-09-282-505-1	Sequence 1, Appl
37	53	67.3	218	4	US-05-054-255-1	Sequence 1, Appl
38	50	64.1	114	4	US-09-109-207C-8	Sequence 8, Appl
39	50	64.1	218	2	US-08-887-352B-15	Sequence 15, Appl
40	50	64.1	218	2	US-08-887-352B-17	Sequence 17, Appl
41	50	64.1	218	2	US-08-887-352B-19	Sequence 19, Appl
42	50	64.1	218	2	US-08-887-352B-24	Sequence 24, Appl
43	50	64.1	218	4	US-09-109-207C-15	Sequence 15, Appl
44	50	64.1	218	4	US-09-109-207C-17	Sequence 17, Appl
45	50	64.1	218	4	US-09-109-207C-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-08-483-636-16  
; Sequence 16, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0539  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-483-636-16

Query Match 96.2%; Score 75; DB 2; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3e-07;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15  
|||||:|||||  
Db 1 KASQSVDYDGD SYMN 15

RESULT 2

US-08-483-632-16  
; Sequence 16, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESS: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-483-632-16

Query Match 96.2%; Score 75; DB 2; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3e-07;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15  
|||||:|||||  
Db 1 KASQSVDYDGD SYMN 15

RESULT 3

US-08-466-151-6  
; Sequence 6, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 06-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/879495  
FILING DATE: 07-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P2C1D1  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

US-08-466-151-6

Query Match 96.2%; Score 75; DB 3; Length 106;  
Best Local Similarity 93.3%; Pred. No. 2.8e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15  
|||||:|||||  
Db 24 KASQSVDYDGD SYMN 38

RESULT 4

US-08-491-845-8  
; Sequence 8, Application US/08491845  
; Patent No. 5773247  
; GENERAL INFORMATION:  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: SHIOSAKI, Kouichi

APPLICANT: OSATOMI, Kiyoshi  
APPLICANT: TOKIYOSHI, Sachio  
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491.845  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00039  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: MAEDA-5  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-491-845-8

Query Match 96.2%; Score 75; DB 1; Length 111;  
Best Local Similarity 93.3%; Pred. No. 3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGD SYNN 15  
|||||:|||||  
Db 24 KASQSVDFDGD SYNN 38

RESULT 5  
US-08-491-845-16  
Sequence 16, Application US/08491845  
Patent No. 5773247  
GENERAL INFORMATION:  
APPLICANT: MAEDA, Hiroaki  
APPLICANT: KIMACHI, Kazuhiko  
APPLICANT: EDA, Yasuyuki  
APPLICANT: SHIOSAKI, Kouichi  
APPLICANT: OSATOMI, Kiyoshi  
APPLICANT: TOKIYOSHI, Sachio  
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491.845  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00039  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: MAEDA-5  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-491-845-16

Query Match 96.2%; Score 75; DB 1; Length 111;  
Best Local Similarity 93.3%; Pred. No. 3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGD SYNN 15  
|||||:|||||  
Db 24 KASQSVDFDGD SYNN 38

RESULT 6  
US-08-483-636-73  
Sequence 73, Application US/08483636  
Patent No. 5914110  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-483-636-73

Query Match 96.2%; Score 75; DB 2; Length 111;  
Best Local Similarity 93.3%; Pred. No. 3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KASQSVDFDGDSDYMN 15  
Db 24 KASQSVDFDGDSDYMN 38

## RESULT 7

US-08-483-632-73  
Sequence 73, Application US/08483632  
Patent No. 5928904  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESS: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-483-632-73

Query Match 96.2%; Score 75; DB 2; Length 111;  
Best Local Similarity 93.3%; Pred. No. 3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KASQSVDFDGDSDYMN 15  
Db 24 KASQSVDFDGDSDYMN 38

## RESULT 8

US-08-887-352B-5  
Sequence 5, Application US/08887352B  
Patent No. 5994511  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
TITLE OF INVENTION: Improving Polypeptides  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-5

Query Match 96.2%; Score 75; DB 2; Length 111;  
Best Local Similarity 93.3%; Pred. No. 3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KASQSVDFDGDSDYMN 15  
Db 24 KASQSVDFDGDSDYMN 38

RESULT 9  
US-08-466-151-2  
Sequence 2, Application US/08466151  
Patent No. 6037453  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: winpatin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,151  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/466163  
 FILING DATE: 06-Jun-1995  
 APPLICATION NUMBER: 08/405617  
 FILING DATE: 15-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/185899  
 FILING DATE: 26-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/879495  
 FILING DATE: 07-MAY-1992  
 APPLICATION DATA:  
 APPLICATION NUMBER: 07/744768  
 FILING DATE: 14-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET INFORMATION: P0718P2C1D1  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 111 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-466-151-2

Query Match 96.2%; Score 75; DB 3; Length 111;  
 Best Local Similarity 93.3%; Pred. No. 3e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15  
 Db 24 KASQSVDFDGD SYMN 38

RESULT 10  
 US-09-109-207C-5  
 ; Sequence 5, Application US/09109207C  
 ; Patent No. 6172213  
 ; GENERAL INFORMATION:  
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
 ; FILE REFERENCE: P1123R1  
 ; CURRENT APPLICATION NUMBER: US/09/109,207C  
 ; PRIOR FILING DATE: 1998-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/051,554  
 ; PRIOR FILING DATE: 1997-07-03  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SEQ ID NO 5  
 ; LENGTH: 111  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-109-207C-5

Query Match 96.2%; Score 75; DB 4; Length 111;  
 Best Local Similarity 93.3%; Pred. No. 3e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15  
 Db 24 KASQSVDFDGD SYMN 38

RESULT 11  
 US-08-513-968-51  
 ; Sequence 51, Application US/08513968  
 ; Patent No. 6114143  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EDA, Yasuyuki.  
 ; APPLICANT: MAEDA, Hiroaki  
 ; APPLICANT: MAKIZUMI, Keiichi  
 ; APPLICANT: SHIOSAKI, Kouichi  
 ; APPLICANT: OSATOMI, Kiyoshi  
 ; APPLICANT: KINACHI, Kazuhiko  
 ; APPLICANT: HIGUCHI, Hiroyumi  
 ; APPLICANT: TOKIYOSHI, Sachio  
 ; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY  
 ; NUMBER OF SEQUENCES: 86  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/513,968  
 ; FILING DATE: 11-SEP-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 78913/1993  
 ; FILING DATE: 11-MAR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: EDA=1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; TELEX: 248633  
 ; INFORMATION FOR SEQ ID NO: 51:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 115 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-513-968-51

Query Match 96.2%; Score 75; DB 4; Length 115;  
 Best Local Similarity 93.3%; Pred. No. 3.1e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15  
 Db 28 KASQSVDFDGD SYMN 42

RESULT 12  
 US-08-111-080-24  
 ; Sequence 24, Application 08/111080  
 ; Patent No. 5558865

Fri Jun 29 08:04:22 2001

us-09-724-406-12.ra1

GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/111.080  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/748,562  
FILING DATE: 22-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-111-080-24

Query Match 96.2%; Score 75; DB 1; Length 120;  
Best Local Similarity 93.3%; Pred. No. 3.3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
| | | | | : | | | | |  
DB 24 KASQSVDFDGSYMN 38

RESULT 13  
US-08-211-980-24  
Sequence 24, Application US/08211980  
Patent No. 5665569  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,980  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-980-24

Query Match 96.2%; Score 75; DB 1; Length 120;  
Best Local Similarity 93.3%; Pred. No. 3.3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
| | | | | : | | | | |  
DB 24 KASQSVDFDGSYMN 38

RESULT 14  
PCT-US93-07967-24  
Sequence 24, Application PC/TUS9307967  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447



REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-07967-24

Query Match 96.2%; Score 75; DB 5; Length 120;  
Best Local Similarity 93.3%; Pred. No. 3.3e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KASQSVDFDGD SYMN 15  
Db 24 KASQSVDFDGD SYMN 38

RESULT 15  
US-08-483-636-14  
Sequence 14, Application US/08483636  
Patent No. 5914110  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-483-636-14

Query Match 96.2%; Score 75; DB 2; Length 131;  
Best Local Similarity 93.3%; Pred. No. 3.6e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KASQSVDFDGD SYMN 15  
Db 43 KASQSVDFDGD SYMN 57

Search completed: June 28, 2001, 16:01:14  
Job time: 522 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:43 ; Search time 234.85 Seconds  
(without alignments)  
4.865 Million cell updates/sec

Title: US-09-724-406-12  
Perfect score: 78  
Sequence: 1 KASQSVDFDGSYMN 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	75	96.2	81	2	S42193	Ig kappa chain V r
2	75	96.2	93	2	A38601	Ig kappa chain V r
3	75	96.2	111	1	KVMS43	Ig kappa chain V r
4	75	96.2	111	1	KVMS83	Ig kappa chain V r
5	75	96.2	111	1	KVMS08	Ig kappa chain V r
6	75	96.2	111	1	KVMS69	Ig kappa chain V r
7	72	92.3	110	1	KVMS10	Ig kappa chain V r
8	72	92.3	112	2	S19971	Ig kappa chain V r
9	72	92.3	131	2	PH1226	Ig kappa chain V-J
10	69	88.5	111	2	S09966	Ig kappa chain V r
11	64	82.1	111	1	KVMS01	Ig kappa chain V r
12	61	78.2	112	2	S19976	Ig kappa chain V r
13	47	60.3	112	2	S19972	Ig kappa chain V r
14	46	59.0	96	2	B49442	Ig kappa chain V r
15	44	56.4	109	2	PH0093	Ig kappa chain V r
16	44	56.4	340	2	E83146	Ig kappa chain V r
17	43	55.1	303	2	A83958	Ig kappa chain V r
18	42	53.8	115	2	S63596	Ig kappa chain V r
19	41	52.6	91	2	S25462	Ig kappa chain V r
20	41	52.6	102	2	PH1079	Ig kappa chain V r
21	41	52.6	107	2	S26343	Ig kappa chain V r
22	41	52.6	107	2	S26344	Ig kappa chain V r
23	41	52.6	108	1	KVMS54	Ig kappa chain V r
24	41	52.6	111	1	KVMS80	Ig kappa chain V r
25	41	52.6	111	1	KVMS37	Ig kappa chain V r
26	41	52.6	111	2	S09963	Ig kappa chain V-J
27	41	52.6	111	2	S09969	Ig kappa chain V-J
28	41	52.6	120	2	S06732	Ig kappa chain pre
29	41	52.6	131	1	KVMSM6	Ig kappa chain pre

## ALIGNMENTS

RESULT 1  
S42193  
Ig kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Oct-1994 #sequence\_revision 26-May-1995 #text\_change 23-Jul-1999  
C:Accession: S42193  
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.  
Eur. J. Immunol. 23, 2503-2510, 1993  
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s  
A:Reference number: 342176; MUID:94009207  
A:Accession: S42193  
A:Status: preliminary  
A:Residues: 1-81 <MO>  
A:Molecule type: DNA  
A:Cross-references: IMBL:225456; NID:9407846; PIDN:CAA80943.1; PID:9407847  
A:Note: the authors translated the codon GTT for residue 36 as Ala  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin

Query Match 96.2% Score 75; DB 2; Length 81;  
Best Local Similarity 93.3%; Pred. No. 8.1e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGSYMN 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 KASQSVDFDGSYMN 20

RESULT 2  
A38601  
Ig kappa chain V region (1c3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999  
C:Accession: A38601  
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A:Title: Common structural features among monoclonal antibodies binding the same anti  
A:Reference number: A38601; MUID:91115823  
A:Accession: A38601  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-93 <GOS>  
A:Cross-references: GB:M57978; NID:9196402; PIDN:AAA63359.1; PID:g196403  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin

Query Match 96.2% Score 75; DB 2; Length 93;  
Best Local Similarity 93.3%; Pred. No. 9.4e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

conserved hypothet  
hypothetical prote  
Ig kappa chain V r  
Ig kappa chain V r  
Ig kappa chain V r  
Ig kappa chain V r  
Ig kappa chain pre  
Ig kappa chain V r  
DNA-directed RNA p  
DNA-directed RNA p  
MGR protein - vari  
RNA polymerase sub  
DNA-directed RNA p  
DNA-directed RNA p  
Ig kappa chain V r  
anti-glycoprotein

30 41 52.6 264 2 H83170  
31 41 52.6 972 2 E84693  
32 40.5 51.9 91 2 S42186  
33 40.5 51.9 101 2 A37330  
34 40.5 51.9 112 2 A36259  
35 40.5 51.9 113 2 F30560  
36 40.5 51.9 132 2 C32513  
37 40 51.3 111 2 S37202  
38 40 51.3 1286 1 H36845  
39 40 51.3 1286 2 T28521  
40 40 51.3 1286 2 A72161  
41 40 51.3 1286 2 T37366  
42 40 51.3 1287 1 RN247  
43 40 51.3 1289 2 T30681  
44 39.5 50.6 89 2 B25155  
45 39 50.0 111 2 D45722

QY 1 KASQSVDFDGSYMN 15  
 DB 5 KASQSVDFDGSYMN 19

RESULT 3  
 KVM543  
 Ig kappa chain V region (PC7043) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
 C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: A01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 R:Mo, J.A.; Bona, C.A.; Holmdahl, R.  
 Eur. J. Immunol. 23, 2503-2510, 1993  
 A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec  
 A:Reference number: S42187; MUID:94009207  
 A:Accession: S42187  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:Cross-references: EMBL:225444; NID:9407832; PIDN:CAA80931.1; PID:9407833  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42194  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MO>  
 A:Cross-references: EMBL:225458; NID:9407844; PIDN:CAA80945.1; PID:9407845  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42190  
 A:Molecule type: DNA  
 A:Residues: 13-99 <MO>  
 A:Cross-references: EMBL:225450; NID:9407838; PIDN:CAA80937.1; PID:9407839  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42189  
 A:Molecule type: DNA  
 A:Residues: 15-99 <MO>  
 A:Cross-references: EMBL:225448; NID:9407836; PIDN:CAA80935.1; PID:9407837  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42188  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MO>  
 A:Cross-references: EMBL:225446; NID:9407834; PIDN:CAA80933.1; PID:9407835  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42191  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:Cross-references: EMBL:225452; NID:9407840; PIDN:CAA80939.1; PID:9407841  
 A:Note: V-kappa-21E; anti-collagen  
 A:Accession: S42192  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:Cross-references: EMBL:225454; NID:9407842; PIDN:CAA80941.1; PID:9407843  
 A:Note: V-kappa-21E; anti-collagen  
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 75; DB 1; Length 111;  
 Best Local Similarity 93.3%; Pred. No. 1.1e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KASQSVDFDGSYMN 15  
 DB 24 KASQSVDFDGSYMN 38

RESULT 4  
 KVM583  
 Ig kappa chain V region (PC7183) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: B01937; A01937  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: B01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (h  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 75; DB 1; Length 111;  
 Best Local Similarity 93.3%; Pred. No. 1.1e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
 DB 24 KASQSVDFDGSYMN 38

RESULT 5  
 KVM508  
 Ig kappa chain V region (PC6308) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: C01937; A01937  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: C01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (h  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 75; DB 1; Length 111;  
 Best Local Similarity 93.3%; Pred. No. 1.1e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
 DB 24 KASQSVDFDGSYMN 38

RESULT 6  
 KVM569  
 Ig kappa chain V region (PC7769) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: E01937; A01937  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: E01937  
 A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes. C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 75; DB 1; Length 111;  
Best Local Similarity 93.3%; Pred. No. 1.1e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15  
|||||:|||||  
DB 24 KASQSVDFDGD SYNN 38

RESULT 7

KVMS10

Ig kappa chain V region (PC7210) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: D01937; A01937  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152  
A:Accession: D01937

A:Molecule type: protein

A:Residues: 1-110 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes. C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 92.3%; Score 72; DB 1; Length 110;  
Best Local Similarity 86.7%; Pred. No. 3.6e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15  
|||||:|||||  
DB 24 KASQSLDYDGD SYNN 38

RESULT 8

SI9971

Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: SI9971; SI9973  
R:Weissenhorn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: SI9963

A:Accession: SI9971

A:Molecule type: mRNA

A:Residues: 1-112 <WEI>

A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289  
A:Experimental source: clone M-T310

A:Accession: SI9973

A:Molecule type: mRNA

A:Residues: 1-112 <WEW>

A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293  
A:Experimental source: M-T404

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 72; DB 2; Length 112;  
Best Local Similarity 86.7%; Pred. No. 3.7e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15  
|||||:|||||  
DB 24 KASQSLDYDGD SYNN 38

RESULT 9

PHI226

Ig kappa chain precursor V region (M-T310) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000  
C:Accession: PHI226  
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L. Gene 121, 271-278, 1992  
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and A:Reference number: PHI224; MUID:93077041  
A:Accession: PHI226

A:Molecule type: mRNA

A:Residues: 1-131 <WEI>

A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766

A:Note: this mouse sequence was hybridized and fused with a human constant region gene C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-131/Product: Ig light chain V region #status predicted <MAT>

F:36-114/Domain: immunoglobulin homology <IMM>

Query Match

92.3%; Score 72; DB 2; Length 131;  
Best Local Similarity 86.7%; Pred. No. 4.3e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15  
|||||:|||||  
DB 44 KASQSLDYDGD SYNN 58

RESULT 10

SO9966

Ig kappa chain V-J region (1E10) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000

C:Accession: SO9966

R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatou, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990

A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibody A:Reference number: SO9955; MUID:90269328

A:Accession: SO9966

A:Molecule type: mRNA

A:Residues: 1-111 <REI>

A:Cross-references: EMBL:X51854; NID:g55397; PIDN:CAA36147.1; PID:g930231

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match

88.5%; Score 69; DB 2; Length 111;  
Best Local Similarity 86.7%; Pred. No. 0.00012;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15  
|||||:|||||  
DB 24 KASQSLDYDGD SYNN 38

RESULT 11

KVMSCI

Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)

C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 31-Mar-2000

C:Accession: A01936  
R:McKean, D.J.; Bell, M.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related molecules  
A:Reference number: A93822; MUID:79012520  
A:Accession: A01936  
A:Molecule type: protein  
A:Residues: 1-111 <MCK>  
C:Comment: This chain was isolated from a myeloma protein.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 82.18; Score 64; DB 1; Length 111;  
Best Local Similarity 80.0%; Pred. No. 0.00082;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
DB 24 KASQSVDFDGSYMN 38  
|||||:|:|||||

RESULT 12  
SI9976  
Ig kappa chain V region (M-T413) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: SI9976  
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: SI9963  
A:Accession: SI9976  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAAA6221.1; PID:g52299  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 78.28; Score 61; DB 2; Length 112;  
Best Local Similarity 73.3%; Pred. No. 0.0026;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
DB 24 KASQSVDFDGSYMN 38  
|||||:|:|||||

RESULT 13  
SI9972  
Ig kappa chain V region (M-T321) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: SI9972  
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: SI9963  
A:Accession: SI9972  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAAA6222.1; PID:g52291  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

C:Accession: A01936  
R:McKean, D.J.; Bell, M.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related molecules  
A:Reference number: A93822; MUID:79012520  
A:Accession: A01936  
A:Molecule type: protein  
A:Residues: 1-111 <MCK>  
C:Comment: This chain was isolated from a myeloma protein.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 82.18; Score 64; DB 1; Length 111;  
Best Local Similarity 80.0%; Pred. No. 0.00082;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
DB 24 KASQSVDFDGSYMN 38  
|||||:|:|||||

RESULT 12  
SI9976  
Ig kappa chain V region (M-T413) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: SI9976  
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: SI9963  
A:Accession: SI9976  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAAA6221.1; PID:g52299  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 78.28; Score 61; DB 2; Length 112;  
Best Local Similarity 73.3%; Pred. No. 0.0026;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
DB 24 KASQSVDFDGSYMN 38  
|||||:|:|||||

RESULT 13  
SI9972  
Ig kappa chain V region (M-T321) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: SI9972  
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: SI9963  
A:Accession: SI9972  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAAA6222.1; PID:g52291  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 60.3%; Score 47; DB 2; Length 112;  
Best Local Similarity 60.0%; Pred. No. 0.62;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
DB 24 RASQSVDYNAISYMH 38  
:|||||:|:|

RESULT 14  
B49442  
Ig light chain V region (50.1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: B49442  
R:Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapié, L.M.  
Proteins 14, 499-508, 1992  
A:Title: Crystallization, sequence, and preliminary crystallographic data for an anti  
A:Reference number: A49442; MUID:93066166  
A:Accession: B49442  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-96 <STU>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:8-86/Domain: immunoglobulin homology <IMM>

Query Match 59.0%; Score 46; DB 2; Length 96;  
Best Local Similarity 53.3%; Pred. No. 0.77;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
DB 16 RASESVDDGNSFLH 30  
:|||||:|:|

RESULT 15  
PH0093  
Ig kappa chain V region (anti-cyclosporin E) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 21-Jan-2000  
C:Accession: PH0093  
R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koehler, H.P.; Quesniaux, V.F.J.  
Mol. Immunol. 27, 1029-1038, 1990  
A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporin  
A:Reference number: PH0087; MUID:91042649  
A:Accession: PH0093  
A:Molecule type: mRNA  
A:Residues: 1-109 <SCH>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:24-38/Region: complementarity-determining 1  
F:54-60/Region: complementarity-determining 2  
F:93-101/Region: complementarity-determining 3

Query Match 56.4%; Score 44; DB 2; Length 109;  
Best Local Similarity 60.0%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
DB 24 RASESVDSNGSFMN 38  
:|||||:|:|

Search completed: June 28, 2001, 15:58:43  
Job time: 371 sec







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:35 ; Search time 105.36 Seconds  
(without alignments)  
4.877 Million cell updates/sec

Title: US-09-724-406-12

Perfect score: 78

Sequence: 1 KASQSVDFDGSYMN 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	75	96.2	111	1	KV3M_MOUSE
2	75	96.2	111	1	KV3N_MOUSE
3	75	96.2	111	1	KV3O_MOUSE
4	75	96.2	111	1	KV3Q_MOUSE
5	72	92.3	110	1	KV3P_MOUSE
6	64	82.1	111	1	KV3L_MOUSE
7	44	56.4	111	1	KV3C_MOUSE
8	41	52.6	108	1	KV3V_MOUSE
9	41	52.6	111	1	KV3A_MOUSE
10	41	52.6	111	1	KV3H_MOUSE
11	41	52.6	111	1	KV3J_MOUSE
12	41	52.6	111	1	KV3K_MOUSE
13	41	52.6	112	1	KV3B_MOUSE
14	41	52.6	131	1	KV3I_MOUSE
15	40.5	51.9	350	1	Y4RM_RHLSN
16	40	51.3	1286	1	RPOI_VACCC
17	40	51.3	1286	1	RPOI_VARCV
18	40	51.3	1287	1	RPOI_VACV
19	39	50.0	112	1	KV3G_MOUSE
20	39	50.0	559	1	KIF2_XENLA
21	39	50.0	749	1	PCRA_LEUCI
22	39	50.0	823	1	SCH9_YEAST
23	39	50.0	1173	1	TSPL_XENLA
24	38	48.7	348	1	CAPG_HUMAN
25	38	48.7	361	1	MLTB_ECOLI
26	38	48.7	405	1	PRSB_YEAST
27	38	48.7	409	1	THIL_PANTH
28	38	48.7	955	1	VP2_BT117
29	38	48.7	956	1	VP2_BT111
30	37	47.4	111	1	KV3R_MOUSE
31	37	47.4	111	1	KV3S_MOUSE
32	37	47.4	111	1	KV3U_MOUSE
33	37	47.4	123	1	Y131_CABEL

34 37 47.4 148 1 CALL\_DROME  
35 37 47.4 243 1 LPSB\_LYTP1  
36 37 47.4 321 1 LPSA\_LYTP1  
37 37 47.4 340 1 PURA\_METH  
38 37 47.4 377 1 AMSH\_HAETN  
39 37 47.4 459 1 CCMH\_ERWAM  
40 37 47.4 465 1 TRAZ\_STRPN  
41 37 47.4 692 1 Y650\_MENJA  
42 37 47.4 1170 1 TSP2\_BOVIN  
43 37 47.4 1172 1 TSP2\_HUMAN  
44 37 47.4 1172 1 TSP2\_MOUSE  
45 37 47.4 1178 1 TSP2\_CHICK

## ALIGNMENTS

RESULT 1  
KV3M\_MOUSE  
ID KV3M\_MOUSE STANDARD; PRT; 111 AA.  
AC P01665;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 7043.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity."  
RL Nature 276:785-790(1978).  
DR PIR: A01937; KVAS43.  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; Ig; 1.  
KW Immunoglobulin v region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 96.2%; Score 75; DB 1; Length 111;  
Best Local Similarity 93.3%; Pred. No. 2.9e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
Db 24 KASQSVDFDGSYMN 38

RESULT 2  
KV3N\_MOUSE  
ID KV3N\_MOUSE STANDARD; PRT; 111 AA.  
AC P01666;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 7183.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

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us-09-724-406-12.rsp

RN SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR PIR: B01937; KVM583.  
DR InterPro: IPR003006; -.  
DR Pfam: PF00047; ig; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 2 38  
FT DOMAIN 3 53  
FT DOMAIN 4 60  
FT DOMAIN 5 60  
FT DOMAIN 6 92  
FT DOMAIN 7 92  
FT DOMAIN 8 101  
FT DOMAIN 9 101  
FT DOMAIN 10 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 96.2%; Score 75; DB 1; Length 111;  
Best Local Similarity 93.3%; Pred. No. 2.9e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDYSYN 15  
|||||:|||||

DB 24 KASQSVDFDGDYSYN 38

RESULT 3

KV3Q\_MOUSE STANDARD; PRT; 111 AA.  
AC P01667;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 6308.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]

RN SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR PIR: C01937; KVM58.  
DR InterPro: IPR003006; -.  
DR Pfam: PF00047; ig; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 2 38  
FT DOMAIN 3 53  
FT DOMAIN 4 60  
FT DOMAIN 5 60  
FT DOMAIN 6 92  
FT DOMAIN 7 92  
FT DOMAIN 8 101  
FT DOMAIN 9 101  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 96.2%; Score 75; DB 1; Length 111;  
Best Local Similarity 93.3%; Pred. No. 2.9e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDYSYN 15  
|||||:|||||

DB 24 KASQSVDFDGDYSYN 38

RESULT 4

KV3Q\_MOUSE STANDARD; PRT; 111 AA.  
AC P01669;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 7769.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]

RN SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR PIR: E01937; KVM569.  
DR InterPro: IPR003006; -.  
DR Pfam: PF00047; ig; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 2 38  
FT DOMAIN 3 53  
FT DOMAIN 4 60  
FT DOMAIN 5 60  
FT DOMAIN 6 92  
FT DOMAIN 7 92  
FT DOMAIN 8 101  
FT DOMAIN 9 101  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 96.2%; Score 75; DB 1; Length 111;  
Best Local Similarity 93.3%; Pred. No. 2.9e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDYSYN 15  
|||||:|||||

DB 24 KASQSVDFDGDYSYN 38

RESULT 5

KV3P\_MOUSE STANDARD; PRT; 110 AA.  
AC P01668;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 7210.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]

RN SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR PIR: D01937; KVM510.  
DR InterPro: IPR003006; -.  
DR Pfam: PF00047; ig; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 2 38  
FT DOMAIN 3 53  
FT DOMAIN 4 60  
FT DOMAIN 5 60  
FT DOMAIN 6 92  
FT DOMAIN 7 92  
FT DOMAIN 8 101  
FT DOMAIN 9 101  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 96.2%; Score 75; DB 1; Length 111;  
Best Local Similarity 93.3%; Pred. No. 2.9e-06;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDYSYN 15  
|||||:|||||

FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 61 92 FRAMEWORK 3.  
 FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 101 110 FRAMEWORK 4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 110 110  
 SQ SEQUENCE 110 AA; 11950 MW; 69FIA5CB86B1249 CRC64;

Query Match 92.3%; Score 72; DB 1; Length 110;  
 Best Local Similarity 86.7%; Pred. No. 9.5e-06;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
 |||||:|||||  
 DB 24 KASQSVDFDGSYMN 38

## RESULT 6

KV3L\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01664;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION CBPC 101.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 related mouse kappa variable regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR: A01936; KVMSC1  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig; 1.  
 DR Immunoglobulin V region.  
 KW DOMAIN 1 23  
 FT DOMAIN 24 38 FRAMEWORK 1.  
 FT DOMAIN 39 53 FRAMEWORK 2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 61 92 FRAMEWORK 3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 23 92 FRAMEWORK 4.  
 FT NON\_TER 111 111 BY SIMILARITY.  
 SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 82.1%; Score 64; DB 1; Length 111;  
 Best Local Similarity 80.0%; Pred. No. 0.00023;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
 |||||:|||||  
 DB 24 KASQSVDFDGSYMN 38

## RESULT 7

KV3C\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01656;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION MOPC 70.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=67056897; PubMed=4162931;  
 RA Gray W.R., Dreyer W.J., Hood L.E.;  
 RT "Mechanism of antibody synthesis: size differences between mouse  
 kappa chains.";  
 RL Science 155:465-467(1967).  
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
 DR PIR: A01930; KVM80.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig; 1.  
 DR Immunoglobulin V region; Bence-Jones protein.  
 KW DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 39 53 FRAMEWORK 2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 61 92 FRAMEWORK 3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 23 92 FRAMEWORK 4.  
 FT NON\_TER 111 111 BY SIMILARITY.  
 SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

Query Match 56.4%; Score 44; DB 1; Length 111;  
 Best Local Similarity 60.0%; Pred. No. 0.65;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
 |||||:|||||  
 DB 24 RASEVDNSGISPMN 38

## RESULT 8

KV3V\_MOUSE STANDARD; PRT; 108 AA.  
 AC P01674;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 2154.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 DR PIR: A01940; KVM854.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig; 1.  
 DR Immunoglobulin V region.  
 KW DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 39 53 FRAMEWORK 2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 23 92 FRAMEWORK 4.  
 FT NON\_TER 108 108 BY SIMILARITY.  
 SQ SEQUENCE 108 AA; 11699 MW; D4092D1D8DAC4B9E CRC64;

Query Match 52.6%; Score 41; DB 1; Length 108;  
 Best Local Similarity 60.0%; Pred. No. 2.1;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 KASQSVDFDGSYMN 15
Db 24 RASQSVSTSGSYNMH 38

RESULT 9
KV3A_MOUSE STANDARD; PRT; 111 AA.
ID KV3A_MOUSE STANDARD; PRT; 111 AA.
AC P01654;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 2880/PC 1229.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
DR PIR; A01930; KVM80.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

Query Match 52.6%; Score 41; DB 1; Length 111;
Best Local Similarity 60.0%; Pred. No. 2.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
Db 24 RASQSVSTSGSYNMH 38

RESULT 10
KV3H_MOUSE STANDARD; PRT; 111 AA.
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KVM86.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

QY 1 KASQSVDFDGSYMN 15
Db 24 RASQSVSTSGSYNMH 38

RESULT 11
KV3J_MOUSE STANDARD; PRT; 111 AA.
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM837.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

QY 1 KASQSVDFDGSYMN 15
Db 24 RASQSVSTSGSYNMH 38

RESULT 12
KV3L_MOUSE STANDARD; PRT; 111 AA.
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KVM86.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;
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Query Match 52.6%; Score 41; DB 1; Length 111;  
 Best Local Similarity 53.3%; Pred. No. 2.1;  
 Matches 8; Conservative 5; Mismatches 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
 :||:|||||:|:|:  
 Db 24 RASESVDSYGNFSMH 38

## RESULT 12

KV3K\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01663;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 4050.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).

DR PIR: A01935; KVM5M6.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 52.6%; Score 41; DB 1; Length 111;  
 Best Local Similarity 53.3%; Pred. No. 2.1;  
 Matches 8; Conservative 5; Mismatches 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
 :||:|||||:|:|:  
 Db 24 RASESVDSYGNFSMH 38

## RESULT 13

KV3B\_MOUSE STANDARD; PRT; 112 AA.  
 AC P01655;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 7132.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 DR PIR: A01930; KVM580.

DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 102  
 FT DOMAIN 103 112  
 FT DISULFID 23 92  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 12054 MW; 5F0DD25EE20BE611 CRC64;

Query Match 52.6%; Score 41; DB 1; Length 112;  
 Best Local Similarity 60.0%; Pred. No. 2.2;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15  
 :||:|||||:|:|:  
 Db 24 RASESVDSYGNFSMH 38

## RESULT 14

KV3L\_MOUSE STANDARD; PRT; 131 AA.  
 AC P01661;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-35.  
 RA MEDLINE=78235887; PubMed=98179;  
 RA Burstein Y., Schechter I.;  
 RT "Primary structures of N-terminal extra peptide segments linked to  
 RT the variable and constant regions of immunoglobulin light chain  
 RT precursors: implications on the organization and controlled  
 RT expression of immunoglobulin genes.";  
 RL Biochemistry 17:2392-2400(1978).  
 RN [2]  
 RP SEQUENCE OF 21-131.  
 RX MEDLINE=73140225; PubMed=4691517;  
 RA McKean D.J., Potter M., Hood L.E.;  
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
 RT kappa chains with limited sequence differences.";  
 RL Biochemistry 12:760-771(1973).  
 RN [3]  
 RP REVISIONS.

RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 RT related mouse kappa variable regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 DR PIR: A01935; KVM5M6.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 131  
 FT DOMAIN 21 43  
 FT DOMAIN 44 58  
 FT DOMAIN 59 73  
 FT DOMAIN 74 80  
 FT DOMAIN 81 112  
 FT DOMAIN 113 121  
 FT DOMAIN 122 131  
 FT DISULFID 43 112  
 IG KAPPA CHAIN V-III REGION MOPC 63.  
 FRAMEWORK 1.  
 COMPLEMENTARITY-DETERMINING 1.  
 FRAMEWORK 2.  
 COMPLEMENTARITY-DETERMINING 2.  
 FRAMEWORK 3.  
 COMPLEMENTARITY-DETERMINING 3.  
 FRAMEWORK 4.  
 BY SIMILARITY.

FT NON\_TER 131 131  
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 52.6%; Score 41; DB 1; Length 131;  
Best Local Similarity 53.3%; Pred. No. 2.6;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGSYMN 15  
Db 44 RASEVDYSGNFMH 58

## RESULT 15

Y4RM\_RHISN STANDARD; PRT; 350 AA.  
AC P55646;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HYPOTHETICAL 39.4 KDA PROTEIN Y4RM.  
GN Y4RM.  
OS Rhizobium sp. (strain NGR234).  
OG Plasmid sym pNGR234a.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97305956; PubMed=9163424;  
RA Freilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
RA Perret X.;  
RT "Molecular basis of symbiosis between Rhizobium and legumes.";  
RL Nature 387:394-401(1997).  
CC -!- SIMILARITY: NONE OBVIOUS OUTSIDE OF SIMILARITY WITH Y4ZA.  
CC POTENTIAL FRAGMENT.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AE000094; AAB91838.1; -  
KW Hypothetical protein; Plasmid.  
FT SIMILAR 258 339 HIGHLY SIMILAR TO Y4ZA 34-115.  
SQ SEQUENCE 350 AA; 39381 MW; 6CBEGFACADD70DFC CRC64;

Query Match 51.9%; Score 40.5; DB 1; Length 350;  
Best Local Similarity 69.2%; Pred. No. 9.2;  
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 4 QSVDFDGS-YMN 15  
Db 230 QGVDFDNDSAFNN 242

Search completed: June 28, 2001, 15:54:35  
Job time: 123 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:20 ; Search time 411.58 Seconds  
(without alignments)  
4.822 Million cell updates/sec

Title: us-09-724-406-12

Perfect score: 78

Sequence: 1 KASQSVDFDGDSDSYN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	56.4	336	2 Q9X6V5	Q9X6V5 pseudomonas
2	44	56.4	340	2 Q9HX24	Q9HX24 pseudomonas
3	44	56.4	542	5 Q9NJD9	Q9NJD9 onchocerca
4	44	56.4	1868	10 Q9LVX3	Q9LVX3 arabidopsis
5	43	55.1	303	2 Q9KA25	Q9KA25 bacillus ha
6	43	55.1	2439	5 Q9VMS2	Q9VMS2 drosophila
7	41	52.6	264	2 Q9HXK0	Q9HXK0 pseudomonas
8	41	52.6	294	2 Q9HY55	Q9HY55 streptomyces
9	41	52.6	400	2 Q9Z4A1	Q9Z4A1 escherichia
10	41	52.6	400	2 Q9R2H5	Q9R2H5 salmonella
11	41	52.6	972	10 Q9ZW06	Q9ZW06 arabidopsis
12	40	51.3	131	10 Q9SRP5	Q9SRP5 arabidopsis
13	40	51.3	137	10 Q9SRP4	Q9SRP4 arabidopsis
14	40	51.3	171	10 Q9M7R0	Q9M7R0 olea europae
15	40	51.3	171	10 Q9M7Q9	Q9M7Q9 olea europae
16	40	51.3	311	2 Q86071	Q86071 pseudomonas
17	40	51.3	356	5 Q9NFF0	Q9NFF0 leishmania
18	40	51.3	985	14 Q9JFB4	Q9JFB4 vaccinia vi
19	40	51.3	1285	14 Q9QBB0	Q9QBB0 yaba monkey

20	40	51.3	1285	14	Q9DHP2
21	40	51.3	1286	14	Q57204
22	40	51.3	1286	14	Q9QNI9
23	40	51.3	1286	14	Q9Q903
24	40	51.3	1286	14	Q9Q8N2
25	40	51.3	1287	14	Q9J593
26	40	51.3	1289	14	Q85289
27	40	51.3	1289	14	Q98246
28	39	50.0	137	11	Q97596
29	39	50.0	186	5	Q9W2L0
30	39	50.0	262	5	Q05432
31	39	50.0	313	13	Q9YHF0
32	39	50.0	336	2	Q69589
33	39	50.0	336	2	Q96253
34	39	50.0	367	2	Q9HVX3
35	39	50.0	379	10	Q9M7R4
36	39	50.0	458	5	Q91079
37	39	50.0	551	10	Q93370
38	39	50.0	609	4	Q9H2V9
39	39	50.0	1024	5	Q9VM97
40	38	48.7	522	3	Q59740
41	38	48.7	761	2	Q9F7S9
42	38	48.7	896	10	Q9FV30
43	38	48.7	896	10	Q9FV29
44	38	48.7	900	5	Q44838
45	38	48.7	907	10	Q9SS78

## ALIGNMENTS

RESULT 1

Q9X6V5 ID Q9X6V5 PRELIMINARY; PRT; 336 AA.  
AC Q9X6V5  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE MEMBRANE-BOUND LYCIC TRANSGLYCOSYLASE PRECURSOR.  
GN MITB.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PA01;  
RA Gagnon L.A., Castro-Urbina I.M., Liao X., Hancock R.E.W., Clarke A.J.,  
RA Huletsky A.;  
RT "Cloning and characterization of PBP5 of Pseudomonas aeruginosa."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF147448; AAD32232.1;  
DR HSSP; P41052; 1fTM.  
KW Signal.  
FT SIGNAL 1 29 POTENTIAL.  
FT SIGNAL 336 336 POTENTIAL.  
SQ SEQUENCE 336 AA; 37423 MW; 1DAFBB8991787BBE CRC64;

Query Match 56.4%; Score 44; DB 2; Length 336;  
Best Local Similarity 63.6%; Pred. No. 12;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDFDGDSDSYN 15

Db 204 AVDFDGDGHIN 214

RESULT 2

Q9HX24 ID Q9HX24 PRELIMINARY; PRT; 340 AA.  
AC Q9HX24;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

01-MAR-2001 (Tremblrel. 16, Last sequence update)  
01-MAR-2001 (Tremblrel. 16, Last annotation update)  
MEMBRANE-BOUND LYTC TRANSGLYCOSYLASE.  
MLT2 OR PA4001.  
Pseudomonas aeruginosa.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
NCBI\_TaxID=287;  
[1]  
SEQUENCE FROM N.A.  
STRAIN-PA01;  
MEDLINE=20437337; PubMed=10984043;  
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
Garber R.L., Goulet L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
"Complete genome sequence of Pseudomonas aeruginosa PA01, an  
opportunistic pathogen";  
Nature 406:959-964(2000).  
EMBL; AE004817; AAC07388.1; 7A00BD23A0695BD8 CRC64;  
SEQUENCE 340 AA; 37867 MW; 7A00BD23A0695BD8 CRC64;  
Query Match 56.4%; Score 44; DB 2; Length 340;  
Best Local Similarity 63.6%; Pred. No. 13;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 5 SVDFDGDGYM 15  
:|||||:  
Db 208 AVDFDGDGHIN 218  
RESULT 3  
ID Q9NJD9 PRELIMINARY; PRT; 542 AA.  
AC Q9NJD9;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE CALCIUM-BINDING PROTEIN CBP-1.  
GN CBP-1.  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=20278137; PubMed=10816503;  
Lizotte-Waniewski M., Tawe W., Guiliano D.B., Lu W., Liu J.,  
Williams S.A., Lustigman S.;  
"Identification of potential vaccine and drug target candidates by  
expressed sequence tag analysis and immunoscreening of Onchocerca  
volvulus larval cDNA libraries";  
Infect. Immun. 68:3491-3501(2000).  
CC -1- SIMILARITY: TO EF-HAND FAMILY.  
DR EMBL; AF153720; AAF64251.1; -.  
DR InterPro; IPR002048; -.  
DR Pfam; PF00036; ehand; 10.  
DR PROSITE; PS00018; EF-HAND; UNKNOWN\_7.  
DR SMART; SM00054; EFH; 1.  
DR KEGG; K01004; Calcium-binding.  
KW Calcium-binding.  
SQ SEQUENCE 542 AA; 61269 MW; 94E3D57FB72D805B CRC64;  
Query Match 56.4%; Score 44; DB 5; Length 542;  
Best Local Similarity 58.3%; Pred. No. 21;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 4 QSVDFDGDGYM 15  
:|||||:  
Db 380 QSVDFDGDGHIN 391

RESULT 4  
Q9LVX3 PRELIMINARY; PRT; 1868 AA.  
ID Q9LVX3  
AC Q9LVX3;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE GENOMIC DNA, CHROMOSOME 3, P1 CLONE: MGF10.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
[1]  
SEQUENCE FROM N.A.  
STRAIN-COLUMBIA;  
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
[2]  
SEQUENCE FROM N.A.  
STRAIN-COLUMBIA;  
RX MEDLINE=20277480; PubMed=10819329;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
clones";  
DNA Res. 7:131-135(2000).  
DR EMBL; AB018114; BAE02691.1; -.  
DR InterPro; IPR000276; -.  
DR InterPro; IPR000345; -.  
DR InterPro; IPR001395; -.  
DR PROSITE; PS00063; ALDORETO\_REDUCTASE\_3; UNKNOWN\_1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; UNKNOWN\_1.  
SQ SEQUENCE 1868 AA; 206711 MW; 0799ADC38CC0C5F0 CRC64;  
Query Match 56.4%; Score 44; DB 10; Length 1868;  
Best Local Similarity 60.0%; Pred. No. 84;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 KASQSVDFDGDGYM 15  
:|||||:  
Db 1074 EASASSDIDSYSRN 1088  
RESULT 5  
Q9KA25 PRELIMINARY; PRT; 303 AA.  
ID Q9KA25  
AC Q9KA25;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE INTEGRASE/RECOMBINASE.  
GN CODV.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=86665;  
[1]  
SEQUENCE FROM N.A.  
STRAIN-C-125 / JCM 9153;  
RA Takami H., Nakasone K., Takaki Y.;  
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF001515; BAB06184.1; -.  
DR InterPro; IPR002104; -.  
DR Pfam; PF00589; Phage integrase; 1.  
SQ SEQUENCE 303 AA; 35035 MW; D10EA8AAFE1D6705 CRC64;  
Query Match 55.1%; Score 43; DB 2; Length 303;



```

Query Match      55.1%; Score 43; DB 5; Length 2439;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

RA	NCBI TaxID=1902;
RP	[1]
RC	SEQUENCE FROM N.A.
RA	STRAIN=A3(2);
RP	RA Brown S.P., Harris
RC	Submitted (MAY-2000
RA	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=A3(2);
RA	Cerdeno A.M., Park
RP	Submitted (MAY-2000
RC	[3]

```

RN  SEQUENCE FROM N.A.
RP  STRAIN=A3(2);
RC  MEDLINE=97000351; PubMed=8843436;
RA  Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RT  Kinashi H., Hopwood D.A.;
RT  "A set of ordered cosmids and a detailed genetic and physical map for
RT  the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL  Mol. Microbiol. 21:77-96(1996).
DR  EMBL; AL356832; CAB92672.1; -.
DR  InterPro; IPR000303; -.
DR  Pfam; PF00549; ligase-CoA; 1.
DR  PROSITE; PS01216; SUCCINYL_COA_LIG_1; UNKNOWN_1.
DR  PROSITE; PS00399; SUCCINYL_COA_LIG_2; 1.
DR  PROSITE; PS00399; SUCCINYL_COA_LIG_2; 1.
SQ  SEQUENCE 294 AA; 30238 MW; ECD4DC830CAE8F09 CRC64;

Query Match 52.6%; Score 41; DB 2; Length 294;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD 11
DB 11 |||||
DB 43 KAGTSVDFDGN 53

RESULT 9
QY24A1 PRELIMINARY; PRT; 400 AA.
AC Q924A1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE TRAF PROTEIN.
GN TRAF.
OS Escherichia coli.
OC Plasmid IncII Colib-p9.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN SEQUENCE FROM N.A.
RA Sempel G., Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete
RT nucleotide sequence of the Colib-p9 genome.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021078; BAA75169.1; -.
KW Plasmid.
SQ SEQUENCE 400 AA; 43180 MW; AB875F3869C7542A CRC64;

Query Match 52.6%; Score 41; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 DFDGDSYMN 15
DB 241 DFDGDKYHN 249
DB 241 DFDGDKYHN 249

RESULT 10
QY2H5 PRELIMINARY; PRT; 400 AA.
AC Q92H5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE TRAF PROTEIN.
GN TRAF.
OS Salmonella typhimurium.
OG Plasmid R64.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;

RN  SEQUENCE FROM N.A.
RP  STRAIN=DRD-11;
RC  Komano T., Narahara K., Yoshida T., Furuya N.;
RT  "The transfer region of IncII plasmid R64: similarities between R64
RT  tra genes and Legionella icm/dot genes.";
RL  Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN  SEQUENCE FROM N.A.
RP  STRAIN=DRD-11;
RC  MEDLINE=92011438; PubMed=1917882;
RA  Furuya N., Komano T.;
RT  "Determination of the nick site at origin of IncII plasmid R64: global
RT  similarity of origin structures of IncII and IncP plasmids.";
RL  J. Bacteriol. 173:6612-6617(1991).
RN  SEQUENCE FROM N.A.
RP  STRAIN=DRD-11;
RC  MEDLINE=98053841; PubMed=9393692;
RA  Furuya N., Komano T.;
RT  "Mutational analysis of the R64 origin region: requirement for precise
RT  location of the Nika-binding sequence.";
RL  J. Bacteriol. 179:7291-7297(1997).
RN  SEQUENCE FROM N.A.
RP  STRAIN=DRD-11;
RC  MEDLINE=98268996; PubMed=9603870;
RA  Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K.,
RA  Ogawa T., Komano T.;
RT  "Purification and characterization of thin pili of IncII plasmids
RT  Colib-p9 and R64: formation of PiliV-specific cell aggregates by type
RT  IV pili.";
RL  J. Bacteriol. 180:2842-2848(1998).
RN  SEQUENCE FROM N.A.
RP  STRAIN=DRD-11;
RC  MEDLINE=94132048; PubMed=8300611;
RA  Pansegrau W., Schroder W., Lanka E.;
RT  "Concerted action of three distinct domains in the DNA cleaving-
RT  joining reaction catalyzed by relaxase (TraI) of conjugative plasmid
RT  RP4.";
RL  J. Biol. Chem. 269:2782-2789(1994).
RN  SEQUENCE FROM N.A.
RP  STRAIN=DRD-11;
RC  MEDLINE=94285211; PubMed=8014987;
RA  Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G.,
RA  Haas D., Helinski D.R., Schwab H., Stanisich V.A., Thomas C.M.;
RT  "Complete nucleotide sequence of Birmingham IncP alpha plasmids.
RT  Compilation and comparative analysis.";
RL  J. Mol. Biol. 239:623-663(1994).
KW EMBL; AB027308; BAA77991.1; -.
SQ SEQUENCE 400 AA; 43194 MW; 55685F2E137B9250 CRC64;

Query Match 52.6%; Score 41; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 DFDGDSYMN 15
DB 241 DFDGDKYHN 249
DB 241 DFDGDKYHN 249

RESULT 11
QY2W06 PRELIMINARY; PRT; 972 AA.
AC Q92W06;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUMILIO-LIKE PROTEIN.

```



Query Match 51.3%; Score 40; DB 10; Length 171;  
 Best Local Similarity 58.3%; Pred. No. 28;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 QSVDFDGDGYNN 15  
 Db 138 KSVDSGDGYVS 149

RESULT 15  
 Q9M7Q9 PRELIMINARY; PRT; 171 AA.  
 AC Q9M7Q9;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE CALCIUM-BINDING PROTEIN.  
 GN PCA23.  
 OS Olea europaea (Common olive).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
 OC Lamiales; Oleaceae; Olea.  
 OX NCBI\_TaxID=4146;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20115491; PubMed=10648840;  
 RX Ledesma A., Villalba M., Rodriguez R.;  
 RT "Cloning, expression and characterization of a novel four EF-hand  
 Ca(2+)-binding protein from olive pollen with allergenic activity.";  
 RL FEBS Lett. 466:192-196(2000).  
 CC -!- SIMILARITY: TO EF-HAND FAMILY.  
 DR EMBL; AF078680; AAF31152.1; -.  
 DR InterPro; IPR002048; -.  
 DR InterPro; IPR003299; -.  
 DR Pfam; PF00036; efhand; 4.  
 DR PRINTS; PR01362; CALFLAGIN.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_4.  
 DR SMART; SM00054; EFh; 1.  
 KW Calcium-binding.  
 SQ SEQUENCE 171 AA; 18957 MW; 207B6F0468FAB83B CRC64;

Query Match 51.3%; Score 40; DB 10; Length 171;  
 Best Local Similarity 58.3%; Pred. No. 28;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 QSVDFDGDGYNN 15  
 Db 138 KSVDSGDGYVS 149

Search completed: June 28, 2001, 16:08:21  
 Job time: 949 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:35 ; Search time 362.28 Seconds

(without alignments)  
1.171 Million cell updates/sec

Title: US-09-724-406-14

Perfect score: 31

Sequence: 1 AASNLES 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
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8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
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11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
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13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	100.0	7	16 AAR70196	Mab 3B9 light chain
2	31	100.0	7	19 AAW83028	Anti-Fas MAB HFE7A
3	31	100.0	7	20 AAY23773	CDR of the light c
4	31	100.0	7	20 AAY18115	Light chain CDR fo
5	31	100.0	7	21 AAB14745	Mouse anti-Fas ant
6	31	100.0	7	21 AAW90895	Murine anti-Fas an
7	31	100.0	7	21 AAY59260	Antibody 4H5 L cha
8	31	100.0	7	21 AAY51137	Murine CD4/CD34 re
9	31	100.0	15	15 AAR66144	IF7 antibody varia
10	31	100.0	41	21 AAY91015	Antibody 4H5 L cha
11	31	100.0	103	21 AAY59263	

12	31	100.0	103	21	AA551140	Murine derived pro
13	31	100.0	106	14	AAR33309	MAE15 light chain.
14	31	100.0	106	21	AA85197	Light chain amino
15	31	100.0	111	10	AA90541	Immunoglobulin L c
16	31	100.0	111	15	AA55123	Mouse anti-HIV mu5
17	31	100.0	111	15	AA55127	Mouse-human chimere
18	31	100.0	111	15	AA60302	Anti HIV antibody
19	31	100.0	111	15	AA60306	Chimeric anti HIV
20	31	100.0	111	20	AA23781	Light chain variab
21	31	100.0	111	20	AA18123	Light chain sequen
22	31	100.0	111	21	AA59267	Antibody 4H5 L cha
23	31	100.0	111	21	AA551144	Murine derived pro
24	31	100.0	111	21	AA551146	Murine derived pro
25	31	100.0	112	13	AA24575	Human x mouse modi
26	31	100.0	113	22	AA671895	Monoclonal antibody
27	31	100.0	115	11	AA04134	Anti-Leu 3a light
28	31	100.0	131	10	AA90543	Amino acids sequen
29	31	100.0	131	11	AA04132	Anti-Leu 3a light
30	31	100.0	131	14	AAR32123	Anti-CD4 antibody
31	31	100.0	131	16	AA75355	Humanized antibody
32	31	100.0	131	16	AA70202	Humanized antibody
33	31	100.0	131	18	AAW34516	Variable kappa cha
34	31	100.0	131	20	AA23779	Light chain variab
35	31	100.0	131	20	AA23771	Light chain variab
36	31	100.0	131	20	AA18126	Light chain sequen
37	31	100.0	131	20	AA18118	Light chain sequen
38	31	100.0	132	16	AA70189	Mouse MAB 3B9 ligh
39	31	100.0	132	20	AA23767	Light chain variab
40	31	100.0	132	20	AA18120	Light chain sequen
41	31	100.0	218	18	AAW13563	Humanized anti-L-s
42	31	100.0	222	18	AAW01751	MH1 monoclonal ant
43	31	100.0	238	19	AAW83031	Anti-Fas humanised
44	31	100.0	238	19	AAW83032	Anti-Fas humanised
45	31	100.0	238	19	AAW83033	Anti-Fas humanised

## ALIGNMENTS

RESULT 1  
AAR70196  
ID AAR70196 standard; Protein; 7 AA.  
XX  
AC AAR70196;  
XX  
DT 20-SEP-1995 (first entry)  
XX  
DE MAB 3B9 light chain CDR.  
XX  
KW Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAB; Interleukin-4; IL-4; allergy; CDR;  
KW complementarity determining region.  
XX  
OS Mus sp.  
XX  
PN WO9507301-A.  
XX  
PD 16-MAR-1995.  
XX  
PF 07-SEP-1994; 94WO-US10308.  
XX  
PR 07-SEP-1993; 93US-0117366.  
XX  
PR 14-OCT-1993; 93US-0136783.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PI Gross MS, Holmes SD, Sylvester DR;  
XX  
XX WPI; 1995-123387/16.  
XX  
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
XX from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions

PS Disclosure; Page 55; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare  
CC hybridomas, which were screened for anti-IL-4 MAB secretion. Only  
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
CC chains were cloned into pGEM7f+ and transformed into E. coli  
CC DH5-alpha. A light chain cDNA clone was sequenced (AA083490) that  
CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were  
CC identified.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 3.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7  
Db 1 aasnles 7

RESULT 2

AAW83028  
ID AAW83028 standard; Peptide; 7 AA.

AC AAW83028;

XX 15-MAR-1999 (first entry)

DE Anti-Fas MAB HFE7A light chain CDR-L2.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy; complementarity determining region;  
CDR.

XX Mus musculus.

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY ) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

XX New antibodies and proteins bind conserved epitope of Fas antigen -  
PT used to evaluate drugs in animal models and to treat Fas-associated  
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
PT myocarditis, hepatitis and AIDS

PS Claim 9; Page 185; 292pp; English.

XX

CC This is the amino acid of complementarity determining region 2  
CC (CDR-L2) of the light chain (see AAW83042) of murine anti-human Fas  
CC monoclonal antibody HFE7A. The invention relates to antibodies,  
CC especially humanised antibodies (see AAW83031-37), recognising the  
CC Fas antigen. Such antibodies preferably comprise a heavy chain and  
CC a light chain including CDRs (see AAW83024-29) from the heavy and  
CC light chains of HFE7A. Humanised antibodies are produced by CDR  
CC grafting. The antibodies are capable of inducing apoptosis in  
CC abnormal cells expressing Fas, and of inhibiting Fas-induced  
CC apoptosis in normal cells. They are used to evaluate, in animal  
CC models, treatments of diseases that involve Fas/Fas ligand  
CC interactions, and also to treat such diseases, including autoimmune  
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,  
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's  
CC disease, thrombopenia purpura and insulin-dependent diabetes),  
CC allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
CC glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and  
CC transplant rejection (all claimed).

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 3.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7  
Db 1 aasnles 7

RESULT 3

AAW23773  
ID AAY23773 standard; Peptide; 7 AA.

AC AAY23773;

XX 13-SEP-1999 (first entry)

XX CDR of the light chain variable region of antibody 3B9.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;  
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;  
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
KW rheumatoid arthritis; host-versus-graft disease; renal disease;  
KW allergy; complementarity determining region.

XX Mus sp.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85890.

XX New DNA molecules encoding recombinant antibodies useful for

PT treating IL4-mediated conditions  
 PS Example 3; Column 43-44; 50pp; English.  
 XX  
 CC The present sequence represents a complementarity determining region  
 CC (CDR) of the light chain variable region of murine interleukin-4  
 CC (IL-4) antibody 3B9. The specification describes chimeric and  
 CC humanised IL-4 monoclonal antibodies. The antibodies of the  
 CC invention are used in therapeutic and pharmaceutical compositions  
 CC for treating IL-4 mediated and immunoglobulin E-mediated allergic  
 CC reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis,  
 CC atopic asthma, anaphylactic shock, rheumatoid arthritis,  
 CC host-versus-graft disease and renal disease. They are also useful  
 CC in the diagnosis of an allergy or condition associated with excess  
 CC IL-4 production through the measurement e.g. by ELISA of circulating  
 CC endogenous IL-4 levels in humans.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
 Db 1 aasnles 7

RESULT 4  
 AAY18115  
 ID AAY18115 standard; peptide; 7 AA.  
 XX  
 AC AAY18115;  
 XX  
 DT 11-AUG-1999 (first entry)  
 DE  
 DE Light chain CDR for hIL-4 specific antibody.

Antibody; Interleukin-4; IL4; immunoglobulin E; IgE mediated disease;  
 allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;  
 atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;  
 autoimmune disease; graft versus host disease;  
 complementarity determining region; CDR.

Synthetic.

US5914110-A.

22-JUN-1999.

07-JUN-1995; 95US-0483636.

07-JUN-1995; 95US-0483636.

07-SEP-1993; 93US-0117366.

14-OCT-1993; 93US-0136783.

07-SEP-1994; 94WO-US10308.

(SMIK ) SMITHKLINE BEECHAM CORP.

(SMIK ) SMITHKLINE BEECHAM PLC.

Gross MS, Holmes SD, Sylvester DR;

WPI; 1999-370482/31.

N-PSDB; AAX79514.

Recombinant IL4 antibodies

Claim 7; Column 43; 50pp; English.

This sequence represents a light chain complementarity determining region  
 (CDR) from an antibody of the invention. The antibody is a chimeric or  
 humanised interleukin-4 (IL4) monoclonal antibody for the treatment of

CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for  
 CC the treatment of allergic disorders such as allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.  
 CC The antibodies are also useful for regulating B and T cell proliferation  
 CC and as such are useful in the treatment of autoimmune diseases and graft  
 CC versus host disease.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
 Db 1 aasnles 7

RESULT 5  
 AAB14745  
 ID AAB14745 standard; peptide; 7 AA.  
 XX  
 AC AAB14745;  
 XX  
 DT 24-NOV-2000 (first entry)  
 DE  
 DE Mouse anti-Fas antibody HFE7A light chain CDR2.

Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 murine; complementarity determining region; CDR; human Fas;  
 Fas ligand; apoptosis modulator; programmed cell death;  
 autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 hepatitis; AIDS; graft rejection; light chain.

Mus musculus.

JP2000169393-A.

20-JUN-2000.

30-SEP-1999; 99JP-0278301.

30-SEP-1998; 98JP-0276883.

(SANY ) SANKYO CO LTD.

WPI; 2000-485645/43.

Preventive or treating agent for the diseases caused by an abnormality  
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 anti-Fas antibody

Claim 10; Page 63; 139pp; Japanese.

The invention relates to compositions for the prevention or treatment  
 of diseases caused by an abnormality in the Fas/Fas ligand system  
 containing an anti-Fas antibody as the active component. The anti-Fas  
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 or a humanised version of HFE7A containing identical CDRs  
 (complementarity determining regions) to antibody HFE7A. Via its  
 interaction with Fas, the antibody of the invention acts as a modulator  
 of apoptosis. The compositions of the invention may therefore be used in  
 the treatment or prevention of conditions such as autoimmune diseases,  
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3  
 of the light chain of the murine anti-human Fas monoclonal antibody  
 HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).

Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 | | | | |  
 Db 1 aasnles 7

## RESULT 6

AAW90895  
 ID AAW90895 standard; peptide; 7 AA.

XX AC AAW90895;

XX 08-AUG-2000 (first entry)

DT Murine anti-Fas antibody peptide fragment #5.

DE Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;  
 XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Mus musculus.

OS EF990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

XX (SANY ) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems

XX Disclosure; Page 98; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like  
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a murine anti-Fas antibody peptide fragment described in the method  
 CC of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 3.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 | | | | |  
 Db 1 aasnles 7

## RESULT 7

AAW59260  
 ID AAW59260 standard; peptide; 7 AA.

XX AC AAW59260;

XX 17-APR-2000 (first entry)

XX Antibody 4H5 L chain variable region CDR2 fragment.

DE CD4 antigen; anti-human; antibody; 4H5; drug; CDR;

KW complementarity determining region.

XX Mus sp.

OS JP11332563-A.

XX 07-DEC-1999.

XX 26-MAY-1998; 98JP-0163034.

XX 26-MAY-1998; 98JP-0163034.

XX (ASAH ) ASAH KASEI KOGYO KK.

XX WPI; 2000-091351/08.

XX An antibody and the nucleic acid coding the antibody -

PS Claim 2; Page 14; 25pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. Sequences  
 CC AAY59259-61 represent the complementarity determining region (CDR)-1,  
 CC CDR-2 and CDR-3 fragments in the L chain variable region of the  
 CC antibody 4H5 respectively.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 3.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 | | | | |  
 Db 1 aasnles 7

## RESULT 8



AA51137  
ID AA51137 standard; Protein; 7 AA.

AC AA51137;

XX 31-MAR-2000 (first entry)

XX Murine CD4/CD34 recognizing antibody light chain CDR-2 region #1.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; complementarity determining region;  
KW CDR-2; light chain; murine.

XX Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH) ASAHI KASEI KOGYO KK.

PA (ASAH) ASAHI MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX Devices containing antibodies recognising CD4 or CD34 and their use for  
PT the separation of CD4 or CD34 positive cells

XX Claim 3; Page 77; 11pp; Japanese.

XX This invention describes a novel device (I) for separating cluster  
CC differentiation (CD)-positive cells using a recombinant (chimeric or  
CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
CC for the separation of CD4 or CD34 positive cells, which is useful for  
CC the collection of hematopoietic undifferentiated cells, elimination of  
CC lymphocytes from cells to be used in bone marrow transplantation, the  
CC detection of leukemic cells and the production of medicinal  
CC compositions for the treatment of HIV infection and autoimmune diseases.  
CC This sequence represents a murine derived complementarity determining  
CC region CDR-2 protein fragment which is used to illustrate the method of  
CC the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 1 aasnles 7

RESULT 9

ID AAR66144 standard; peptide; 15 AA.

XX AAR66144;

XX 12-JUL-1995 (first entry)

XX CD-4 antibody variable region complementary peptide.

XX CD-4 antibody variable region; complementary peptide;  
KW extra-corporeal blood circulation; cell filter material.

XX Synthetic.

XX JP06269663-A.

XX 27-SEP-1994.

XX 17-MAR-1993; 93JP-0057206.

XX 17-MAR-1993; 93JP-0057206.

XX (TOYM) TOYOKO KK.

XX WPI; 1994-346316/43.

XX Material for collecting cells positive for CD-4 antibody -  
PT comprises nonwoven fabric having keto-alkyl halide functional gp  
XX Example 2; Page 7; 9pp; Japanese.

XX AAR66140-R66146 are peptides complementary to the variable region  
CC of the CD-4 antibody, these peptides are fixed onto a claimed  
CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with  
CC keto-alkyl halide functional groups. This material can be used  
CC as a filter for CD-4 positive cells in a medical treatment  
CC involving the extra-corporeal circulation of blood.

XX Sequence 15 AA;

Query Match 100.0%; Score 31; DB 15; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.95;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 9 aasnles 15

RESULT 10

AA51137

ID AA51137 standard; protein; 41 AA.

XX AA51137;

XX 05-SEP-2000 (first entry)

XX 1F7 antibody variable light chain L2 amino acid sequence SEQ ID NO:6.  
XX 1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;  
KW AIDS; anti-HIV; human immunodeficiency virus; detection;  
KW acquired immunodeficiency syndrome.

XX Mus sp.

XX US6057421-A.

XX 02-MAY-2000.

XX 03-DEC-1997; 57US-0984277.

XX 30-NOV-1994; 54US-0351193.

XX (IMMP-) IMMOPHON INC.

XX Muller S, Kohler H;

XX WPI; 2000-338622/29.

XX Variable heavy and light chain regions of murine monoclonal antibody  
PT 1F7, useful for treating HIV infection and AIDS  
XX Claim 1; Fig 8; 45pp; English.

XX The present invention describes the variable heavy and light chain  
 CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAY91014 to  
 CC AAY91016 represent specifically claimed amino acid sequences of the  
 CC variable light chain, and AAY91017 to AAY91019 represent specifically  
 CC claimed amino acid sequence of the variable heavy chain. The antibodies  
 CC are used for treatment of HIV (human immunodeficiency virus) infection  
 CC and AIDS (acquired immunodeficiency syndrome). They are also used for  
 CC detecting HIV in serum and for stimulating HIV antigen related and  
 CC committed B cells to produce broadly reactive and neutralising antibodies  
 CC by clonotypic stimulation.

XX Sequence 41 AA;

Query Match 100.0%; Score 31; DB 21; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 Db 12 aasnles 18  
 |||||

RESULT 11  
 ID AAY59263  
 ID AAY59263 standard; protein; 103 AA.

XX AC AAY59263;  
 XX DT 17-APR-2000 (first entry)  
 XX DE Antibody 4H5 L chain variable region.  
 XX KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX OS Mus sp.

XX JP11332563-A.  
 XX PD 07-DEC-1999.  
 XX PF 26-MAY-1998; 98JP-0163034.  
 XX PR 26-MAY-1998; 98JP-0163034.  
 XX PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX DR WPI; 2000-091351/08.  
 XX DR N-PSDB; AAZ58662.

XX An antibody and the nucleic acid coding the antibody -  
 XX Claim 5; Page 15-16; 23pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the L chain variable region of the antibody 4H5.

XX Sequence 103 AA;

Query Match 100.0%; Score 31; DB 21; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 Db 46 aasnles 52  
 |||||

RESULT 12

AAY51140  
 ID AAY51140 standard; Protein; 103 AA.

XX AC AAY51140;  
 XX DT 31-MAR-2000 (first entry)  
 XX DE Murine derived protein fragment #2.  
 XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX OS Mus sp.

XX WO9961629-A1.

XX PD 02-DEC-1999.

XX PF 24-MAY-1999; 99WO-JP02711.

XX PR 25-MAY-1998; 98JP-0159957.

XX PR 26-MAY-1998; 98JP-0163023.

XX PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX PA (ASAH ) ASAH MEDICAL CO LTD.

XX PI Ono M, Soka T, Morimoto I, Miyamura K;

XX DR WPI; 2000-086720/07.

XX DR N-PSDB; AAZ44204.

XX Devices containing antibodies recognising CD4 or CD34 positive cells  
 PT the separation of CD4 or CD34 positive cells -

XX Claim 22; Page 79; 111pp; Japanese.

XX This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.

XX Sequence 103 AA;

Query Match 100.0%; Score 31; DB 21; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 Db 46 aasnles 52  
 |||||

RESULT 13

AAAR33309

ID AAR33309 standard; Protein; 106 AA.

XX AC AAR33309;

XX DT 05-JUL-1993 (first entry)

XX DE MAE15 light chain.

XX KW Antibody; high affinity; FCEH; low affinity; FCEL;  
 KW IgE receptor; histamine; mast cell; basophil; Kabat;  
 KW CDR; murine; MAE11; MAE13; MAE15; MAE17.

XX OS Synthetic.  
 XX PN WO9304173-A.  
 XX PD 04-MAR-1993.  
 XX PF 14-AUG-1992; 92WO-US06860.  
 XX PR 14-AUG-1991; 91US-0744768.  
 XX PR 07-MAY-1992; 92US-0879495.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Jardieu PM, Presta LG;  
 XX WPI; 1993-094004/11.  
 XX DR Polypeptide(s) binding to specific Fc epsilon receptors - act as  
 XX PT IgE antagonists; useful for treating and preventing IgE-mediated  
 XX PT disorders e.g. allergies  
 XX PS Disclosure: Fig 2; 113pp; English.  
 XX CC Antibodies capable of binding FcEL-bound IgE but which are  
 XX CC substantially incapable of binding FcEL-bound IgE or inducing  
 XX CC histamine release from mast cells or basophils, comprise a human  
 XX CC Kabat CDR domain into which has been substituted a positionally  
 XX CC analogous residue from a Kabat CDR domain of the murine anti-huIgE  
 XX CC antibodies MAE11, MAE13, MAE15 or MAE17.  
 XX SQ Sequence 106 AA;

Query Match 100.0%; Score 31; DB 14; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 7.7; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7  
 DB 54 aasnles 60

RESULT 14  
 AAY85197  
 ID AAY85197 standard; protein; 106 AA.  
 XX AC AAY85197;  
 XX DT 29-JUN-2000 (first entry)  
 XX DE Light chain amino acid sequence of mouse antibody MAE15.  
 XX KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcEL; FcEH;  
 XX KW low affinity binding receptor; high affinity binding receptor; allergy;  
 XX KW diagnosis; treatment; histamine release; prevent; light chain.  
 XX OS Mus sp.  
 XX PN US6037453-A.  
 XX PD 14-MAR-2000.  
 XX PF 06-JUN-1995; 95US-0466151.  
 XX PR 15-MAR-1995; 95US-0405617.  
 XX PR 14-AUG-1992; 92WO-US06860.  
 XX PR 26-JAN-1994; 94US-0185899.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Presta LG, Jardieu PM;

DR WPI; 2000-269913/23.  
 XX New bispecific antibodies, useful for treating immunoglobulin  
 XX PT E-mediated disease, binds to IgE, but only when on the low affinity  
 XX PT receptor, and to an antigen other than IgE  
 XX PS Claim 1; Fig 2; 48pp; English.  
 XX CC This sequence represents the light chain amino acid sequence of a mouse  
 XX CC anti-human immunoglobulin E (IgE) antibody. The invention relates to a  
 XX CC bispecific antibody that binds specifically to IgE when IgE is bound to  
 XX CC its low affinity receptor (FcEL), but does not bind to IgE, when IgE is  
 XX CC bound to its high affinity receptor (FcEH). The bispecific antibody  
 XX CC comprises an IgE-binding arm with human framework residues of a recipient  
 XX CC human antibody and donor murine CDR (complementarity determining region)  
 XX CC residues, but with at least one human CDR residue replacing the analogous  
 XX CC murine residue. The antibody also comprises an Fv that is specific for a  
 XX CC predetermined antigen other than IgE. The antibodies work by displacing  
 XX CC bound IgE from its receptor, or via competitive inhibition of its  
 XX CC binding. The bispecific antibodies are used for diagnosis, treatment and  
 XX CC prevention of allergy and other IgE-mediated diseases, also, when  
 XX CC immobilised, for the isolation of FcEL from cells (for research or  
 XX CC therapy). The bispecific antibodies of the invention do not cause  
 XX CC granulation or release of histamine from mast cells.  
 XX SQ Sequence 106 AA;

Query Match 100.0%; Score 31; DB 21; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 7.7; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7  
 DB 54 aasnles 60

RESULT 15  
 AAP90541  
 ID AAP90541 standard; protein; 111 AA.  
 XX AC AAP90541;  
 XX DT 20-OCT-1989 (first entry)  
 XX DE Immunoglobulin L chain variable region.  
 XX KW Immunoglobulin; L chain variable region; HIV.  
 XX OS Mus musculus.  
 XX PN EP327000-A.  
 XX PD 09-AUG-1989.  
 XX PF 30-JAN-1989; 83EP-0101583.  
 XX PR 30-JAN-1988; 83JP-0020255.  
 XX PR 08-JUL-1988; 83JP-0171385.  
 XX PA (KAGA ) THE CHEMO-SERO-THERAPEUTIC RESEARCH INSTITUTE.  
 XX PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T;  
 XX PI Takatsuki K;  
 XX WPI; 1989-229050/32.  
 XX DR N-PSDB; AAN90491, AAN90492, AAN90493.  
 XX XX Chimeric anti-human immune virus antibodies - contg. mouse variable  
 XX PT regions and human constant regions for diagnosis, treatment and  
 XX PT prevention of AIDS  
 XX PS Claim 5; page 15; 33pp; English.

XX

CC The sequence is an L chain variable region from an immunoglobulin with  
 CC anti-HIV neutralising activity. See AAN90491-3, and AAN90495.  
 XX

SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 10; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 54 aasnles 60

Search completed: June 28, 2001, 16:14:35  
 Job time: 1323 sec

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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds  
(without alignments)  
1.019 Million cell updates/sec

Title: us-09-724-406-14

Perfect score: 31

Sequence: 1 AASNLES 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	2	US-08-483-636-18
2	31	100.0	7	2	US-08-483-632-18
3	31	100.0	41	3	US-08-984-277-6
4	31	100.0	106	3	US-08-466-151-6
5	31	100.0	111	1	US-08-491-845-8
6	31	100.0	111	1	US-08-491-845-8
7	31	100.0	111	2	US-08-483-636-73
8	31	100.0	111	2	US-08-483-632-73
9	31	100.0	115	4	US-08-513-968-51
10	31	100.0	131	2	US-08-483-636-14
11	31	100.0	131	2	US-08-483-636-58
12	31	100.0	131	2	US-08-483-632-14
13	31	100.0	131	2	US-08-483-632-58
14	31	100.0	131	3	US-08-589-939-3
15	31	100.0	131	4	US-08-579-378A-14
16	31	100.0	131	4	US-08-579-378A-18
17	31	100.0	132	2	US-08-483-632-2
18	31	100.0	132	2	US-08-483-636-2
19	31	100.0	218	5	PCT-US96-13152-2
20	28	90.3	7	2	US-08-650-262-11
21	28	90.3	98	3	US-08-881-037-75
22	28	90.3	108	2	US-08-650-262-2
23	28	90.3	120	1	US-08-111-080-24
24	28	90.3	120	1	US-08-211-980-24
25	28	90.3	120	5	PCT-US93-07967-24
26	27	87.1	6	1	US-08-137-1170-137
27	27	87.1	6	2	US-08-436-717-137

28	27	87.1	17	2	US-08-712-212-5	Sequence 5, Appl
29	27	87.1	17	5	PCT-US95-05160-5	Sequence 5, Appl
30	27	87.1	64	2	US-08-765-179B-10	Sequence 10, Appl
31	27	87.1	106	1	US-08-202-047-26	Sequence 26, Appl
32	27	87.1	106	3	US-08-964-690-26	Sequence 26, Appl
33	27	87.1	111	1	US-07-634-278-46	Sequence 46, Appl
34	27	87.1	111	1	US-07-634-278-46	Sequence 47, Appl
35	27	87.1	111	1	US-08-111-080-30	Sequence 30, Appl
36	27	87.1	111	1	US-08-111-080-30	Sequence 32, Appl
37	27	87.1	111	1	US-08-477-728-47	Sequence 46, Appl
38	27	87.1	111	1	US-08-477-728-47	Sequence 11, Appl
39	27	87.1	111	1	US-08-275-053-14	Sequence 14, Appl
40	27	87.1	111	1	US-08-275-053-14	Sequence 30, Appl
41	27	87.1	111	1	US-08-211-980-30	Sequence 32, Appl
42	27	87.1	111	1	US-08-211-980-30	Sequence 30, Appl
43	27	87.1	111	1	US-08-207-169A-4	Sequence 4, Appl
44	27	87.1	111	1	US-08-474-040-46	Sequence 46, Appl
45	27	87.1	111	1	US-08-474-040-47	Sequence 47, Appl

#### ALIGNMENTS

RESULT 1  
US-08-483-636-18  
; Sequence 18, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

us-09-724-406-14.ra

Fri Jun 29 08:04:26 2001

US-08-483-636-18

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
| | | | |  
DB 1 AASNLES 7

RESULT 2

US-08-483-632-18  
; Sequence 18, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/483,632  
; FILING DATE: 14-OCT-1993  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-483-632-18

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
| | | | |  
DB 1 AASNLES 7

RESULT 3

US-08-984-277-6  
; Sequence 6, Application US/08984277  
; Patent No. 6057421  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Sybille  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY IF7  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: U.S.  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/984,277  
; FILING DATE: 3-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca, Daniel  
; REGISTRATION NUMBER: 42,368  
; REFERENCE/DOCKET NUMBER: 50200-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-756-8600  
; TELEFAX: 202-756-8699  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 41 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; US-08-984-277-6

Query Match 100.0%; Score 31; DB 3; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
| | | | |  
DB 12 AASNLES 18

RESULT 4

US-08-466-151-6  
; Sequence 6, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardiou, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,151

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/466163

FILING DATE: 06-Jun-1995

APPLICATION NUMBER: 08/405617

FILING DATE: 15-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/185899

FILING DATE: 26-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/879495

FILING DATE: 07-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744768

FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P0718P2C1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-466-151-6

Query Match 100.0%; Score 31; DB 3; Length 106;

Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 54 AASNLES 60

RESULT 5

US-08-491-845-8

Sequence 8, Application US/08491845

Patent No. 5773247

GENERAL INFORMATION:

APPLICANT: MAEDA, Hiroaki

APPLICANT: KIMACHI, Kazuhiko

APPLICANT: EDA, Yasuyuki

APPLICANT: SHIOSAKI, Kouichi

APPLICANT: OSATOMI, Kiyoshi

APPLICANT: TOKIYOSHI, Sachio

TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street N.W. Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/491,845

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00039

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: MAEDA-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-491-845-8

Query Match 100.0%; Score 31; DB 1; Length 111;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 54 AASNLES 60

RESULT 6

US-08-491-845-16

Sequence 16, Application US/08491845

Patent No. 5773247

GENERAL INFORMATION:

APPLICANT: MAEDA, Hiroaki

APPLICANT: KIMACHI, Kazuhiko

APPLICANT: EDA, Yasuyuki

APPLICANT: SHIOSAKI, Kouichi

APPLICANT: OSATOMI, Kiyoshi

APPLICANT: TOKIYOSHI, Sachio

TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street N.W. Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/491,845

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00039

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: MAEDA-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

; LENGTH: 111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-491-845-16

Query Match 100.0%; Score 31; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 7  
US-08-483-636-73  
; Sequence 73, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5090  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-483-636-73

Query Match 100.0%; Score 31; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 8  
US-08-483-632-73  
; Sequence 73, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,632  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-483-632-73

Query Match 100.0%; Score 31; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 9  
US-08-513-968-51  
; Sequence 51, Application US/08513968  
; Patent No. 6114143



;; GENERAL INFORMATION:  
;; APPLICANT: EDA, Yasuyuki  
;; APPLICANT: MAEDA, Hiroaki  
;; APPLICANT: MAKIZUMI, Keiichi  
;; APPLICANT: SHIOSAKI, Kouichi  
;; APPLICANT: OSATOMI, Kiyoshi  
;; APPLICANT: KINACHI, Kazuhiko  
;; APPLICANT: HIGUCHI, Hirofumi  
;; APPLICANT: TOKIYOSHI, Sachio  
;; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY  
;; NUMBER OF SEQUENCES: 86  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BROWDY AND NEIMARK  
;; STREET: 419 Seventh Street, N.W., Suite 300  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/513,968  
;; FILING DATE: 11-SEP-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 78913/1993  
;; FILING DATE: 11-MAR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BROWDY, Roger L.  
;; REGISTRATION NUMBER: 25,618  
;; REFERENCE/DOCKET NUMBER: EDA-1  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; TELEX: 248633  
;; INFORMATION FOR SEQ ID NO: 51:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 115 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-513-968-51

Query Match 100.0%; Score 31; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
Db 58 AASNLES 64

RESULT 10  
US-08-483-636-14  
; Sequence 14, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TREATMENT OF IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA

;; COUNTRY: USA  
;; ZIP: 19406-0939  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/483,636  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/117366  
;; FILING DATE: 07-SEP-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/136783  
;; FILING DATE: 14-OCT-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US/94/10308  
;; FILING DATE: 07-SEP-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sutton, Jeffrey A.  
;; REGISTRATION NUMBER: 34,028  
;; REFERENCE/DOCKET NUMBER: P50186-3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 270-5024  
;; TELEFAX: (215) 270-5090  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 131 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-483-636-14

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
Db 73 AASNLES 79

RESULT 11  
US-08-483-636-58  
; Sequence 58, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TREATMENT OF IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-636-58

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 73 AASNLES 79

RESULT 12
US-08-483-632-14
; Sequence 14, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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```
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-632-14

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 73 AASNLES 79

RESULT 13
US-08-483-632-58
; Sequence 58, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-483-632-58

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 73 AASNLES 79

RESULT 14

US-08-589-939-3  
; Sequence 3, Application US/08589939  
; Patent No. 6015662  
; GENERAL INFORMATION:  
; APPLICANT: Hackett, Jr., John R.  
; APPLICANT: Hoff, Jane A.  
; APPLICANT: Ostrow, David H.  
; APPLICANT: Golden, Alan M.  
; TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: US  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/589,939  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5865.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-935-1729  
; TELEFAX: 847-938-2623  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-589-939-3

Query Match 100.0%; Score 31; DB 3; Length 131;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 74 AASNLES 80

RESULT 15

US-08-579-378A-14  
; Sequence 14, Application US/08579378A  
; Patent No. 6210671  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; TITLE OF INVENTION: Humanized Antibodies Reactive with

; TITLE OF INVENTION: L-Selectin  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/579,378A  
; FILING DATE: 27-DEC-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/160,074  
; FILING DATE: 30-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/983,946  
; FILING DATE: 01-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95112895.8  
; FILING DATE: 17-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95114696.8  
; FILING DATE: 19-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebescheutz, Joe O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 11823-002220  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-579-378A-14

Query Match 100.0%; Score 31; DB 4; Length 131;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 74 AASNLES 80

Search completed: June 28, 2001, 16:01:14  
Job time: 522 sec





us-09-724-406-14.rpr

Fri Jun 29 08:04:27 2001

```

Db      7 AASNLES 13
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RESULT  3
A38601
Ig kappa chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601
R:Cosborn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAAG3359.1; PID:g196403
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 AASNLES 7
Db  35 AASNLES 41
      |||||

RESULT  4
KVMS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: D01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: D01937
A:Molecule type: protein
A:Residues: 1-110 <WEI>
A:Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42194
A:Molecule type: DNA
A:Residues: 12-99 <MO>
A:Cross-references: EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PID:g407845
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42190
A:Molecule type: DNA
A:Residues: 13-99 <MOF>
A:Cross-references: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PID:g407839
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42189
A:Molecule type: DNA
A:Residues: 15-99 <MOA>
A:Cross-references: EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PID:g407837
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42188
A:Molecule type: DNA
A:Residues: 12-99 <MOZ>
A:Cross-references: EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42191
A:Molecule type: DNA
A:Residues: 10-99 <MOY>
A:Cross-references: EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42192
A:Molecule type: DNA
A:Residues: 10-99 <MOO>
A:Cross-references: EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PID:g407843
A:Note: V-kappa-2Ie; anti-collagen
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

Db      7 AASNLES 13
      |||||
RESULT  3
A38601
Ig kappa chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601
R:Cosborn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAAG3359.1; PID:g196403
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 AASNLES 7
Db  35 AASNLES 41
      |||||

RESULT  4
KVMS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: D01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: D01937
A:Molecule type: protein
A:Residues: 1-110 <WEI>
A:Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42194
A:Molecule type: DNA
A:Residues: 12-99 <MO>
A:Cross-references: EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PID:g407845
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42190
A:Molecule type: DNA
A:Residues: 13-99 <MOF>
A:Cross-references: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PID:g407839
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42189
A:Molecule type: DNA
A:Residues: 15-99 <MOA>
A:Cross-references: EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PID:g407837
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42188
A:Molecule type: DNA
A:Residues: 12-99 <MOZ>
A:Cross-references: EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42191
A:Molecule type: DNA
A:Residues: 10-99 <MOY>
A:Cross-references: EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A:Note: V-kappa-2Ie; anti-collagen
A:Accession: S42192
A:Molecule type: DNA
A:Residues: 10-99 <MOO>
A:Cross-references: EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PID:g407843
A:Note: V-kappa-2Ie; anti-collagen
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

Db      7 AASNLES 13
      |||||
RESULT  3
A38601
Ig kappa chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601
R:Cosborn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAAG3359.1; PID:g196403
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      100.0%; Score 31; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 AASNLES 7
Db  54 AASNLES 60
      |||||

RESULT  5
KVMSC1
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A:Reference number: A93822; MUID:79012520
A:Accession: A01936

```

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 7  
KVMS83  
Ig kappa chain V region (PC7183) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: B01937; A01937  
R:Weigert, M.; Galmat, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152  
A:Accession: B01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 8  
KVMS69  
Ig kappa chain V region (PC7769) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: E01937; A01937  
R:Weigert, M.; Galmat, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152  
A:Accession: E01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AASNLES 7  
Db 54 AASNLES 60

Db 54 AASNLES 60

RESULT 9

SI9971  
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: SI9971; SI9973  
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: SI9963  
A:Accession: SI9971  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289  
A:Experimental source: clone M-T310  
A:Accession: SI9973  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293  
A:Experimental source: M-T404  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 10

SI9976  
Ig kappa chain V region (M-T413) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: SI9976  
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: SI9963  
A:Accession: SI9976  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 11

PHI226  
Ig kappa chain precursor V region (M-T310) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000  
C:Accession: PHI226  
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L

Gene 121, 271-278, 1992  
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on  
A:Reference number: PH1224; MUID:93077041  
A:Accession: PH1226  
A:Molecule type: mRNA  
A:Residues: 1-131 <WEI>  
A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766  
A:Note: This mouse sequence was hybridized and fused with a human constant region gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-131/Product: Ig light chain V region #status predicted <MAT>  
F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 AASNLES 7  
|||||||  
DB 74 AASNLES 80

RESULT 12  
B64160  
hypothetical protein HI0852 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: B64160  
R:Flaeschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.  
Gocayne, J.D.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: B64160  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-463 <TIGR>  
A:Cross-references: GB:U32766; GB:I42023; NID:gl573854; PIDN:AAC22509.1; PID:gl573866; T  
A:Note: best homolog was a hypothetical protein from Escherichia coli  
C:Superfamily: multidrug-efflux transporter  
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 100.0%; Score 31; DB 2; Length 463;  
Best Local Similarity 100.0%; Pred. No. 6.3; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 AASNLES 7  
|||||||  
DB 94 AASNLES 100

RESULT 13  
T39624  
6-phosphofructokinase beta subunit - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000  
C:Accession: T39624  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.  
submitted to the EMBL Data Library, March 1998  
A:Reference number: Z21843  
A:Accession: T39624  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-942 <WOO>  
A:Cross-references: EMBL:AL022104; PIDN:CAAL17900.1; GSPDB:GN00067; SPDB:SPBPC16H5.02  
A:Experimental source: strain 972h; cosmid c16H5  
C:Genetics:  
A:Gene: SPDB:SPBPC16H5.02

A:Map position: 2  
A:Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology  
C:Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology

Query Match 100.0%; Score 31; DB 2; Length 942;  
Best Local Similarity 100.0%; Pred. No. 14; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 AASNLES 7  
|||||||  
DB 165 AASNLES 171

RESULT 14  
T00362  
hypothetical protein KIAA0675 - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 02-Sep-2000  
C:Accession: T00362  
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura,  
DNA Res. 5, 169-176, 1998  
A:Title: Prediction of the coding sequences of unidentified human genes. X. The compl  
A:Reference number: Z14142; MUID:98403880  
A:Accession: T00362  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1208 <ISH>  
A:Cross-references: EMBL:AB014575; NID:g3327163; PIDN:BAA31650.1; PID:g3327164  
A:Experimental source: brain; clone HK02566  
C:Genetics:  
A:Note: KIAA0675  
C:Superfamily: RING finger homology  
F:1144-1193/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 31; DB 2; Length 1208;  
Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 AASNLES 7  
|||||||  
DB 896 AASNLES 902

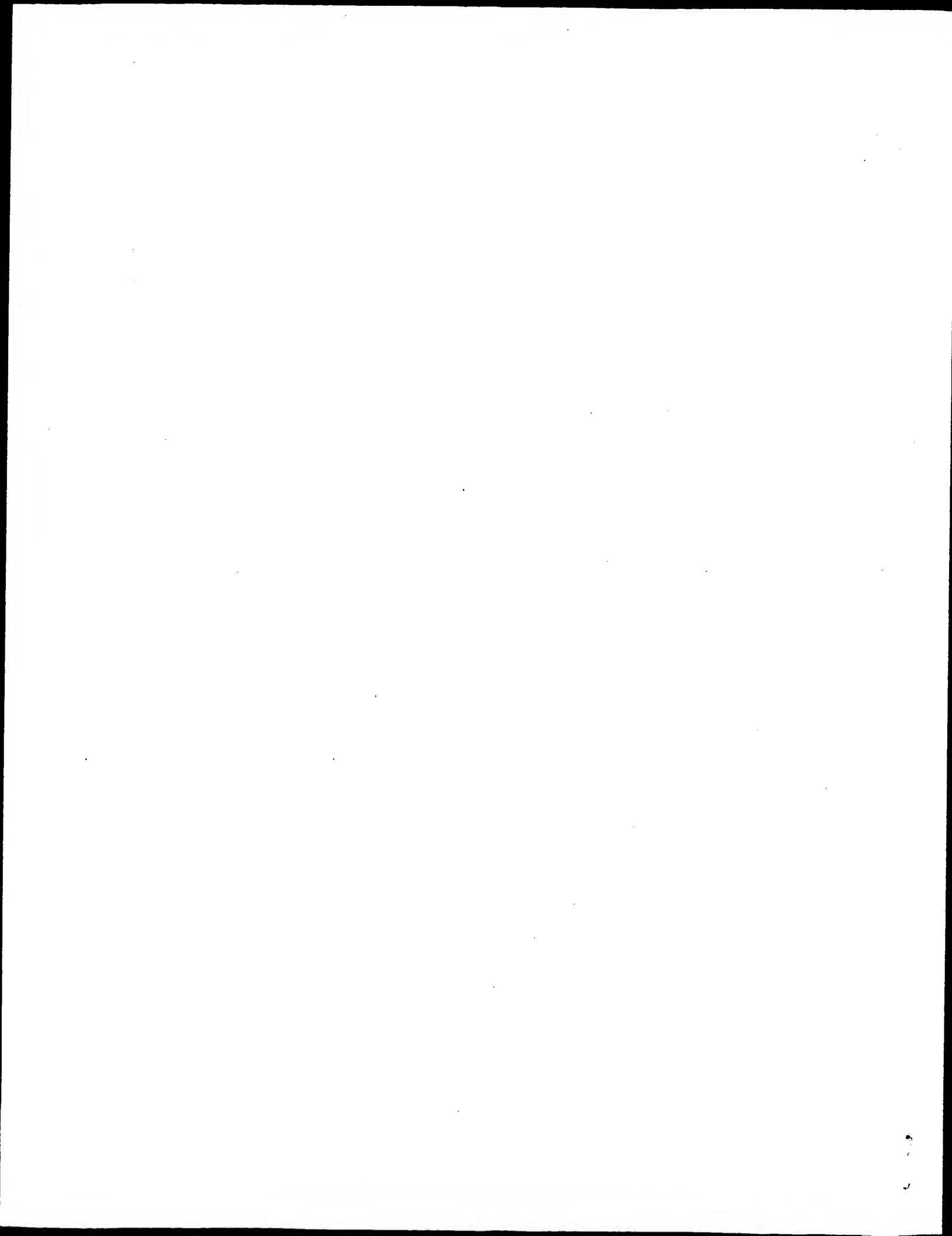
RESULT 15  
K1HUGL  
Ig kappa chain V-I region (Gal) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000  
C:Accession: A01867  
R:Laure, C.J.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973  
A:Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal)  
A:Reference number: A01867; MUID:75059122  
A:Accession: A01867  
A:Molecule type: protein  
A:Residues: 1-108 <LAU>  
A:Note: the C region of this chain has the Inv (3) marker  
C:Comment: This chain was isolated from a Waldenström's macroglobulin.  
C:Genetics:  
A:Gene: GDB:IGKV1  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (h  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:18-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status predicted

Query Match 90.3%; Score 28; DB 1; Length 108;  
Best Local Similarity 85.7%; Pred. No. 7.2;



	Matches	6;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	AASNLES	7							
			1							
Db	50	AASNLOS	56							

Search completed: June 28, 2001, 15:58:44  
Job time: 372 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:35 ; Search time 105.36 Seconds  
(without alignments)  
2.276 Million cell updates/sec

Title: US-09-724-406-14  
Perfect score: 31  
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues  
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	110	1 KV3P_MOUSE	P01668 mus musculus
2	31	100.0	111	1 KV3L_MOUSE	P01664 mus musculus
3	31	100.0	111	1 KV3M_MOUSE	P01665 mus musculus
4	31	100.0	111	1 KV3N_MOUSE	P01666 mus musculus
5	31	100.0	111	1 KV3O_MOUSE	P01669 mus musculus
6	31	100.0	463	1 Y1EO_HAEN	P44903 haemophilus
7	28	90.3	108	1 KVIG_HUMAN	P01599 homo sapien
8	28	90.3	313	1 VP9_WTVJ	P12326 wound tumor
9	28	90.3	313	1 VP9_WTVNJ	P13611 wound tumor
10	28	90.3	632	1 FTSH_HELPJ	Q92m66 helicobacte
11	28	90.3	784	1 KL68_DROME	P46867 drosophila
12	27	87.1	108	1 KV1B_HUMAN	P01594 homo sapien
13	27	87.1	108	1 KV3V_MOUSE	P01674 mus musculus
14	27	87.1	111	1 KV3H_MOUSE	P01660 mus musculus
15	27	87.1	111	1 KV3J_MOUSE	P01662 mus musculus
16	27	87.1	111	1 KV3K_MOUSE	P01663 mus musculus
17	27	87.1	111	1 KV3Q_MOUSE	P01667 mus musculus
18	27	87.1	111	1 KV3R_MOUSE	P01670 mus musculus
19	27	87.1	111	1 KV3S_MOUSE	P01671 mus musculus
20	27	87.1	111	1 KV3T_MOUSE	P01672 mus musculus
21	27	87.1	131	1 KV3I_MOUSE	P01661 mus musculus
22	27	87.1	177	1 PSS_BACSU	P39823 bacillus su
23	27	87.1	230	1 CUTI_FUSCO	Q99174 fusarium so
24	27	87.1	230	1 CUTI_FUSSO	P00590 fusarium so
25	27	87.1	260	1 UPSP_BACSU	Q31751 bacillus su
26	27	87.1	486	1 YN8U_YEAST	P53742 saccharomyc
27	27	87.1	662	1 UVRB_RICPR	Q9zd42 rickettsia
28	26	83.9	112	1 KV3G_MOUSE	P01659 mus musculus
29	26	83.9	132	1 KV3F_MOUSE	P01658 mus musculus
30	26	83.9	456	1 RICH_HUMAN	P35790 homo sapien
31	26	83.9	1407	1 CYAA_DICDI	Q03100 dictyosteli
32	26	83.9	2017	1 MYSN_DROME	Q99323 drosophila
33	25	80.6	259	1 FLA2_NATMA	Q93718 natrialba m

## ALIGNMENTS

RESULT 1

KV3P\_MOUSE  
ID KV3P\_MOUSE STANDARD; PRT; 110 AA.  
AC P01668;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 7210.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
RT diversity";  
RL Nature 276:785-790(1978).  
DR PIR; D01937; KVM510.  
DR InterPro; IPR003006; -  
DR Pfam; PF00047; Ig: 1.  
KW Immunoglobulin V region.

DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 100  
FT DOMAIN 101 110  
FT DISULFID 23 92  
FT NON\_TER 110 110  
SQ SEQUENCE 110 AA; 11950 MW; 69FIA5CE886B1249 CRC64;  
FRAMEWORK 1.  
COMPLEMENTARITY-DETERMINING 1.  
FRAMEWORK 2.  
COMPLEMENTARITY-DETERMINING 2.  
FRAMEWORK 3.  
COMPLEMENTARITY-DETERMINING 3.  
FRAMEWORK 4.  
BY SIMILARITY.

Query Match 100.0%; Score 31; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
| | | | | | |  
Db 54 AASNLES 60

RESULT 2

KV3L\_MOUSE  
ID KV3L\_MOUSE STANDARD; PRT; 111 AA.  
AC P01664;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION CBPC 101.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

```
RN
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01936; KVMSC1.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 3
KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM543.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60
```

```
DB 54 AASNLES 60
|||||||
RESULT 4
KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: B01937; KVM583.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60
|||||||

RESULT 5
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: E01937; KVM569.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 54 AASNLES 60
|||||||
```

FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.65;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 DB 54 AASNLES 60

RESULT 6  
 YIEO\_HAEIN  
 ID YIEO\_HAEIN STANDARD; PRT; 463 AA.  
 AC P44903;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE HYPOTHETICAL PROTEIN HI0852.  
 GN HI0852.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RD / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus  
 influenzae Rd.";  
 RL Science 269:496-512(1995).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE  
 CC (PROBABLE).  
 CC -!- SIMILARITY: STRONG. TO E.COLI YIEO.  
 CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN  
 CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).  
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 CC -----  
 DR EMBL: U32765; AAC22509.1; -  
 DR TIGR: HI0852; -  
 KW Hypothetical protein; Transport; Transmembrane; Inner membrane.

FT TRANSMEM 10 30 POTENTIAL.  
 FT TRANSMEM 49 69 POTENTIAL.  
 FT TRANSMEM 82 102 POTENTIAL.  
 FT TRANSMEM 107 127 POTENTIAL.  
 FT TRANSMEM 139 159 POTENTIAL.  
 FT TRANSMEM 165 185 POTENTIAL.  
 FT TRANSMEM 197 217 POTENTIAL.  
 FT TRANSMEM 225 245 POTENTIAL.

FT TRANSMEM 267 287 POTENTIAL.  
 FT TRANSMEM 298 318 POTENTIAL.  
 FT TRANSMEM 328 348 POTENTIAL.  
 FT TRANSMEM 354 374 POTENTIAL.  
 FT TRANSMEM 393 413 POTENTIAL.  
 FT TRANSMEM 429 449 POTENTIAL.  
 SQ SEQUENCE 463 AA; 50002 MW; D725EFFD50F9F23F CRC64;

Query Match 100.0%; Score 31; DB 1; Length 463;  
 Best Local Similarity 100.0%; Pred. No. 3.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 DB 94 AASNLES 100

RESULT 7  
 KVIG\_HUMAN  
 ID KVIG\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01599;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION GAL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75059122; PubMed=4215718;  
 RA Laure C.J., Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal IgM-immunoglobulin  
 RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of  
 RT kappa-type, subgroup I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN.  
 DR PIR: A01867; KIHUGL.  
 DR HSSP: P01607; IREI.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 108;  
 Best Local Similarity 85.7%; Pred. No. 3.6;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 DB 50 AASNLES 56

RESULT 8  
 VP9\_WTV  
 ID VP9\_WTV STANDARD; PRT; 313 AA.  
 AC P12326;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)

us-09-724-406-14.rsp

Fri Jun 29 08:04:28 2001

Best Local Similarity 85.7%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 1;

01-JUL-1993 (Rel. 26, Last annotation update)  
 DE STRUCTURAL PROTEIN P9 (CAPSOMERE PROTEIN P9) (PROTEIN PNS11).  
 GN S11.  
 OS Wound tumor virus (WTV).  
 OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.  
 OX NCBI\_TaxID=10987;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=89263810; PubMed=2726499;  
 RX Dall D.J., Anzola J.V., Xu Z., Nuss D.L.;  
 RA "Complete nucleotide sequence of wound tumor virus genomic segment  
 RT S11."  
 RL Nucleic Acids Res. 17:3599-3599(1989).  
 CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.  
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 CC -----  
 CC EMBL; X14219; CAA324239.1; -  
 CC PIR; S04139; QMXRWT.  
 CC SEQUENCE 313 AA; 35606 MW; 6746F59840AD17F2 CRC64;  
 SQ

Query Match 90.3%; Score 28; DB 1; Length 313;  
 Best Local Similarity 85.7%; Pred. No. 12;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7  
 DB 294 AASNL5 300

RESULT 9  
 VP9\_WTVNJ STANDARD; PRT; 313 AA.  
 ID VP9\_WTVNJ  
 AC P31611;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE STRUCTURAL PROTEIN P9 (CAPSOMERE PROTEIN P9) (PROTEIN PNS11).  
 OS Wound tumor virus (strain NJ) (WTV).  
 OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.  
 OX NCBI\_TaxID=31595;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=92074261; PubMed=1962460;  
 RX Hillman B.I., Anzola J.V., Halpern B.T., Cavileer T.D., Nuss D.L.;  
 RA "First field isolation of wound tumor virus from a plant host:  
 RT minimal sequence divergence from the type strain isolated from an  
 RT insect vector".  
 RL Virology 185:896-900(1991).  
 CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.  
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 CC -----  
 CC EMBL; M77020; AAA48500.1; -  
 CC PIR; C41705; QMXRWN.  
 CC Nonstructural protein.  
 KW SEQUENCE 313 AA; 35551 MW; D9B904785C601C34 CRC64;  
 SQ

Query Match 90.3%; Score 28; DB 1; Length 313;

QY 1 AASNL5 7  
 DB 294 AASNL5 300

RESULT 10  
 FTSH\_HELPJ STANDARD; PRT; 632 AA.  
 ID FTSH\_HELPJ  
 AC Q9ZM66; 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).  
 GN FTSH OR JHP0356.  
 OS Helicobacter pylori J99 (Campylobacter pylori J99).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 OC Helicobacter.  
 OX NCBI\_TaxID=85963;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=99120557; PubMed=9923682;  
 RX Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
 RA Smith D.R., Noonan B., Guild B.C., deJonghe B.L., Carmel G.,  
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives G.F.,  
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.;  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen Helicobacter pylori".  
 RL Nature 397:176-180(1999).  
 CC -!- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE  
 CC (BY SIMILARITY).  
 CC -!- COFACTOR: BINDS ONE ZINC ION (POTENTIAL).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC  
 CC METALLOPROTEASE).  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; AE001471; AAD05932.1; -  
 CC InterPro; IPR000642; -  
 CC InterPro; IPR001939; -  
 CC Pfam; PF00004; AAA; 1.  
 CC Pfam; PF01434; Peptidase\_M41; 1.  
 CC PROSITE; PS00674; AAA; 1.  
 CC Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;  
 KW Zinc.  
 CC DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 10 31 POTENTIAL.  
 FT DOMAIN 32 116 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 117 137 POTENTIAL.  
 FT DOMAIN 138 632 CYTOPLASMIC (POTENTIAL).  
 FT NP\_BIND 210 217 ATP (POTENTIAL). (BY SIMILARITY).  
 FT METAL 434 434 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT\_SITE 435 435 BY SIMILARITY.  
 FT METAL 438 438 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT SEQUENCE 632 AA; 69765 MW; 2FB67B43C51559FB CRC64;  
 SQ

Query Match 90.3%; Score 28; DB 1; Length 632;  
 Best Local Similarity 85.7%; Pred. No. 25;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7

Db 616 AANNLES 622

RESULT 11  
KL68\_DROME  
ID KL68\_DROME STANDARD; PRT; 784 AA.  
AC P48867;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE KINESIN-LIKE PROTEIN KL68D.  
GN KLP68D OR KLP5.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Phrygotea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95050960; PubMed=7525600;  
RA Pesavento P.A., Stewart R.J., Goldstein L.S.B.;  
RT "Characterization of the KLP68D kinesin-like protein in Drosophila;  
RL Possible roles in axonal transport.";  
RN J. Cell Biol. 127:1041-1048(1994).  
[2]  
RP SEQUENCE OF 220-342 FROM N.A.  
RX MEDLINE=92020874; PubMed=1924306;  
RA Stewart R.J., Pesavento P.A., Woerpel D.N., Goldstein L.S.B.;  
RT "Identification and partial characterization of six members of the  
RL kinesin superfamily in Drosophila.";  
RN Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(1991).  
CC -1- FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR  
CC ANTEROGRADE AXONAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES IN  
CC FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OR  
CC OTHER PLUS-END DIRECTED MOTORS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS  
CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING  
CC EMBRYOGENESIS.  
CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN  
CC II SUBFAMILY.

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-----  
EMBL; U15974; AAA69929.1; -  
EMBL; M74431; AAA28658.1; -  
HSSP; P56536; 2KIN.  
DR FlyBase; FBgn004381; klp68D.  
DR InterPro; IPR001752; -  
PFam; PF00225; kinesin; 1.  
DR PRINTS; PR00380; KINESINHEAVY.  
DR PROSITE; PS00411; KINESIN\_MOTOR\_DOMAIN1; 1.  
DR PROSITE; PS00057; KINESIN\_MOTOR\_DOMAIN2; 1.  
KW Motor protein; Microtubules; ATP-binding; Coiled coil.  
FT DOMAIN 16 275 MECHANOCHEMICAL (MOTOR).  
FT DOMAIN 351 385 COILED COIL (POTENTIAL).  
FT NP\_BIND 426 582 COILED COIL (POTENTIAL).  
FT NP\_BIND 106 113 ATP (POTENTIAL).  
FT CONFLICT 220 221 SS -> TC (IN REF. 2).  
FT CONFLICT 338 342 GSRK -> VRGV (IN REF. 2).  
SQ SEQUENCE 784 AA; 88193 MW; 94BB9BDAF072DFC0 CRC64;

Query Match 90.38; Score 28; DB 1; Length 784;  
Best Local Similarity 85.79; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7  
Db 751 AASNLES 757

RESULT 12  
KVIB\_HUMAN  
ID KVIB\_HUMAN STANDARD; PRT; 108 AA.  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-I REGION AU.  
GN KLP68D OR KLP5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;  
RA Schiechl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RL immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
protein Au).";  
RN Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
[2]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehnhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
RT Schwager P., Steigemann W., Schramm H.J.;  
RL "The structure determination of the variable portion of the  
RL Bence-Jones protein Au.";  
CC Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
CC REGION OF THE KAPPA CHAIN REI.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
CC PIR; A01862; KIHUAU.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; -  
DR Pfam; PF00047; ig; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 35 49 FRAMEWORK 2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 57 88 FRAMEWORK 3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 98 107 FRAMEWORK 4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 87.18; Score 27; DB 1; Length 108;  
Best Local Similarity 100.08; Pred. No. 6.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AASNLES 7  
Db 51 AASNLES 56

RESULT 13  
KV3V\_MOUSE  
ID KV3V\_MOUSE STANDARD; PRT; 108 AA.  
AC P01674;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 2154.  
OS Mus musculus (Mouse).

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Fri Jun 29 08:04:28 2001

FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 111  
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;  
 Query Match 87.1%; Score 27; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7  
 Db 55 ASNLES 60

RESULT 15  
 KV3J\_MOUSE STANDARD; PRT: 111 AA.  
 ID KV3J\_MOUSE  
 AC P01662;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

RP SEQUENCE (ABPC 22).  
 RX MEDLINE=79073152; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 related mouse kappa variable regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 RN [1]  
 RN [2]  
 RP SEQUENCE (PC 9245).  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity.";  
 RL Nature 276:785-790(1978).  
 CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.  
 DR PIR; A01935; KVM56.  
 DR InterPro; IPR003006;  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111  
 SQ SEQUENCE 111 AA; 12041 MW; D7DF06090303453CE CRC64;

Query Match 87.1%; Score 27; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 6.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7  
 Db 55 ASNLES 60

RESULT 14  
 KV3H\_MOUSE STANDARD; PRT: 111 AA.  
 ID KV3H\_MOUSE  
 AC P01660;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN [2]  
 RP SEQUENCE (PC 3741).  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity.";  
 RL Nature 276:785-790(1978).  
 CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.  
 DR PIR; A01934; KVM37.  
 DR InterPro; IPR003006;  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111

Query Match 87.1%; Score 27; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7  
 Db 55 ASNLES 60

Search completed: June 28, 2001, 15:54:36  
 Job time: 124 sec



.Fri Jun 29 08:04:28 2001

us-09-724-406-14.rsp

Page 7



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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:21 ; Search time 411.58 Seconds  
(without alignments)  
2.250 Million cell updates/sec

Title: US-09-724-406-14  
Perfect score: 31  
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16:\*\*

- 1: sp-archaea:\*\*
- 2: sp-bacteria:\*\*
- 3: sp-fungi:\*\*
- 4: sp-human:\*\*
- 5: sp-invertebrate:\*\*
- 6: sp-mammal:\*\*
- 7: sp-mhc:\*\*
- 8: sp-organelle:\*\*
- 9: sp-phage:\*\*
- 10: sp-plant:\*\*
- 11: sp-rodent:\*\*
- 12: sp-unclassified:\*\*
- 13: sp-vertebrate:\*\*
- 14: sp-virus:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	942	3	042938
2	31	100.0	1208	4	075162
3	28	90.3	103	11	09JL80
4	28	90.3	204	5	09U2Y4
5	28	90.3	784	5	09VFN8
6	27	87.1	310	2	P94981
7	27	87.1	389	10	09SAF7
8	27	87.1	419	10	09M887
9	27	87.1	443	10	09L176
10	27	87.1	468	10	09L176
11	27	87.1	457	3	074901
12	27	87.1	576	14	09JGJ9
13	27	87.1	619	2	09F9H4
14	27	87.1	643	10	09LSX2
15	27	87.1	689	1	09HMT9
16	27	87.1	746	3	008754
17	27	87.1	826	13	09YHD5
18	27	87.1	832	5	016360
19	27	87.1	856	5	09V706

20	27	87.1	927	2	09PGG3
21	27	87.1	1195	13	09PUM2
22	27	87.1	1425	2	085862
23	27	87.1	2406	5	09N905
24	27	87.1	4880	11	09JLT1
25	27	87.1	5085	11	09JKS6
26	26	83.9	292	5	023983
27	26	83.9	297	2	050805
28	26	83.9	367	10	09SE32
29	26	83.9	367	10	09FPB1
30	26	83.9	408	4	094798
31	26	83.9	444	4	09UHX4
32	26	83.9	547	5	09VWD9
33	26	83.9	585	13	09FVN8
34	26	83.9	588	4	09H3W6
35	26	83.9	589	4	09HAZ5
36	26	83.9	589	4	09H3R4
37	26	83.9	589	4	09H0T8
38	26	83.9	595	4	09UMX0
39	26	83.9	601	4	09NKR5
40	26	83.9	624	4	09UHD9
41	26	83.9	624	4	09HAZ4
42	26	83.9	624	4	09UHD9
43	26	83.9	638	11	09QZM0
44	26	83.9	664	10	022834
45	26	83.9	750	5	001348
	26	83.9	801	5	09VTD3

## ALIGNMENTS

RESULT 1  
O42938 ID O42938 PRELIMINARY; PRT; 942 AA.  
AC O42938  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE PROBABLE 6-PHOSPHOFRUCTOKINASE BETA SUBUNIT (EC 2.7.1.11)  
DE (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (6PF-1-K BETA SUBUNIT).  
GN SPEC16H5.02.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
CC -! CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-FRUCTOSE 1,6-BISPHOSPHATE.  
CC -! PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.  
CC -! SUBUNIT: HETEROOCTAMER OF 4 ALPHA AND 4 BETA CHAINS (BY EMIL; AL022104; CAAL17900.1; -;  
DR HSP; P00512; 3PFK  
DR InterPro; IPR000023; -;  
DR Pfam; PF00365; PFK; 3.  
DR PRINTS; PR00476; PHFRCTKINASE.  
DR PRODOM; PD000707; -; 2.  
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.  
KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme;  
KW Phosphorylation; Magnesium  
SQ SEQUENCE 942 AA; 102554 MW; C6052AF7C1DB75B4 CRC64;

Query Match 100.0%; Score 31; DB 3; Length 942;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

us-09-724-406-14.rspt

Fri Jun 29 08:04:28 2001

Query Match 90.3%; Score 28; DB 11; Length 103;  
 Best Local Similarity 85.7%; Pred. No. 17;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 Db 46 AASNLES 52

RESULT 4  
 Q9U2Y4 PRELIMINARY; PRT; 204 AA.

ID Q9U2Y4  
 AC Q9U2Y4  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE Y113G7A.14 PROTEIN.  
 GN Y113G7A.14  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peleoderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lennard N.  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=99069613; PubMed=9851916;  
 RX none;  
 RA "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL: AL132858; CAB60484.1; -. 8968065DF2EA9C7E CRC64;  
 SQ SEQUENCE 204 AA; 23067 MW; 8968065DF2EA9C7E CRC64;

Query Match 90.3%; Score 28; DB 5; Length 204;  
 Best Local Similarity 85.7%; Pred. No. 35;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 Db 134 AASNLES 140

RESULT 5  
 Q9VTN8 PRELIMINARY; PRT; 784 AA.

ID Q9VTN8  
 AC Q9VTN8  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE KLP68D PROTEIN.  
 DE KLP68D OR CG7293.  
 GN Drosophila melanogaster (fruit fly).  
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=BERKELEY;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Db 165 AASNLES 171

RESULT 2  
 Q9JL80 PRELIMINARY; PRT; 1208 AA.

ID Q9JL80  
 AC Q9JL80  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE KIAA0675 PROTEIN.  
 GN KIAA0675.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=BRAIN;  
 RC MEDLINE=98403880; PubMed=9734811;  
 RX Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RA "Prediction of the coding sequences of unidentified human genes. X.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Res. 5:169-176(1998).  
 CC -|- SIMILARITY: CONTAINS A RING (C3HC4-CLASS) ZINC FINGER.  
 DR EMBL: AB014575; BAA31650.1; -.  
 DR HSSP: P28990; 1CHC.  
 DR InterPro: IPR001841; -.  
 DR Pfam: PF000097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW Zinc-finger. 1208 AA; 138603 MW; 76945A63AF85207E CRC64;  
 SQ SEQUENCE 1208 AA; 138603 MW; 76945A63AF85207E CRC64;

Query Match 100.0%; Score 31; DB 4; Length 1208;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 Db 896 AASNLES 902

RESULT 3  
 Q9JL80 PRELIMINARY; PRT; 103 AA.

ID Q9JL80  
 AC Q9JL80  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 DE Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=BALB/C;  
 RC Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RA "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
 RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF206026; AAF69324.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR NON\_TER 1  
 FT NON\_TER 103  
 FT NON\_TER 103  
 SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.A., Bouck J., Brokstein P., Bottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrelli J.H., Gu Z., Kennison J.P., Houck J.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hough M.,  
 RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.P., Houck J.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.P., Houck J.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.L.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2193(2000).  
 DR EMBL: AE003543; AAF50008.1; -;  
 DR HSSP: P17119; 3KAR.  
 DR FLYBase: FBgn0004381; Klp68D.  
 DR InterPro: IPR001752; -;  
 DR Pfam: PF00225; kinesin; 1.  
 DR PRINTS: PR00380; KINESINHEAVY.  
 DR PROSITE: PS00411; KINESIN\_MOTOR\_DOMAIN1; 1.  
 DR PROSITE: PS00467; KINESIN\_MOTOR\_DOMAIN2; 1.  
 DR SMART: SM00129; KISC; 1.  
 KW ATP-binding; Coiled coil; Microtubules; Motor protein.  
 SQ SEQUENCE 784 AA; 8820 MW; 7A3C6716D22BC05D CRC64;

Query Match 90.3%; Score 28; DB 5; Length 784;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLS 7  
 |||||  
 DB 751 AASNLS 757

RESULT 6  
 P94981 ID P94981 PRELIMINARY; PRT; 310 AA.  
 AC P94981;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DE HYPOTHETICAL 30.2 KDA PROTEIN.  
 GN RV1646 OR MTCY06H11.1.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Mycobacterium.  
 OX Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 RN NCBI\_TaxID=1773;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV.  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,  
 RA Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 DR EMBL: Z85982; CAB06640.1; -;  
 DR TubercuList; RV1646; -;  
 DR InterPro: IPR000084; -;  
 DR Pfam: PF00934; PE; 1.  
 DR ProDom: PD001223; -; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 310 AA; 30219 MW; F51DFE4CC2D9EDAD CRC64;

Query Match 87.1%; Score 27; DB 2; Length 310;  
 Best Local Similarity 85.7%; Pred. No. 96;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLS 7  
 |||||  
 DB 14 AAGNLS 20

RESULT 7  
 Q9SAF7 ID Q9SAF7 PRELIMINARY; PRT; 389 AA.  
 AC Q9SAF7;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE F3F19.26 PROTEIN.  
 GN F3F19.26.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lenz C.,  
 RA Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A.,  
 RA Alcafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,  
 RA Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,  
 RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,  
 RT "Arabidopsis thaliana chromosome 1 BAC F3F19 sequence."  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Theologis A.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Theologis;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC007357; AAC31076.1; -;  
 DR InterPro: IPR001350; -;  
 DR InterPro: IPR001611; -;  
 DR InterPro: IPR003592; -;  
 DR Pfam: PF00560; LRR; 7.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR PROSITE: PS00572; GLYCOSYL\_HYDROL\_F1\_1; UNKNOWN\_1.  
 DR SMART: SM00370; LRR; 1.  
 SQ SEQUENCE 389 AA; 43216 MW; 1DC342A0BF4B7EBF CRC64;

Query Match 87.1%; Score 27; DB 10; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

us-09-724-406-14.rspt

Fri Jun 29 08:04:28 2001

Sequence features of the regions of 4,251,695 bp covered by ninety Pl.

RT TAC and BAC clones.  
 RL DNA Res. 7:217-221(2000).  
 DR EMBL: AF001313; BAB03087.1; --  
 DR InterPro: IPR001360; --  
 DR InterPro: IPR001611; --  
 DR InterPro: IPR003592; --  
 DR Pfam: PF00560; LRR: 4.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR PROSITE: PS00572; GLYCOSYL\_HYDROL\_F1\_1; UNKNOWN1.  
 DR SMART: SM00370; LRR: 1.  
 KW Receptor. 443 AA; 49318 MW; 1E2D37B3F9066F4C CRC64;  
 SQ SEQUENCE

Query Match 87.1%; Score 27; DB 10; Length 443;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7  
 DB 106 ASNLES 111

RESULT 8  
 Q9M887 PRELIMINARY; PRT; 419 AA.

AC Q9M887;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE PUTATIVE RAD23.

GN F16B3.17.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;  
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,  
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,  
 RA Bowman C.B., White O., Nierman W.C., Fraser C.M.;  
 RA "Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence."  
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL: AC021640; AAF32461.1; --  
 DR InterPro: IPR000449; --  
 DR InterPro: IPR002965; --  
 DR Pfam: PF00240; ubiquitin; 1.  
 DR PRINTS: PR00627; UBA: 2.  
 DR PROSITE: PS0053; UBQUITIN.2; 1.  
 DR SEQUENCE 419 AA; 44247 MW; CAAL3BC4FFEB1E25 CRC64;

Query Match 87.1%; Score 27; DB 10; Length 419;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 DB 183 AGSNLES 189

RESULT 9  
 Q9LI76 PRELIMINARY; PRT; 443 AA.

AC Q9LI76;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE SIMILARITY TO ELICITOR-INDUCIBLE RECEPTOR EIR.

OS Arabidopsis thaliana (Mouse-ear cress).  
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-COLUMBIA;  
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-COLUMBIA;  
 RX PubMed=10907853;  
 RA Nakamura Y.;  
 RA "Structural analysis of Arabidopsis thaliana chromosome 3. II.

RT

Q9LFX3 PRELIMINARY; PRT; 468 AA.

AC Q9LFX3;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE T7N9.21.

OS Arabidopsis thaliana (Mouse-ear cress).  
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;  
 RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,  
 RA Shinn P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,  
 RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,  
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,  
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
 RA Ecker J.R.;  
 RA "Genomic sequence for Arabidopsis thaliana BAC T7N9 from chromosome I."

RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

RL [2]  
 RN SEQUENCE FROM N.A.  
 RP Ecker J.R.;  
 RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

RL [3]  
 RN SEQUENCE FROM N.A.  
 RP Ecker J.R.;  
 RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RL [4]  
 RN SEQUENCE FROM N.A.  
 RP Ecker J.R.;  
 RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RL [5]  
 RN SEQUENCE FROM N.A.  
 RP Ecker J.R.;  
 RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RL [6]  
 RN SEQUENCE FROM N.A.  
 RP Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Lam B.,  
 RA Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,  
 RA Nguyen M., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 RA Ecker J.R.;  
 RA "Structural analysis of Arabidopsis thaliana chromosome 3. II.

RT

RA Theologis A., Ecker J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC000348; AAF79860.1; -;  
 SQ SEQUENCE 468 AA; 53589 MW; F140B6E374024FEB CRC64;

Query Match  
 Best Local Similarity 87.1%; Score 27; DB 10; Length 468;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AASNLE 6  
 |||||  
 Db 78 AASNLE 83

RESULT 11  
 074901  
 ID 074901 PRELIMINARY; PRT; 497 AA.  
 AC 074901  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DE HYPOPHETICAL 55.1 KDA PROTEIN.  
 GN SPCC613.01 OR SPCC757.14.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972H-;  
 RA Bothe G., Pohl T., Lyne M., Rajandream M.A., Barrell B.G., Pohl T.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-260 FROM N.A.  
 RC STRAIN=972H-;  
 RA Lyne M., Rajandream M.A., Barrell B.G., Bothe G., Pohl T.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL031644; CAA21053.1; -;  
 DR EMBL; AL031825; CAA21239.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 497 AA; 55125 MW; 63D113F831A602C7 CRC64;

Query Match  
 Best Local Similarity 87.1%; Score 27; DB 3; Length 497;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 |||||  
 Db 62 ATSNLES 68

RESULT 12  
 09JGJ9  
 ID 09JGJ9 PRELIMINARY; PRT; 576 AA.  
 AC 09JGJ9;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE 64-KDA READTHROUGH PROTEIN (FRAGMENT).  
 GN RT.  
 OS soil-borne wheat mosaic virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Furovirus.  
 OX NCBI\_TaxID=28375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAPANESE;  
 RX MEDLINE=20238044; PubMed=10772992;  
 RA Shiroko Y., Suzuki N., French R.C.;  
 RT "Similarity and divergence among viruses in the genus Furovirus.";  
 RL Virology 270:201-207(2000).

DR EMBL; AB033690; BAA94800.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 575 AA; 63984 MW; 8DF91221FD61E1F7 CRC64;

Query Match  
 Best Local Similarity 87.1%; Score 27; DB 14; Length 576;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AASNLES 7  
 |||||  
 Db 453 AASNLES 459

RESULT 13  
 09F9H4  
 ID 09F9H4 PRELIMINARY; PRT; 619 AA.  
 AC 09F9H4;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE OUTER MEMBRANE PROTEIN A.  
 GN OMPA.  
 OS Rickettsia felis (Rickettsia azadi).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsieae; Rickettsia.  
 OX NCBI\_TaxID=42862;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bouyer D.H., Stenos J., Crocquet-Valdes P.A., Foll L.D., Walker D.H.;  
 RT "The identification and characterization of a previously undiscovered  
 rOmpA-encoding gene in Rickettsia felis.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191026; AAG17185.1; -;  
 SQ SEQUENCE 619 AA; 60547 MW; 1AA112066EEFFA1B CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 27; DB 2; Length 619;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLE 6  
 |||||  
 Db 508 AASNLE 513

RESULT 14  
 09LSX2  
 ID 09LSX2 PRELIMINARY; PRT; 643 AA.  
 AC 09LSX2;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE EMBI|CAB86628.1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=20181125; PubMed=10718197;  
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence  
 RT features of the regions of 3,076,755 bp covered by sixty pl and TAC  
 RL clones.";  
 RL DNA Res. 7:31-63(2000).  
 DR EMBL; AB025638; BAA97418.1; -;  
 DR InterPro; IPR001471; -;  
 DR ProDom; PD001423; -; 1.  
 SQ SEQUENCE 643 AA; 73049 MW; 58B44A6C4A18DA21 CRC64;

us-09-724-406-14.rspt

Fri Jun 29 08:04:28 2001

Query Match 87.1%; Score 27; DB 10; Length 643;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7  
 Db 541 ASNLES 546

RESULT 15  
 Q9HMT9 PRELIMINARY; PRT; 689 AA.  
 AC Q9HMT9;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE EXCISION NUCLEASE CHAIN B.  
 GN UVRB OR VNG2390G.  
 OS Halobacterium sp. (strain NRC-1).  
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;  
 OC Halobacterium.  
 OX NCBI\_TaxID=64091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20504483; PubMed-11016950;  
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
 RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W., Dale H.,  
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Spudich J.L., Jung K.-H.,  
 RA Isenbarger T.A., Peck R.F., Fohlschroder M., Dennis P.P., Omer A.D.,  
 RA Alam M., Freitas T., Hou S., Daniels C.J., Hood L., Dassarma S.,  
 RA Eberhardt H., Lowe T.M., Liang P., Riley M.,  
 RA "Genome sequence of Halobacterium species NRC-1.",  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
 RL EMBL; AE005120; AAG20482.1; -.  
 DR InterPro; IPR001410; -.  
 DR InterPro; IPR001650; -.  
 DR InterPro; IPR001943; -.  
 DR Pfam; PF00271; helicase\_C; 1.  
 DR Pfam; PF02151; UVR; 1.  
 SQ SEQUENCE 689 AA; 77507 MW; BED16C96A94E93B8 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 689;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLE 6  
 Db 645 AASNLE 650

Search completed: June 28, 2001, 16:08:22  
 Job time: 950 sec



GenCore version 4.5  
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OM protein - protein search, using sw model  
Run on: June 28, 2001, 16:14:35 ; Search time 362.28 Seconds  
(without alignments)  
1.506 Million cell updates/sec

Title: US-09-724-406-16  
Perfect score: 54  
Sequence: 1 QQSNEPWT 9  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 54 100.0 111 15 AAR55123 Mouse anti-HIV mu5

2 54 100.0 111 15 AAR55127 Mouse-human chimera

3 54 100.0 111 15 AAR60302 Anti HIV antibody

4 54 100.0 111 15 AAR60306 Chimeric anti HIV

5 54 100.0 113 22 AAB71895 Monoclonal antibody

6 54 100.0 218 18 AAW13563 Humanised anti-L-s

7 54 100.0 222 18 AAW01751 MHL monoclonal ant

8 51 94.4 110 15 AAR60810 Light chain variab

9 51 94.4 111 15 AAR53930 Light chain variab

10 51 94.4 112 17 AAW00830 Variable light cha

11 51 94.4 112 18 AAW19016 Anti-human FasL an

12	48	88.9	246	18	AAW09434
13	48	88.9	247	18	AAW09443
14	48	88.9	281	19	AAW82314
15	48	88.9	288	19	AAW82316
16	48	88.9	288	19	AAW82317
17	48	88.9	483	19	AAW82315
18	48	88.9	531	21	AAW43749
19	48	88.9	539	21	AAW50823
20	48	88.9	554	21	AAW50822
21	45	83.3	9	16	AAW75477
22	44	81.5	9	16	AAW75478
23	44	81.5	9	17	AAW01149
24	44	81.5	9	19	AAW44172
25	44	81.5	106	14	AAW33309
26	44	81.5	106	21	AAW85197
27	44	81.5	111	10	AAW90541
28	44	81.5	112	13	AAW24575
29	44	81.5	131	10	AAW90543
30	44	81.5	131	17	AAW01143
31	44	81.5	131	19	AAW44168
32	43.5	80.6	132	14	AAW37716
33	42	77.8	9	18	AAW27346
34	42	77.8	107	18	AAW27353
35	42	77.8	112	16	AAW79158
36	42	77.8	112	16	AAW79156
37	42	77.8	112	18	AAW27358
38	42	77.8	112	18	AAW27527
39	42	77.8	132	12	AAW10920
40	42	77.8	237	20	AAW73873
41	42	77.8	240	20	AAW73875
42	41	75.9	112	12	AAW13089
43	41	75.9	215	16	AAW64202
44	40	74.1	9	19	AAW83029
45	40	74.1	9	21	AAW14746

# ALIGNMENTS

RESULT 1  
AAR55123  
ID AAR55123 standard; Protein; 111 AA.  
XX AAR55123;  
XX AC AAR55123;  
XX DE 27-JAN-1995 (first entry)  
XX DT  
XX DE Mouse anti-HIV mu5.5 light chain variable region.  
XX KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;  
XX KW human immunodeficiency virus; variable region; VH chain; murine.  
XX OS Mus musculus.  
XX FH Key  
XX FT Region  
XX FT Location/Qualifiers  
XX FT 1..23  
XX FT /label= FR1  
XX FT 24..38  
XX FT /label= CDR1  
XX FT 39..53  
XX FT /label= FR2  
XX FT 54..60  
XX FT /label= CDR2  
XX FT 61..92  
XX FT /label= FR3  
XX FT 93..101  
XX FT /label= CDR3  
XX FT 102..111  
XX FT /label= FR4  
XX PN JP06125783-A.  
XX PD 10-MAY-1994.

Anti-CD19 antibody  
Modified single ch  
Human SKVCD19 pro  
Mouse OFT3 variant  
Mouse bispecific a  
Chimeric CD19/crCR  
Amino acid sequen  
Fv-antibody constr  
Fv-antibody constr  
Mouse antibody lig  
Mouse antibody lig  
Mab 1.4 light chai  
Monoclonal antibod  
Mab15 light chain.  
Light chain amino  
Immunoglobulin L c  
Human x mouse modl  
Amino acids sequen  
Mab 1.4 light chai  
Monoclonal antibod  
CDR3 from murine a  
Light chain variab  
Human IgE receptor  
Human IgE receptor  
Light chain variab  
Light chain variab  
kappa light chain  
Human antiFc epsil  
Human antiFc epsil  
Murine I84 light c  
Monoclonal antibod  
Anti-Fas Mab HPE7A  
Mouse anti-Fas ant



PF 14-JAN-1993; 93WO-JP000039.  
 XX 14-JAN-1993; 93AU-0032671.  
 PR 14-JAN-1993; 93WO-JP000039.  
 XX  
 PA (KAGA) CHERO SERO THERAPEUTIC RES INST.  
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
 PI Tokiyoshi S;  
 XX WPI: 1994-249145/30.  
 DR N-PSDB; AA070372.  
 XX  
 PT Recombinant chimeric anti HIV antibody - useful for the treatment  
 PT and prevention of HIV  
 PS Claim 15; Figure 4; 51pp; Japanese.  
 XX  
 CC The recombinant antibody light chain has neutralising activity  
 CC against HIV. Chimeric antibodies comprising both mouse and human  
 CC sequences are useful in the treatment/prevention of AIDS caused by  
 CC HIV.  
 XX  
 SQ Sequence 111 AA;

Query Match 100.0%; Score 54; DB 15; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.016;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QOSNEPWT 9  
 DB 93 qgsnedpwt 101

RESULT 4  
 AAR60306  
 ID AAR60306 standard; protein; 111 AA.  
 AC AAR60306;  
 XX  
 DT 13-MAR-1995 (first entry)  
 DE Chimeric anti HIV antibody light chain variable region.  
 KW Antibody; heavy chain; light chain; human immunodeficiency virus;  
 KW HIV; acquired immune deficiency syndrome; AIDS; treatment;  
 KW prophylaxis; Mus musculus; Homo sapiens.  
 XX Chimeric Homo sapiens.  
 OS Chimeric Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= Framework region 1.  
 FT Region 24..38  
 FT /label= CDR1.  
 FT /note= "Mouse derived amino acid sequence."  
 FT Region 39..53  
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 FT Region 54..60  
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 FT /note= "Mouse derived amino acid sequence."  
 FT Region 61..92  
 FT /label= Framework region 3.  
 FT Region 93..101  
 FT /label= CDR3.  
 FT /note= "Mouse derived amino acid sequence."  
 FT Region 102..111  
 FT /label= Framework region 4.  
 PN W09415969-A.  
 XX

PD 21-JUL-1994.  
 XX  
 PF 14-JAN-1993; 93WO-JP000039.  
 XX  
 PR 14-JAN-1993; 93AU-0032671.  
 PR 14-JAN-1993; 93WO-JP000039.  
 XX  
 PA (KAGA) CHERO SERO THERAPEUTIC RES INST.  
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;  
 PI Tokiyoshi S;  
 XX WPI: 1994-249145/30.  
 DR N-PSDB; AAR60306.  
 XX  
 PT Recombinant chimeric anti HIV antibody - useful for the treatment  
 PT and prevention of HIV  
 PS Claim 14; Figure 12; 51pp; Japanese.  
 XX  
 CC The recombinant antibody light chain has neutralising activity  
 CC against HIV. Chimeric antibodies comprising both mouse and human  
 CC sequences are useful in the treatment/prevention of AIDS caused by  
 CC HIV.  
 XX  
 SQ Sequence 111 AA;

Query Match 100.0%; Score 54; DB 15; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.016;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QOSNEPWT 9  
 DB 93 qgsnedpwt 101

RESULT 5  
 AAB71895  
 ID AAB71895 standard; protein; 113 AA.  
 AC AAB71895;  
 XX  
 DT 09-MAY-2001 (first entry)  
 DE Monoclonal antibody ST40 light chain.  
 KW Antibody; ST40; molecular mimetic; CD4; human immunodeficiency virus;  
 KW HIV; infection.  
 XX Unidentified.  
 OS  
 FT Region 1..23  
 FT /label= Framework region 1.  
 FT Region 24..38  
 FT /label= CDR1.  
 FT /note= "Mouse derived amino acid sequence."  
 FT Region 39..53  
 FT /label= Framework region 2.  
 FT Region 54..60  
 FT /label= CDR2.  
 FT /note= "Mouse derived amino acid sequence."  
 FT Region 61..92  
 FT /label= Framework region 3.  
 FT Region 93..101  
 FT /label= CDR3.  
 FT /note= "Mouse derived amino acid sequence."  
 FT Region 102..111  
 FT /label= Framework region 4.  
 PN W09415969-A.  
 XX

Designing molecular mimetics to mimic a parent molecule activity,  
 useful e.g. therapeutically and diagnostically, uses computational  
 screening to identify active chemical groups by accessibility within  
 the parent molecule.  
 Example 1; Fig 1; 85pp; English.

us-09-724-406-16.rag

Fri Jun 29 08:04:29 2001

CC The present sequence was used in a method for designing a mimetic which  
 CC exhibits an activity associated with a parent molecule. Such mimetics  
 CC may be smaller than the parent molecule and correspondingly easier and  
 CC cheaper to make, since the active region of the parent molecule is  
 CC normally relatively small. The method is useful for an antibody or other  
 CC is a binding domain or the hypervariable region of an antibody when the parent  
 CC member of the immunoglobulin superfamily. It is useful when the parent  
 CC molecule is an antibody and the mimetic a peptide, especially an antibody  
 CC which binds CD4 and a peptide which binds CD4. The mimetics designed and  
 CC produced are useful diagnostically to detect cells bearing CD4 on their  
 CC surfaces or may be included in pharmaceuticals e.g. to treat conditions  
 CC in which CD4 is implicated (e.g. HIV).

XX SQ Sequence 113 AA;  
 Query Match 100.0%; Score 54; DB 22; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 0.016;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 |||||  
 Db 93 qgsnedpwt 101

## RESULT 6

AAW13563

ID AAW13563 standard; Protein; 218 AA.

XX AC AAW13563;

XX DT 03-JUN-1997 (first entry)

XX DE Humanised anti-L-selectin antibody Hudreg 55 light chain.

XX DE L-selectin; humanised antibody; Hudreg 55; acute organ damage;  
 KW organ failure; poly-trauma; haemorrhagic-traumatic shock.

XX OS Chimeric Mus sp.;  
 OS Chimeric Homo sapiens.

XX PN W09706822-A1.

XX PD 27-FEB-1997.

XX PF 14-AUG-1996; 96WO-US13152.

XX PR 27-DEC-1995; 95US-0578953.

XX PR 17-AUG-1995; 95EP-0112895.

XX PR 19-SEP-1995; 95EP-0114696.

XX PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Co M, Haselbeck A, Martin U, Schumacher G;

XX PI WPI: 1997-165036/15.

XX DR N-PSDB; AAT61280.

XX PT Using anti-selectin antibody to prevent acute organ damage and  
 XX PT multiple organ failure - during extracorporeal circulation or  
 XX PT following polytrauma, e.g. haemorrhagic-traumatic shock

XX PS Disclosure: Page 32-33; 52pp; English.

XX CC Humanised anti-L-selectin antibody Hudreg 55 comprises 2 light  
 XX CC chains each having the sequence given in AAW13563 and 2 heavy chains  
 XX CC each having the sequence given in AAW13564. These are encoded by the  
 XX CC cDNA clones given in AAT61280 and AAT61281. Hudreg 55 can be used to  
 XX CC prevent multiple organ failure associated with polytrauma and for  
 XX CC the prevention of acute organ damage associated with extracorporeal  
 XX CC blood circulation. The antibody inhibits interaction between the  
 XX CC carbohydrate-recognising domain of the selectin and the

CC corresponding cell surface receptor.

XX SQ Sequence 218 AA;  
 Query Match 100.0%; Score 54; DB 18; Length 218;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 |||||  
 Db 93 qgsnedpwt 101

## RESULT 7

AAW01751

ID AAW01751 standard; Protein; 222 AA.

XX AC AAW01751;

XX DT 21-AUG-1997 (first entry)

XX DE MHL monoclonal antibody kappa chain.

XX DE CDR; light chain; antigen binding site; antigen free animal;  
 KW germfree animal; immunoreactive; thrombotic event.

XX OS Mus musculus.  
 XX FH Key  
 XX FT Domain  
 XX FT /label= CDR1  
 XX FT 19...39  
 XX FT Domain  
 XX FT 63...68  
 XX FT /label= CDR2  
 XX FT 99...104  
 XX FT /label= CDR3

Location/Qualifiers

19...39

/label= CDR1

63...68

/label= CDR2

99...104

/label= CDR3

XX PN W09640986-A1.

XX PD 19-DEC-1996.

XX PF 29-APR-1996; 96WO-US07891.

XX PR 07-JUN-1995; 95US-0486420.

XX PA (AMBI-) AMERICAN BIOGENETIC SCI INC.

XX PI Dimitrijevic N, Dimitrijevic N;

XX PI WPI: 1997-052360/05.

XX DR N-PSDB; AAT59338.

XX PT Calibrator comprising lyophilised compsn contg. DesAABB fibrin  
 XX PT polymers, buffer and stabilising agent - for use in soluble fibrin  
 XX PT assays used for evaluating pre-disposition to thrombotic event

XX PS Disclosure: Page 96; 120pp; English.

XX CC The present sequence represents the MHL monoclonal antibody kappa  
 XX CC (light) chain, which was produced in antigen free (germfree) mice. A new  
 XX CC invention contemplates the production and use of recombinantly produced  
 XX CC derivatives of monoclonal antibody MHL and fusion proteins containing a  
 XX CC portion of MHL that bind to the same epitope recognised by monoclonal  
 XX CC antibody MHL, such as single chain antigen binding proteins comprising  
 XX CC the antigen binding site of monoclonal antibody MHL. A calibrator for  
 XX CC use in an in vitro assay for detecting the presence of soluble  
 XX CC crosslinked and soluble non-crosslinked DesAABB fibrin polymers, is  
 XX CC claimed. This calibrator can be used in kits which use an antibody that  
 XX CC specifically binds to an epitope which recognises the MHL monoclonal  
 XX CC antibody. This calibrator is useful for evaluating predisposition to a  
 XX CC thrombotic event, supporting a diagnosis of an occurrence of a  
 XX CC thrombotic event or monitoring a thrombotic event in a mammal.  
 XX CC The lyophilised calibrator exhibits excellent immunoreactive stability

CC in storage in the lyophilised state and after reconstitution.  
 XX  
 SQ Sequence 222 AA;

Query Match  
 Best Local Similarity 100.0%; Score 54; DB 18; Length 222;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QOSNEDEPWT 9  
 Db 97 qqsndepwt 105  
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RESULT 8  
 AAR60810  
 ID AAR60810 standard; Protein; 110 AA.  
 AC AAR60810;  
 DT 06-DEC-1994 (first entry)  
 DE Light chain variable region of antibody HCMV16.  
 KW Antibody; humanised antibody; variable region; immune response;  
 KW cytomegalovirus; glycoprotein; complementarity determining region;  
 KW CDR; heavy chain; light chain; ds.  
 OS Mus musculus.  
 XX WO9409136-A.  
 PN 28-APR-1994.  
 PD 15-OCT-1993; 93WO-GB02134.  
 PF 15-OCT-1992; 92GB-0021654.  
 PR (KETT-) KETTOCK LODGE CAMPUS 2.  
 PA Carr FJ, Hamilton AA, Harris WJ;  
 PI WPI; 1994-151321/18.  
 DR N-PSDB; AAQ73749.  
 XX New humanised monoclonal antibodies against Human Cytomegalovirus  
 PT specificity or affinity, for treatment or prevention of HCMV  
 PT infection.  
 XX Disclosure; Figure 2; 53pp; English.

Human monoclonal antibodies may be made specific for a pathogen by substituting the complementarity determining regions (CDR's) from the murine antibody variable domains which show desirable binding properties to that pathogen, into the human immunoglobulin heavy and light chain variable domains. These "humanised" antibodies should elicit a considerably reduced immune response in humans compared to chimeric antibodies as they contain considerably less murine components and their half life in the circulation should approach that of natural human antibodies. This sequence is taken from a donor monoclonal antibody HCMV16, specific for the human cytomegalovirus gH glycoprotein from which CDR's were taken to construct humanised antibodies. Humanised antibodies are described in AAQ63902-063908.

SQ Sequence 110 AA;

Query Match  
 Best Local Similarity 94.4%; Score 51; DB 15; Length 110;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QOSNEDEPWT 9  
 Db 97 qqsndepwt 105  
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QY 1 QOSNEDEPWT 9  
 Db 93 qqsndepwt 101  
 ||:|||||

RESULT 9  
 AAR53930  
 ID AAR53930 standard; Protein; 111 AA.  
 AC AAR53930;  
 DT 05-DEC-1994 (first entry)  
 DE Light chain variable region of humanised antibody 16HuVK.  
 KW Antibody; humanised antibody; variable region; immune response;  
 KW cytomegalovirus; glycoprotein; complementarity determining region;  
 KW CDR; heavy chain; light chain.  
 OS Homo sapiens.  
 OS Mus musculus.  
 XX WO9409136-A.  
 PN 28-APR-1994.  
 PD 15-OCT-1993; 93WO-GB02134.  
 PF 15-OCT-1992; 92GB-0021654.  
 PR (KETT-) KETTOCK LODGE CAMPUS 2.  
 PA Carr FJ, Hamilton AA, Harris WJ;  
 PI WPI; 1994-151321/18.  
 DR N-PSDB; AAQ63908.  
 XX New humanised monoclonal antibodies against Human Cytomegalovirus  
 PT specificity or affinity, for treatment or prevention of HCMV  
 PT infection.  
 XX Example 1; Figure 5; 53pp; English.

Human monoclonal antibodies may be made specific for a pathogen by substituting the complementarity determining regions (CDR's) from the murine antibody variable domains which show desirable binding properties to that pathogen, into the human immunoglobulin heavy and light chain variable domains. These "humanised" antibodies should elicit a considerably reduced immune response in humans compared to chimeric antibodies as they contain considerably less murine components and their half life in the circulation should approach that of natural human antibodies. This sequence is a humanised heavy chain variable region comprising CDR's from the donor monoclonal antibody HCMV16, specific for the human cytomegalovirus gH glycoprotein. The framework region of the human heavy chain has been modified. Humanised antibodies are described in AAQ63902-063908.

SQ Sequence 111 AA;

Query Match  
 Best Local Similarity 94.4%; Score 51; DB 15; Length 111;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QOSNEDEPWT 9  
 Db 93 qqsndepwt 101  
 ||:|||||

RESULT 10  
 AAR00830  
 ID AAR00830 standard; Protein; 112 AA.

us-09-724-406-16.rag

Fri Jun 29 08:04:29 2001

hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis;  
liver cell; glutamate oxaloacetate; pyruvate transaminase.

XX AC AAW00830;  
XX DT 19-MAY-1997 (first entry)  
XX DE Variable light chain of anti-human Fas ligand antibody NOK-4.  
XX DE Variable region; light chain; human; Fas ligand; monoclonal;  
XX KW antibody; NOK-4; hybridoma; inhibition; apoptosis; assay;  
XX KW diagnosis; disease; hepatitis; infectious mononucleosis;  
XX KW systemic lupus erythematosus.  
XX OS Mus musculus.  
XX PN W09629350-A1.  
XX PD 26-SEP-1996.  
XX PF 21-MAR-1996; 96WO-JP00734.  
XX PR 27-OCT-1995; 95JP-0303492.  
XX PR 20-MAR-1995; 95JP-0087420.  
XX PA (SUME ) SUMITOMO ELECTRIC IND CO.  
XX PI Kayagaki N, Nakata M, Okumura K, Yagita H;  
XX PI WPI: 1996-443140/44.  
XX DR N-PSDB; AAT39556.  
XX DR Monoclonal antibody specifically recognising the Fas ligand - useful  
XX PT for the detection of Fas ligands either on cell surface or in  
XX PT solution  
XX PS Claim 26; Page 88; 133pp; Japanese.  
XX CC The present sequence is the light chain variable region of the  
XX CC anti-human Fas ligand monoclonal antibody (MAB) NOK-4. NOK-4 is  
XX CC produced by the hybridoma NOK-4 (FERM BP-5047), which was prepared  
XX CC by immunising mice with transformed human Fas ligand expressing COS  
XX CC cells, and fusing spleen cells isolated from the mice with myeloma  
XX CC P3x63Ag8.653 (ATCC CRL-1580) cells. The MAB recognises the human  
XX CC Fas ligand on the cell surface or in solution, and can be used to  
XX CC inhibit the apoptosis inducing cell surface Fas ligand/Fas  
XX CC reaction. The MAB can also be used for a Fas ligand assay in  
XX CC biological samples (e.g. human blood), especially for disease  
XX CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic  
XX CC lupus erythematosus.  
XX SQ Sequence 112 AA;  
Query Match 94.4%; Score 51; DB 17; Length 112;  
Best Local Similarity 88.9%; Pred. No. 0.054; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 0;  
OY 1 QOSNEDEPWT 9  
DB 93 qgnnedpwt 101  
RESULT 11  
AAW19016  
ID AAW19016 standard; Protein; 112 AA.  
XX AC AAW19016;  
XX DT 14-JAN-1998 (first entry)  
XX DE Anti-human FasL antibody (NOK4) light chain variable region.  
XX DE Light chain; variable region; mouse; murine; human; Fas ligand;  
XX KW FasL; monoclonal antibody; MAB; hybridoma; treatment; hepatitis;  
KW

XX KW  
XX OS  
XX PN  
XX PD  
XX PF  
XX PR  
XX PA  
XX PI  
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XX PT  
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XX CC  
XX SQ  
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Best Local Similarity 88.9%; Pred. No. 0.054; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 0;  
OY 1 QOSNEDEPWT 9  
DB 93 qgnnedpwt 101  
RESULT 12  
AAW09434  
ID AAW09434 standard; Protein; 246 AA.  
XX AC AAW09434;  
XX DT 23-SEP-1997 (first entry)  
XX DE Anti-CD19 antibody B43 single chain variable region.  
XX DE CD19; antibody; variable region; B43; SU25C1; BLV3; targeting;  
XX KW cytotoxin conjugate; cancer treatment; leukaemia; B cell lymphoma;  
XX KW variable; heavy; light chain.  
XX OS Synthetic.  
XX XX Key Location/Qualifiers  
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XX FT 1..26 /label= FRL  
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FT Region 46..62
FT /label= CDR2
FT Region 63..94
FT /label= FR3
FT Region 95..117
FT /label= CDR3
FT Peptide 118..132
FT Domain 133..246
FT /label= linker
FT Region 133..155
FT /label= light_chain
FT Region 156..170
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FT Region 171..185
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FT Region 186..192
FT /label= FR2
FT Region 193..224
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FT /label= FR3
FT Region 225..246
FT /label= CDR3
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PN WO9636360-A1.
XX
PD 21-NOV-1996.
XX
PF 15-MAY-1996; 96WO-US06941.
XX
PR 17-MAY-1995; 95US-0443408.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Bejcek BE, Kersey JH, Uckun FM, Wang D;
XX WPI: 1997-042642/04.
XX N-PSDB: AAT47732.
XX
PT DNA encoding a single chain variable region polypeptide which binds
PT CD19 - used in the treatment of leukaemia and B-cell lymphoma
XX Claim 2: Page 99-100; 143pp; English.
XX
CC AAW09434 represents a single chain variable region polypeptide
CC (heavy chain-linker-light chain) of anti-CD19 antibody B43. Single
CC chain polypeptides were conjugated to at least one cytotoxic agent and
CC used to target the agent(s) to cancerous cells expressing CD19. The
CC immunoconjugates can be used treatment of cancer, especially leukaemia
CC and B-cell lymphoma.
XX
SQ Sequence 246 AA;

Query Match 88.9%; Score 48; DB 18; Length 246;
Best Local Similarity 88.9%; Pred. NO. 0.43;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
Db 225 qqstedpwt 233
||| |||||

RESULT 13
ID AAW09443
XX AAW09443 standard; Protein; 247 AA.
XX
AC AAW09443;
XX
DT 26-SEP-1997 (first entry)

```

```

XX
DE Modified single chain anti-CD19 antibody B43.
XX
KW CD19; antibody; variable region; B43; SJ25C1; BLX3; targeting;
KW cytotoxin conjugate; cancer treatment; leukaemia; B cell lymphoma;
XX variable; heavy; light chain.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 1..117
FT /label= heavy_chain
FT Region 1..26
FT /label= FR1
FT Region 27..31
FT /label= CDR1
FT Region 32..45
FT /label= FR2
FT Region 46..62
FT /label= CDR2
FT Region 63..94
FT /label= FR3
FT Region 95..117
FT /label= CDR3
FT Peptide 118..132
FT /label= linker
FT Domain 133..246
FT /label= light_chain
FT Region 133..155
FT /label= FR1
FT Region 156..170
FT /label= CDR1
FT Region 171..185
FT /label= FR2
FT Region 186..192
FT /label= CDR2
FT Region 193..224
FT /label= FR3
FT Region 225..246
FT /label= CDR3
FT Misc-difference 247
FT /note= "additional C-terminal Cys residue"
XX
PN WO9636360-A1.
XX
PD 21-NOV-1996.
XX
PF 15-MAY-1996; 95WO-US06941.
XX
PR 17-MAY-1995; 95US-0443408.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Bejcek BE, Kersey JH, Uckun FM, Wang D;
XX WPI: 1997-042642/04.
XX
PT DNA encoding a single chain variable region polypeptide which binds
PT CD19 - used in the treatment of leukaemia and B-cell lymphoma
XX Disclosure; Page 108-109; 143pp; English.
XX
CC AAW09443 represents a modified single chain variable region polypeptide
CC (heavy chain-linker-light chain) of anti-CD19 antibody B43. The modified
CC polypeptide has an additional C-terminal Cys residue, as compared to
CC the unmodified polypeptide (no further information is given in the
CC specification). Single chain polypeptides were conjugated to at least
CC one cytotoxic agent and used to target the agent(s) to cancerous cells
CC expressing CD19. The immunoconjugates can be used treatment of cancer,
CC especially leukaemia and B-cell lymphoma.
XX
SQ Sequence 247 AA;

```

us-09-724-406-16.rag

Fri Jun 29 08:04:29 2001

AAW82316  
ID AAW82316 standard; Protein; 288 AA.  
XX  
AC AAW82316;  
XX  
DT 26-FEB-1999 (first entry)  
XX  
DE Mouse OKT3 variant antibody protein.  
XX  
KW OKT3; monoclonal antibody; MAB; point mutation; transplant rejection;  
organ recipient; diagnosis; tumour; therapy.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
FN DEL9721700-Cl.  
XX  
PD 19-NOV-1998.  
XX  
PF 23-MAY-1997; 97DE-1021700.  
XX  
PR 23-MAY-1997; 97DE-1021700.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
XX Kipriyanov S, Little M, Moldenhauer G;  
XX  
XX WPI: 1998-596150/51.  
DR N-PSDB; AAV73335.  
XX  
PT Monoclonal antibody OKT3 with point-mutation - where cysteine is  
replaced by another polar amino acid, useful for controlling  
transplant rejection, and in tumour diagnostics and therapy  
XX  
PS Claim 3; Fig 2; 8pp; German.  
XX  
CC This sequence represents a monoclonal antibody (MAB) derived from OKT3  
with a point-mutation where Cys at position H100A is replaced with  
another polar amino acid, in this example Ser. The MAB is used in  
lowering or eliminating the transplant rejection in an organ recipient,  
and for diagnostic methods for tumours and tumour therapy.  
XX  
SQ Sequence 288 AA;

Query Match 88.9%; Score 48; DB 19; Length 288;  
Best Local Similarity 88.9%; Pred. No. 0.5; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 1;  
QY 1 QOSNEDPWT 9  
DB 243 qgstedpwt 251

Search completed: June 28, 2001, 16:14:36  
Job time: 1324 sec

Query Match 88.9%; Score 48; DB 18; Length 247;  
Best Local Similarity 88.9%; Pred. No. 0.43; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 1;  
QY 1 QOSNEDPWT 9  
DB 225 qgstedpwt 233

RESULT 14  
AAW82314  
ID AAW82314 standard; Protein; 281 AA.  
XX  
AC AAW82314;  
XX  
DT 26-FEB-1999 (first entry)  
XX  
DE Human ScFvCD19 protein.  
XX  
KW ScFvCD19; anti-CD19; single chain; antibody; B-cell marker; CD19; T cell;  
retroviral vector; gene therapy; tumour-associated antigen; cancer.  
XX  
OS Homo sapiens.  
XX  
FN DEL9720152-Al.  
XX  
PD 05-NOV-1998.  
XX  
PF 02-MAY-1997; 97DE-1020152.  
XX  
PR 02-MAY-1997; 97DE-1020152.  
XX  
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
XX Bargou R, Schroeder A, Schwenkenbecher J;  
XX  
XX WPI: 1998-584686/50.  
DR N-PSDB; AAV73323.  
XX  
PT Retroviral vector system for gene therapy - by expression of  
therapeutic gene in T cells  
XX  
PS Claim 8; Page 5; 10pp; German.

This sequence represents a novel human recombinant anti-CD19 single chain  
antibody, ScFvCD19 which recognizes the extracellular domain of the  
B-cell marker CD19. This sequence is used in a retroviral vector system  
for gene transfer and expression in primary human T cells which involves  
a retroviral vector containing CDNA corresponding to a therapeutic gene,  
a promoter selected from the SV40 immediate early promoter or the human  
IL-2 or MHC I promoter and a selectable marker, and a packaging cell  
line (i.e. a modified retroviral packaging line for enhanced transfer  
into primary human T lymphocytes). This vector system in which the CDNA  
encodes a single-chain antibody (scfv) specific for a tumour-associated  
antigen can be used for gene therapy of cancer, especially by isolating  
T cells from the patient's blood, stimulating the T cells in vitro,  
introducing the retroviral vector into the T cells and returning the T  
cells to the patient, preferably by intravenous injection.

Query Match 88.9%; Score 48; DB 19; Length 281;  
Best Local Similarity 88.9%; Pred. No. 0.49; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 1;  
QY 1 QOSNEDPWT 9  
DB 253 qgstedpwt 261

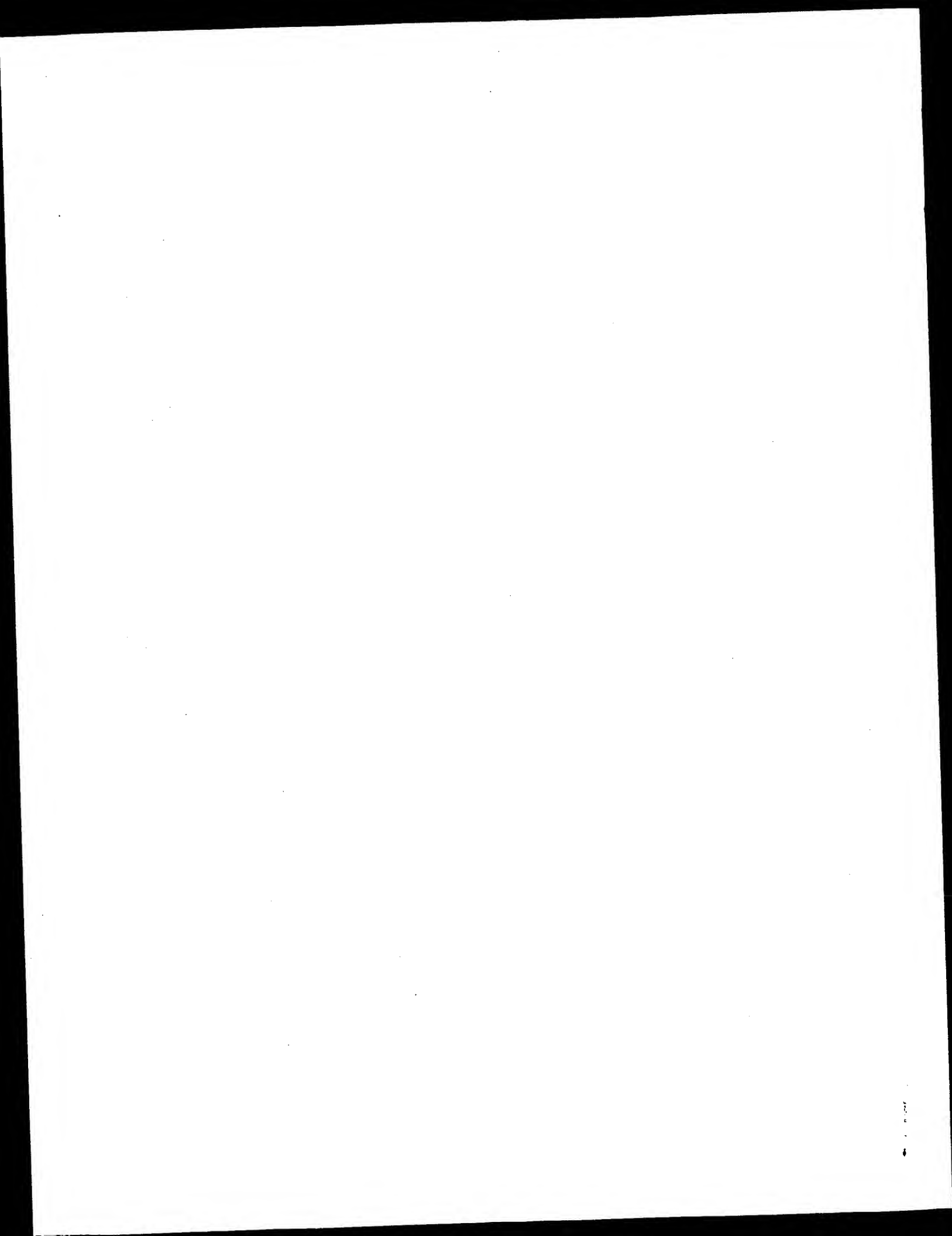
RESULT 15



Fri Jun 29 08:04:29 2001

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Page 9



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds  
(without alignments)  
1.311 Million cell updates/sec

Title: US-09-724-406-16  
Perfect score: 54  
Sequence: 1 QOSNEDPWT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pap:\*
- 2: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pap:\*
- 3: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pap:\*
- 4: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pap:\*
- 5: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pap:\*
- 6: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	111	1	US-08-491-845-8
2	54	100.0	111	1	US-08-491-845-16
3	54	100.0	115	4	US-08-513-968-51
4	54	100.0	131	4	US-08-579-378A-14
5	54	100.0	131	4	US-08-579-378A-18
6	54	100.0	218	5	PCT-US96-13152-2
7	51	94.4	112	3	US-09-065-059-13
8	45	83.3	9	5	PCT-US94-14106-42
9	44	81.5	9	5	PCT-US94-14106-43
10	44	81.5	106	3	US-08-466-151-6
11	40	74.1	111	2	US-08-887-352B-5
12	40	74.1	111	2	US-08-887-352B-6
13	40	74.1	111	3	US-08-887-352B-9
14	40	74.1	111	4	US-09-109-207C-5
15	40	74.1	111	4	US-09-109-207C-6
16	40	74.1	114	2	US-08-887-352B-8
17	40	74.1	114	2	US-08-887-352B-9
18	40	74.1	114	2	US-08-887-352B-10
19	40	74.1	114	4	US-09-109-207C-8
20	40	74.1	114	4	US-09-109-207C-9
21	40	74.1	218	2	US-08-887-352B-10
22	40	74.1	218	2	US-08-887-352B-13
23	40	74.1	218	2	US-08-887-352B-15
24	40	74.1	218	2	US-08-887-352B-17
25	40	74.1	218	2	US-08-887-352B-19
26	40	74.1	218	2	US-08-887-352B-24
27	40	74.1	218	3	US-08-466-151-9

28	40	74.1	218	4	US-09-109-207C-13
29	40	74.1	218	4	US-09-109-207C-15
30	40	74.1	218	4	US-09-109-207C-17
31	40	74.1	218	4	US-09-109-207C-19
32	40	74.1	218	4	US-09-109-207C-24
33	40	74.1	218	4	US-09-282-505-1
34	40	74.1	218	4	US-09-054-255-1
35	40	74.1	248	2	US-08-887-352B-22
36	40	74.1	248	2	US-08-887-352B-23
37	40	74.1	248	4	US-09-109-207C-22
38	40	74.1	248	4	US-09-109-207C-23
39	39	72.2	9	2	US-08-483-636-20
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41	39	72.2	111	1	US-07-634-278-54
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45	39	72.2	111	1	US-08-477-728-55

ALIGNMENTS

RESULT 1  
US-08-491-845-8  
; Sequence 8, Application US/08491845  
; Patent No. 5773247  
; GENERAL INFORMATION:  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: SHIOSAKI, Kouichi  
; APPLICANT: OSATANI, Kiyoshi  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
; NUMBER OF INVENTION: PROCESS FOR PREPARING THE SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/491,845  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP93/00039  
; FILING DATE: 14-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: MAEDA-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-491-845-8

Query Match 100.0%; Score 54; DB 1; Length 111;

us-09-724-406-16.ra1

Fri Jun 29 08:04:30 2001

Best Local Similarity 100.0%; Pred. No. 0.0076; Indels 0; Gaps 0; Mismatches 0; Matches 9; Conservative 0;

QY 1 QOSNEDPWT 9  
| | | | | | | | | |  
DB 93 QOSNEDPWT 101

RESULT 2  
US-08-491-845-16  
; Sequence 16, Application US/08491845  
; Patent No. 5773247  
; GENERAL INFORMATION:  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: SHIOSAKI, Kouichi  
; APPLICANT: OSATOMI, Kiyoshi  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/491,845  
; FILING DATE: 14-JAN-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP93/00039  
; FILING DATE: 14-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: MAEDA=5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-491-845-16

Query Match 100.0%; Score 54; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 0.0076;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
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DB 93 QOSNEDPWT 101

RESULT 3  
US-08-513-968-51  
; Sequence 51, Application US/08513968  
; Patent No. 6114143  
; GENERAL INFORMATION:  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: MAEDA, Hiroaki

APPLICANT: MAKIZUMI, Keiichi  
APPLICANT: SHIOSAKI, Kouichi  
APPLICANT: OSATOMI, Kiyoshi  
APPLICANT: KIMACHI, Kazuhiko  
APPLICANT: HIGUCHI, Hirofumi  
APPLICANT: TOKIYOSHI, Sachio  
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,968  
FILING DATE: 11-SEP-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 78913/1993  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: EDA=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-513-968-51

Query Match 100.0%; Score 54; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 0.0078;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
| | | | | | | | | |  
DB 97 QOSNEDPWT 105

RESULT 4  
US-08-579-378A-14  
; Sequence 14, Application US/08579378A  
; Patent No. 6210671  
; GENERAL INFORMATION:  
; APPLICANT: Co. Man Sung  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: L-Selectin  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/579,378A
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-14

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Query Match      100.0%; Score 54; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QOSNEDPWT 9
Db 113 QOSNEDPWT 121

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RESULT 5
US-08-579-378A-18
; Sequence 18, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; NUMBER OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-18

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Query Match      100.0%; Score 54; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QOSNEDPWT 9
Db 113 QOSNEDPWT 121

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RESULT 6
PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid

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APPLICANT:  
 TITLE OF INVENTION: Process for Generating Specific Antibodies  
 NUMBER OF SEQUENCES: 61  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII (text)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/14106  
 FILING DATE:  
 CLASSIFICATION:  
 INFORMATION FOR SEQ. ID NO. 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 PCT-US94-14106-42

```

Query Match      83.3%; Score 45; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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1 QQSNEPWT 9
1 QQSNEPWT 9

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1  RESULT          9
2  PCT-US94-14106-43
3  ; Sequence 43, Application PC/TUS9414106
4  ; GENERAL INFORMATION:
5  ;
6  ; APPLICANT: Process for Generating Specific Antibodies
7  ;
8  ; TITLE OF INVENTION: 61
9  ; NUMBER OF SEQUENCES: 61
10 ; COMPUTER READABLE FORM:
11 ; MEDIUM TYPE: Floppy disk
12 ; COMPUTER: IBM PC compatible
13 ; OPERATING SYSTEM: PC-DOS/MS-DOS
14 ; SOFTWARE: ASCII (text)
15 ; CURRENT APPLICATION NUMBER: PCT/US94/14106
16 ; FILING DATE:
17 ; CLASSIFICATION:
18 ; INFORMATION FOR SEQ. ID. NO: 43:
19 ; SEQUENCE CHARACTERISTICS:
20 ; LENGTH: 9 amino acids
21 ; TYPE: amino acid
22 ; TOPOLOGY: linear
23 ; MOLECULE TYPE: peptide
24 ; FRAGMENT TYPE: internal
25 ; PCT-US94-14106-43

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Query Match	81.5%	Score 44;	DB 5;	Length 9;
Best Local Similarity	88.9%	pred. No. 1.4e+05;		
Matches	8;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 QQSNEPWT 9  
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ph 1 QQSNEPFT 9

RESULT 10  
US-08-466-151-6  
; Sequence 6, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.

```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
CT-US96-13152-2

Query Match      100.0%; Score 54; DB 5; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.016;
Best Local Identity 99.5%; Mismatches 0; Indels 0; Gaps 0;
Conservative

```

Query Match	100.0%;	Score 54;	DB 5;	Length 218;
Best Local Similarity	100.0%;	Pred. No. 0.016;		
9. Conservative	0;	Mismatches	0;	Indels

1 QQSNEPWT 9  
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93 QQSNEPWT 101

RESULT 7  
US-09-065-059-13  
; Sequence 13, Application US/09065059  
; Patent No. 6068841  
; GENERAL INFORMATION:  
; APPLICANT: SEINO, Ken-ichiro  
; APPLICANT: KAYAGAKI, No. 6068841uhiko  
; APPLICANT: YAGITA, Hideo  
; APPLICANT: OKUMURA, KO  
; APPLICANT: NAKATA, Motomi  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA

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FILING DATE: 424  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bucca Ph.D., Daniel  
REGISTRATION NUMBER: P-42,368  
REFERENCE/DOCKET NUMBER: 50356-151  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-518-5100  
TELEFAX: 703-684-1124

TELEFAX: 703-684-1124  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 112 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-00-0655-059-13

Query Match 94.4%; Score 51; DB 3; Length 112;  
Best Local Similarity 88.9%;  
Pred. No. 0.026;  
8: Conservative 1; Mismatches 0; Indels

1 QQSNEPWT 9  
||:|||||  
93 QQNEPWT 101

RESULT 8  
PCT-US94-14106-42  
; Sequence 42, Application PC/TUS9414106  
: GENERAL INFORMATION:

;; TITLE OF INVENTION: Immunoglobulin Variants  
;; NUMBER OF SEQUENCES: 65  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 1 DNA Way  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/466,151  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/466163  
;; FILING DATE: 06-JUN-1995  
;; APPLICATION NUMBER: 08/405617  
;; FILING DATE: 15-MAR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/185899  
;; FILING DATE: 26-JAN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/879495  
;; FILING DATE: 07-MAY-1992  
;; APPLICATION DATA:  
;; APPLICATION NUMBER: 07/744768  
;; FILING DATE: 14-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svoboda, Craig G.  
;; REGISTRATION NUMBER: 39,044  
;; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
;; TELEPHONE: 650/225-1489  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 106 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
;;  
;; US-08-466-151-6

Query Match 81.5%; Score 44; DB 3; Length 106;  
Best Local Similarity 88.9%; Pred. No. 0.42;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNEPWT 9  
Db 93 QQSNEPFT 101

RESULT 11  
US-08-887-352B-5  
; Sequence 5, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/887,352B  
;; FILING DATE: 03-JUL-1997  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svoboda, Craig G.  
;; REGISTRATION NUMBER: 39,044  
;; REFERENCE/DOCKET NUMBER: P1123  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-1489  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 111 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
;;  
;; US-08-887-352B-5

Query Match 74.1%; Score 40; DB 2; Length 111;  
Best Local Similarity 77.8%; Pred. No. 2.2;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNEPWT 9  
Db 93 QQSNEPFT 101

RESULT 12

US-08-887-352B-6  
; Sequence 6, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/887,352B  
;; FILING DATE: 03-JUL-1997  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svoboda, Craig G.  
;; REGISTRATION NUMBER: 39,044  
;; REFERENCE/DOCKET NUMBER: P1123  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-1489  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 111 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
;;  
;; US-08-887-352B-6

Query Match 74.1%; Score 40; DB 2; Length 111;

us-09-724-406-16.ra1

Fri Jun 29 08:04:30 2001

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; Sequence 5, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-109-207C-5

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Query Match 74.1%; Score 40; DB 4; Length 111;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QQSNEDEPWT 9
   111:111:1
DB 93 QQSHEDPYT 101

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RESULT 15
US-09-109-207C-6
; Sequence 6, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 6
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-111
; OTHER INFORMATION: F(ab) light chain sequence derived from MAEL1
; US-09-109-207C-6

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Query Match 74.1%; Score 40; DB 4; Length 111;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QQSNEDEPWT 9
   111:111:1
DB 93 QQSHEDPYT 101

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Search completed: June 28, 2001, 16:01:14  
Job time: 522 sec

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; Sequence 2, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-2

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Query Match 74.1%; Score 40; DB 3; Length 111;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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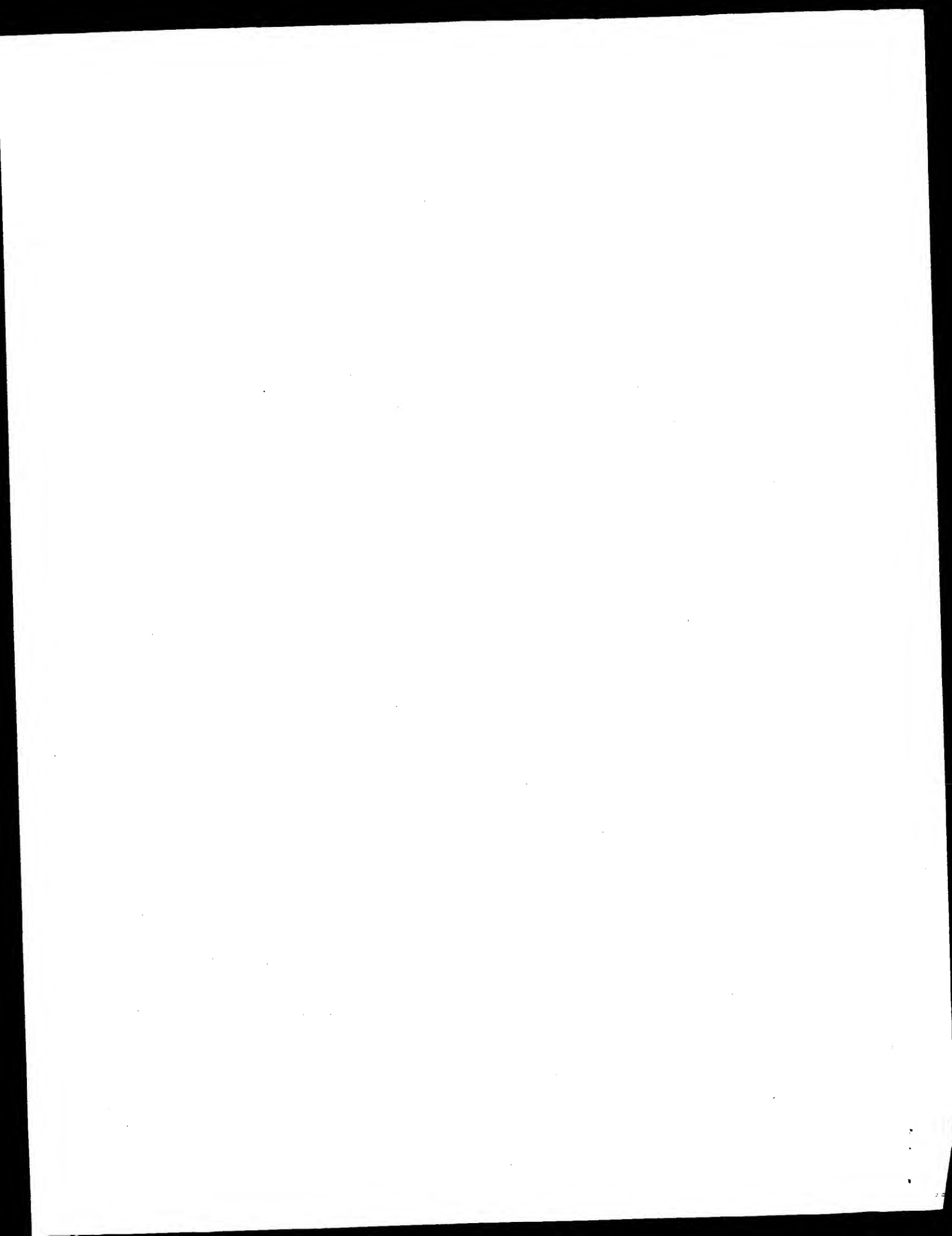
QY 1 QQSNEDEPWT 9
   111:111:1
DB 93 QQSHEDPYT 101

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RESULT 14  
US-09-109-207C-5







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:44 ; Search time 234.85 seconds  
(without alignments)  
2.919 Million cell updates/sec

Title: US-09-724-406-16  
Perfect score: 54  
Sequence: 1 QOSNEDPWT 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR\_68:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	111	1	Ig kappa chain v r
2	54	100.0	111	1	Ig kappa chain v r
3	51	94.4	131	1	Ig kappa chain v r
4	45	83.3	107	2	Ig kappa chain pre
5	45	83.3	111	1	Ig kappa chain v r
6	45	83.3	111	1	Ig kappa chain v r
7	45	83.3	111	2	Ig kappa chain v r
8	45	83.3	111	2	Ig kappa chain v r
9	44	81.5	107	2	Ig kappa chain v r
10	44	81.5	111	1	Ig kappa chain v r
11	44	81.5	111	1	Ig kappa chain v r
12	42	77.8	132	1	Ig kappa chain v r
13	41	75.9	824	2	Ig kappa chain v r
14	41	75.9	96	2	Ig kappa chain v r
15	40	74.1	65	2	Ig kappa chain v r
16	40	74.1	65	2	Ig kappa chain v r
17	40	74.1	112	2	Ig kappa chain v r
18	40	74.1	127	2	Ig kappa chain v r
19	39	72.2	109	2	Ig kappa chain v r
20	39	72.2	111	1	Ig kappa chain v r
21	39	72.2	704	2	Ig kappa chain v r
22	39	72.2	2059	2	Ig kappa chain v r
23	38	70.4	81	2	Ig kappa chain v r
24	37	68.5	111	2	Ig kappa chain v r
25	37	68.5	130	2	Ig kappa chain v r
26	37	68.5	483	2	Ig kappa chain v r
27	37	68.5	483	2	Ig kappa chain v r
28	36	66.7	65	2	Ig kappa chain v r
29	36	66.7	93	2	Ig kappa chain v r

30	36	66.7	109	2	S31998
31	36	66.7	482	2	S65766
32	36	66.7	549	2	T50295
33	36	66.7	805	2	T19936
34	36	66.7	971	1	T01634
35	36	66.7	994	1	T08CR3
36	36	66.7	1171	2	T12936
37	36	66.7	1279	2	A47363
38	36	66.7	1287	2	I46032
39	35	64.8	107	2	JL0139
40	35	64.8	110	1	KVMS10
41	35	64.8	204	2	T36466
42	35	64.8	299	2	T35561
43	35	64.8	403	2	E84935
44	35	64.8	519	2	S36808
45	35	64.8	567	2	F64453

## ALIGNMENTS

RESULT 1

KVMS08  
Ig kappa chain v region (PC6308) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
R:Accession: C01937; A01937  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152  
A:Accession: C01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin v region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status Predicted

Query Match  
Best Local Similarity 100.0%; Score 54; DB 1; Length 111;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QOSNEDPWT 9  
DB 93 QOSNEDPWT 101

RESULT 2

KVMS69  
Ig kappa chain v region (PC7769) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
R:Accession: E01937; A01937  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152  
A:Accession: E01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin v region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status Predicted

Query Match  
Best Local Similarity 100.0%; Score 54; DB 1; Length 111;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-724-406-16.rpr

Fri Jun 29 08:04:31 2001

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Query Match          94.4%; Score 51; DB 1; Length 131;
Best Local Similarity 88.9%; Pred. No. 0.031; 0; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;

QY 1 QQSNEPWT 9
   |||
Db 113 QQSNEPWT 121

RESULT 4
KWSM6 Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26344
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421
A:Accession: S26344
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: EMBL:X59209; NID:g52336; PIDN:CAA41919.1; PID:g1334074
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>

Query Match          83.3%; Score 45; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.3; 0; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;

QY 1 QQSNEPWT 9
   |||
Db 92 QQSNEPWT 100

RESULT 5
KWSM37 Ig kappa chain V regions (PC3741, T111) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
C:Accession: A93204; A93822; A01934
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Contents: PC3741
A:Accession: A93204
A:Molecule type: protein
A:Residues: 1-111 <WEI>
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related
A:Reference number: A93822; MUID:79012520
A:Contents: T111
A:Accession: A93822
A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          83.3%; Score 45; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 0.32; 0; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;

QY 1 QQSNEPWT 9
   |||
Db 93 QQSNEPWT 101

RESULT 3
KWSM6 Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
C:Accession: B90412; B90374; B93822; C93204; D93204; PH1078; A01935
R:Burslein, V.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A:Title: Primary structures of N-terminal extra peptide segments linked to the variable
A:Reference number: A90412; MUID:78235887
A:Contents: M63
A:Accession: B90412
A:Molecule type: protein
A:Residues: 1-35 <BUR>
R:McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains
A:Reference number: A90374; MUID:75140225
A:Contents: M63
A:Accession: B90374
A:Molecule type: protein
A:Residues: 21-46, 'Q' 48-53, 'B' 55-57, 'Z' 59-86, 'F' 88-131 <MCK>
A:Note: this sequence has since been revised in reference A93822
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related
A:Reference number: A93822; MUID:79012520
A:Contents: M63; AB22
A:Accession: B93822
A:Molecule type: protein
A:Residues: 1-53; 69-107 <MC2>
A:Accession: C93822
A:Molecule type: protein
A:Residues: 21-119, 'Y' 121-131 <MC3>
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Contents: PC9245; PC4050
A:Accession: C93204
A:Molecule type: protein
A:Residues: 21-119, 'Y' 121-131 <WEI>
A:Accession: D93204
A:Molecule type: protein
A:Residues: 21-119, 'L' 121-123, 'A' 125-129, 'L' 131 <WE2>
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1078
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 21-122 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73
C:Comment: The M63 precursor sequence is shown.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status experimental <SIG>
F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>
F:43-112/Disulfide bonds: #status predicted

```

QY 1 QOSNEDPWT 9  
 |||||:|  
 Db 93 QOSNEDPYT 101

## RESULT 6

KVMS43

Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 31-Mar-2000  
 C:Accession: A01936  
 R:McKean, D.J.; Bell, M.; Potter, M.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
 A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related molecules  
 A:Reference number: A93822; MUID:79012520  
 A:Accession: A01936  
 A:Molecule type: protein  
 A:Residues: 1-111 <MCK>  
 C:Comment: This chain was isolated from a myeloma protein.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 83.3%; Score 45; DB 1; Length 111;  
 Best Local Similarity 88.9%; Pred. No. 0.32;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 |||||:|  
 Db 93 QOSNEDPYT 101

## RESULT 7

S09966

Ig kappa chain V-J region (LE10) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000  
 C:Accession: S09966  
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
 Eur. J. Immunol. 20, 771-777, 1990  
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies  
 A:Reference number: S09955; MUID:90269328  
 A:Accession: S09966  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <RET>  
 A:Cross-references: EMBL:X51854; NID:955397; PIDN:CAA36147.1; PID:9930231  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 111;  
 Best Local Similarity 88.9%; Pred. No. 0.32;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 |||||:|  
 Db 93 QOSNEDPYT 101

## RESULT 8

A33936

Ig kappa chain V region (VM201) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 21-Jan-2000  
 C:Accession: A33936  
 R:Meek, K.; Johanson, B.; Schulman, J.; Bona, C.; Capra, J.D.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989  
 A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene

A:Reference number: A33936; MUID:89282831  
 A:Accession: A33936  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <MEK>  
 A:Cross-references: GB:J04575; NID:9623194; PIDN:AAA60448.1; PID:9623196  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:14-94/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 111;  
 Best Local Similarity 88.9%; Pred. No. 0.32;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 |||||:|  
 Db 93 QOSNEDPYT 101

## RESULT 9

S26343

Ig kappa chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C:Accession: S26343  
 R:Stark, S.E.; Caton, A.J.  
 J. Exp. Med. 174, 613-624, 1991  
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein  
 A:Reference number: S26309; MUID:91341421  
 A:Accession: S26343  
 A:Molecule type: preliminary  
 A:Status: preliminary  
 A:Residues: 1-107 <STA>  
 A:Cross-references: EMBL:X59207; NID:952334; PIDN:CAA41917.1; PID:91334073  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 44; DB 2; Length 107;  
 Best Local Similarity 88.9%; Pred. No. 0.46;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 |||||:|  
 Db 92 QOSNEDPYT 100

## RESULT 10

KVMS43

Ig kappa chain V region (PC7043) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
 C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: A01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 R:Mo, J.A.; Bona, C.A.; Holmdahl, R.  
 Eur. J. Immunol. 23, 2503-2510, 1993  
 A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s

A:Reference number: S42176; MUID:94009207  
 A:Accession: S42187  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MOJ>  
 A:Cross-references: EMBL:225444; NID:9407832; PIDN:CAA80931.1; PID:9407833  
 A:Note: V-kappa-2IE; anti-collagen  
 A:Accession: S42194  
 A:Molecule type: DNA



Query Match 75.9%; Score 41; DB 2; Length 96;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 DB 85 QOSNEDPWT 93

RESULT 14  
 KYMS83  
 Ig kappa chain V region (PC7183) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: B01937; A01937  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152  
 A:Accession: B01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/disulfide bonds: #status predicted

Query Match 75.9%; Score 41; DB 1; Length 111;  
 Best Local Similarity 88.9%; Pred. No. 1.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 DB 93 QOSNEDPWT 101

RESULT 15  
 C38601  
 Ig kappa chain V region (2B5) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999  
 C:Accession: C38601  
 R:Goshorn, S.C.; Retzel, E.; Jemerson, R.  
 J. Biol. Chem. 266, 2134-2142, 1991  
 A:Title: Common structural features among monoclonal antibodies binding the same antigen  
 A:Reference number: A38601; MUID:91115823  
 A:Accession: C38601  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-65 <GOS>  
 A:Cross-references: GB:M57980; NID:g196406; PIDN:AAA63361.1; PID:g196407  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 74.1%; Score 40; DB 2; Length 65;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 DB 46 QOSNEDPWT 54





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:36 ; Search time 105.36 Seconds  
(without alignments)  
2.926 Million cell updates/sec

Title: US-09-724-406-16  
Perfect score: 54  
Sequence: 1 QQSNEPWT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	111	1	P01667 mus musculus
2	54	100.0	111	1	P01669 mus musculus
3	51	94.4	131	1	P01661 mus musculus
4	45	83.3	111	1	P01660 mus musculus
5	45	83.3	111	1	P01664 mus musculus
6	44	81.5	111	1	P01665 mus musculus
7	44	81.5	132	1	P01658 mus musculus
8	42	77.8	111	1	P01662 mus musculus
9	41	75.9	111	1	P01654 mus musculus
10	39	72.2	111	1	P01656 mus musculus
11	39	72.2	111	1	P01655 mus musculus
12	38	70.4	111	1	P01657 mus musculus
13	38	70.4	112	1	P01659 mus musculus
14	37	68.5	671	1	P01659 mus musculus
15	36	66.7	417	1	P41889 schizosacch
16	36	66.7	417	1	P54998 rhodococcus
17	36	66.7	482	1	Q16581 homo sapien
18	36	66.7	971	1	Q00273 epizootic h
19	36	66.7	994	1	P08504 escherichia
20	36	66.7	1004	1	Q03277 sclara copr
21	36	66.7	1270	1	Q08211 homo sapien
22	36	66.7	1287	1	Q28141 bos taurus
23	36	66.7	1380	1	O70133 mus musculus
24	35	64.8	110	1	P01668 mus musculus
25	35	64.8	403	1	P57158 buchera ap
26	35	64.8	567	1	Q58628 methanococc
27	35	64.8	1023	1	Q27179 methanobact
28	35	64.8	1023	1	P55019 pseudopleur
29	35	64.8	1102	1	Q93009 homo sapien
30	34	63.0	1592	1	P53855 saccharomyc
31	34	63.0	204	1	P05379 thermus aqu
32	34	63.0	232	1	P27983 simian immu
33	34	63.0	373	1	Q58365 methanococc
34	34	63.0	374	1	P18632 cryptomeria

34 34 63.0 436 1 60A\_DROVI Q24735 drosophila  
35 34 63.0 572 1 TC17\_MOUSE Q61751 mus musculus  
36 34 63.0 576 1 TC17\_MOUSE Q61751 mus musculus  
37 34 63.0 605 1 TC17\_MOUSE Q61751 mus musculus  
38 34 63.0 605 1 TC17\_MOUSE Q61751 mus musculus  
39 34 63.0 605 1 TC17\_MOUSE Q61751 mus musculus  
40 34 63.0 632 1 NTP1\_SFVKA Q9q814 myxoma viru  
41 34 63.0 906 1 CBL\_HUMAN Q9q822 Shope fibro  
42 33.5 62.0 885 1 CHB\_SERMA P22681 Shope fibro  
43 33 61.1 322 1 VP40\_NPVHZ Q54468 serratia ma  
44 33 61.1 378 1 RSL\_PROSP P36345 heliothis z  
45 33 61.1 403 1 SHBG\_MOUSE P14128 providencia  
P97497 mus musculus

## ALIGNMENTS

RESULT 1  
KV3Q\_MOUSE  
ID KV3Q\_MOUSE STANDARD; PRT; 111 AA.  
AC P01667;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 6308.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
RT diversity.";  
RL Nature 276:785-790(1978).  
DR PIR: C01937; KWS08.  
DR InterPro: IPR003006;  
DR Pfam: PF00047; Ig; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPWT 9  
Db 93 QQSNEPWT 101

RESULT 2  
KV3Q\_MOUSE  
ID KV3Q\_MOUSE STANDARD; PRT; 111 AA.  
AC P01669;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 7769.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

Fri Jun 29 08:04:32 2001

EN SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RL Nature 276:785-790(1978).  
 DR PIR: E01937; KVM569.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.0035;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEPWT 9  
 DB 93 QOSNEPWT 101

RESULT 3  
 ID KV3H\_MOUSE STANDARD; PRT; 131 AA.  
 AC P01661;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-35.  
 RX MEDLINE=78235887; PubMed=98179;  
 RA Burstein Y., Schechter I.;  
 RT "Primary structures of N-terminal extra peptide segments linked to  
 RT the variable and constant regions of immunoglobulin light chain  
 RT precursors: implications on the organization and controlled  
 RT expression of immunoglobulin genes";  
 RL Biochemistry 17:2392-2400(1978).  
 RN [2]  
 RP SEQUENCE OF 21-131.  
 RX MEDLINE=73140225; PubMed=4691517;  
 RA McKean D.J., Potter M., Hood L.E.;  
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
 RT kappa chains with limited sequence differences";  
 RL Biochemistry 12:760-771(1973).  
 RN [3]  
 RP REVISIONS.  
 RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 RT related mouse kappa variable regions";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 DR PIR: A01935; KVM56.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20 IG KAPPA CHAIN V-III REGION MOPC 63.  
 FT CHAIN 21 131

FT DOMAIN 21 43  
 FT DOMAIN 44 58  
 FT DOMAIN 59 73  
 FT DOMAIN 74 80  
 FT DOMAIN 81 112  
 FT DOMAIN 113 121  
 FT DOMAIN 122 131  
 FT DISULFID 43 112  
 FT NON\_TER 131 131  
 SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 94.4%; Score 51; DB 1; Length 131;  
 Best Local Similarity 88.9%; Pred. No. 0.014;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEPWT 9  
 DB 113 QOSNEPWT 121

RESULT 4  
 ID KV3H\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01660;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE (PC 3741).  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RL Nature 276:785-790(1978).  
 RN [2]  
 RP SEQUENCE (TEPC 111).  
 RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 RT related mouse kappa variable regions";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.  
 DR PIR: A01934; KVM537.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 83.3%; Score 45; DB 1; Length 111;  
 Best Local Similarity 88.9%; Pred. No. 0.15;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEPWT 9  
 DB 93 QOSNEPWT 101

RESULT 5  
KV3L\_MOUSE  
ID KV3L\_MOUSE STANDARD; PRT; 111 AA.  
AC P01664;  
DT 21-JUL-1986 (Rel. 01, Created)  
DE 21-JUL-1986 (Rel. 01, Last sequence update)  
DE IG KAPPA CHAIN V-III REGION CBPC 101.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
RN NCBI\_TaxID=10090;  
RP SEQUENCE.  
RX MEDLINE=79012520; PubMed=95744;  
RA McKean D.J., Bell M., Potter M.;  
RT "Mechanisms of antibody diversity: multiple genes encode structurally  
related mouse kappa variable regions.";  
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01936; KVMSC1.  
DR InterPro: IPR003006;  
DR Pfam: PF00047; Ig; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111  
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 83.3%; Score 45; DB 1; Length 111;  
Best Local Similarity 88.9%; Pred. No. 0.15;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QOSNEPWT 9  
Db 93 QOSNEPWT 101  
|||||:|

RESULT 6  
KV3M\_MOUSE  
ID KV3M\_MOUSE STANDARD; PRT; 111 AA.  
AC P01665;  
DT 21-JUL-1986 (Rel. 01, Created)  
DE 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 7043.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
RN NCBI\_TaxID=10090;  
RP SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR PIR; A01937; KVMSC1.  
DR InterPro: IPR003006;  
DR Pfam: PF00047; Ig; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 102 111 FRAMEWORK 4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 111  
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 81.5%; Score 44; DB 1; Length 111;  
Best Local Similarity 88.9%; Pred. No. 0.22;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QOSNEPWT 9  
Db 93 QOSNEPWT 101  
|||||:|

RESULT 7  
KV3F\_MOUSE  
ID KV3F\_MOUSE STANDARD; PRT; 132 AA.  
AC P01658;  
DT 21-JUL-1986 (Rel. 01, Created)  
DE 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
RN NCBI\_TaxID=10090;  
RP SEQUENCE OF 1-37.  
RX MEDLINE=78235887; PubMed=98179;  
RA Burstein Y., Schechter I.;  
RT "Primary structures of N-terminal extra peptide segments linked to  
the variable and constant regions of immunoglobulin light chain  
precursors: implications on the organization and controlled  
expression of immunoglobulin genes.";  
RL Biochemistry 17:2392-2400(1978).  
RN [1]  
RP SEQUENCE OF 21-132.  
RX MEDLINE=73140224; PubMed=4120629;  
RA McKean D.J., Potter M., Hood L.E.;  
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa  
chain.";  
RL Biochemistry 12:749-759(1973).  
CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS  
BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT  
REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY  
RESIDUES.  
CC PIR; A01933; KVMSC2.  
CC InterPro: IPR003006;  
CC Pfam: PF00047; Ig; 1.  
KW Immunoglobulin V region; Bence-Jones protein; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.  
FT DOMAIN 21 43 FRAMEWORK 1.  
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 59 73 FRAMEWORK 2.  
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 81 112 FRAMEWORK 3.  
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 122 131 FRAMEWORK 4.  
FT DISULFID 43 112 BY SIMILARITY.  
FT NON\_TER 132 132  
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 81.5%; Score 44; DB 1; Length 132;  
Best Local Similarity 44.4%; Pred. No. 0.27;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QOSNEPWT 9  
Db 113 ZZSBZBPWT 121  
|||||:|

Fri Jun 29 08:04:32 2001

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RESULT 8
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RN SEQUENCE (ABPC 22); PubMed=99744;
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
EL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
[2]
RN SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
CC Nature 276:785-790(1978).
DR PIR: A01935; KVM56.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 77.8%; Score 42; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 0.51; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0;

Qy 1 QQSNEPWT 9
Db 93 QQNEDPYT 101

RESULT 9
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
CC Nature 276:785-790(1978).

Query Match 72.2%; Score 39; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2;

Qy 1 QQSNEPWT 9
Db 93 QQSKEVPWT 101

RESULT 11
KV3C_MOUSE
ID KV3C_MOUSE STANDARD; PRT; 111 AA.

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PIR: B01937; KVM583.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 75.9%; Score 41; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 0.77; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

Qy 1 QQSNEPWT 9
Db 93 QQSNEPWT 101

RESULT 10
KV3A_MOUSE
ID KV3A_MOUSE STANDARD; PRT; 111 AA.
AC P01654;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 2880/PC 1229.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
CC Nature 276:785-790(1978).
DR PIR: A01930; KVM580.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

Query Match 72.2%; Score 39; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2;

Qy 1 QQSNEPWT 9
Db 93 QQSKEVPWT 101

RESULT 11
KV3C_MOUSE
ID KV3C_MOUSE STANDARD; PRT; 111 AA.

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AC P01656;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION MOPC 70.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=67056897; PubMed=4162931;  
 RA Gray W.R., Dreyer W.J., Hood L.E.;  
 RT "Mechanism of antibody synthesis: size differences between mouse  
 RT kappa chains."  
 RL Science 155:465-467(1967).  
 CC -1- MISCELLANEOUS; THIS IS A BENICE-JONES PROTEIN.  
 DR PIR: A01930; KWSM80.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 2 38  
 FT DOMAIN 3 53  
 FT DOMAIN 4 60  
 FT DOMAIN 5 61  
 FT DOMAIN 6 92  
 FT DOMAIN 7 93  
 FT DOMAIN 8 101  
 FT DOMAIN 9 102  
 FT DOMAIN 10 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

Query Match 72.2%; Score 39; DB 1; Length 111;  
 Best Local Similarity 77.8%; Pred. No. 1.8;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 DB 93 QOSKEVFWT 101  
 RESULT 12  
 ID KV3K\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01663;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION PC 4050.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity."  
 RL Nature 276:785-790(1978).  
 DR PIR: A01935; KWSM6.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 2 38  
 FT DOMAIN 3 53  
 FT DOMAIN 4 60  
 FT DOMAIN 5 61  
 FT DOMAIN 6 92  
 FT DOMAIN 7 93  
 FT DOMAIN 8 101  
 FT DOMAIN 9 102  
 FT DOMAIN 10 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;  
 Query Match 70.4%; Score 38; DB 1; Length 111;  
 Best Local Similarity 77.8%; Pred. No. 2.7;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 DB 93 QONNEDPLT 101

RESULT 13  
 ID KV3G\_MOUSE STANDARD; PRT; 112 AA.  
 AC P01659;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION TEPC 124.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=73140225; PubMed=4691517;  
 RA McKean D.J., Potter M., Hood L.E.;  
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
 RT kappa chains with limited sequence differences."  
 RL Biochemistry 12:760-771(1973).  
 DR PIR: A01933; KWSM32.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 2 38  
 FT DOMAIN 3 53  
 FT DOMAIN 4 60  
 FT DOMAIN 5 61  
 FT DOMAIN 6 92  
 FT DOMAIN 7 93  
 FT DOMAIN 8 101  
 FT DOMAIN 9 102  
 FT DOMAIN 10 111  
 FT DISULFID 23 92  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 12339 MW; 7CFD328DBE8E9D71 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 112;  
 Best Local Similarity 44.4%; Pred. No. 2.7;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9  
 DB 93 ZZSBZAPWT 101

RESULT 14  
 ID CUT9\_SCHPO STANDARD; PRT; 671 AA.  
 AC P41889; O14231;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE CUT9 PROTEIN.  
 GN CUT9 OR SPAC6F12.15C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.

Fri Jun 29 08:04:32 2001

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RT "Characterization of the desulfurization genes from Rhodococcus sp.
RT strain IGTS8."
RL J. Bacteriol. 176:6707-6716(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96031556; PubMed=7574582;
RA Piddington C.S., Kovacevich B.R., Rambosek J.;
RT "Sequence and molecular characterization of a DNA region encoding the
RT dibenzothiophene desulfurization operon of Rhodococcus sp. strain
RT IGTS8."
RL Appl. Environ. Microbiol. 61:468-475(1995).
CC -!- FUNCTION: PART OF A PATHWAY TO REMOVE COVALENTLY BOUND SULFUR FROM
CC DIBENZOTHIOPHENE (DBT) WITHOUT BREAKING CARBON-CARBON BONDS.
CC SULFUR DIOXYGENASE WHICH CONVERTS DBT TO DBT-SULFONE (DBT02 OR DBT
CC 5,5-DIOXIDE)
CC -!- PATHWAY: FIRST STEP IN PATHWAY FROM DBT TO 2-HBP.
CC -!- SIMILARITY: SOME, TO ACYL COENZYME A DEHYDROGENASES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U08850; AAA56673.1; -
CC DR EMBL; L37363; AAA99484.1; -
CC DR InterPro; IPR001552; -
CC DR Pfam; PF00441; Acyl-CoA_dh; 3.
CC KW Oxidoreductase; Plasmid.
CC FT CONFLICT 251 56 G -> A (IN REF. 2).
CC FT CONFLICT 251 251 A -> R (IN REF. 2).
CC SQ SEQUENCE 417 AA; 45027 MW; CDBCF0054AE2FD0 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 417;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSNEDPWT 9
Db 290 QQATDPYT 298

Search completed: June 28, 2001, 15:54:37
Job time: 125 sec

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RX MEDLINE=95096177; PubMed=7798319;
RA Samejima I., Yanagida M.;
RT "Bypassing anaphase by fission yeast cut9 mutation: requirement of
RT cut9+ to initiate anaphase."
RL J. Cell Biol. 127:1655-1670(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RA Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A PIVOTAL ROLE IN THE CONTROL OF ANAPHASE.
CC COMPONENT OF THE 20S CYCLOSOME/ANAPHASE-PROMOTING COMPLEX (APC),
CC WHICH IS NECESSARY FOR CYCLIN DESTRUCTION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- SIMILARITY: CONTAINS 10 TPR REPEATS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D31844; BAA06630.1; -
CC DR EMBL; 298533; BAB11098.1; -
CC DR InterPro; IPR001440; -
CC DR Pfam; PF00515; TPR; 5.
CC KW Cell division; Cell cycle; Mitosis; Repeat; TPR repeat;
CC FT REPEAT 117 149 TPR 1.
CC FT REPEAT 117 184 TPR 2.
CC FT REPEAT 150 184 TPR 3.
CC FT REPEAT 200 233 TPR 4.
CC FT REPEAT 339 372 TPR 5.
CC FT REPEAT 373 406 TPR 6.
CC FT REPEAT 407 440 TPR 7.
CC FT REPEAT 441 474 TPR 8.
CC FT REPEAT 475 508 TPR 9.
CC FT REPEAT 515 549 TPR 10.
CC FT REPEAT 550 583 TPR 10.
CC FT MUTAGEN 412 412 G->D: IN TEMPERATURE SENSITIVE MUTANT.
CC FT MUTAGEN 535 535 A->T: IN TEMPERATURE SENSITIVE MUTANT.
CC FT CONFLICT 103 103 A -> C (IN REF. 1).
CC SQ SEQUENCE 671 AA; 75888 MW; 5300382396270BE2 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 671;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNEDPW 8
Db 509 QSNEXPW 515

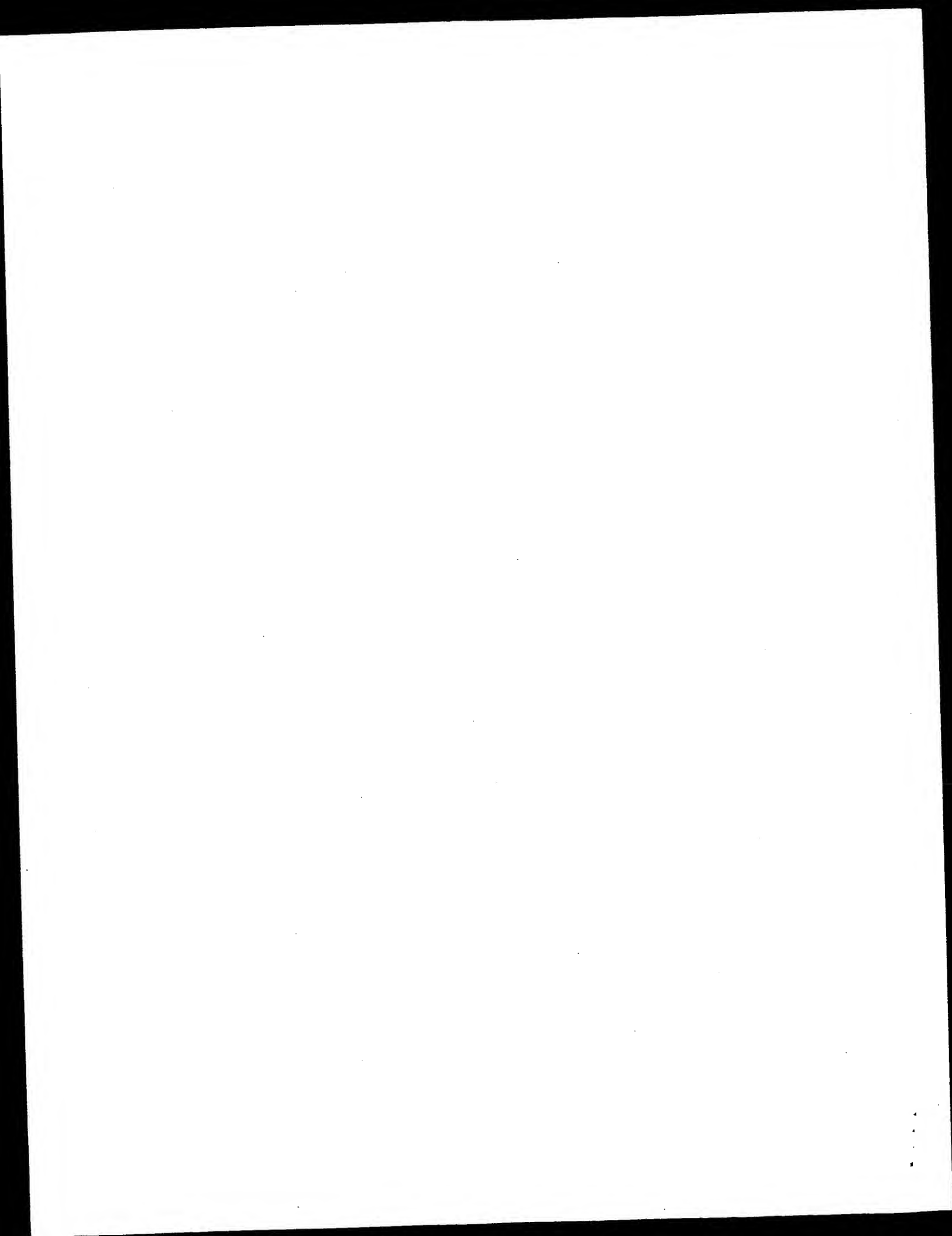
RESULT 15
SOXC_RHOSO
ID SOXC_RHOSO STANDARD; PRT; 417 AA.
AC P54998;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DIBENZOTHIOPHENE DESULFURIZATION ENZYME C (DBT SULFUR DIOXYGENASE).
GN SOXC OR DS2C.
OS Rhodococcus sp. (strain IGTS8).
OG Plasmid.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1831;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95050232; PubMed=7961424;
RA Denome S.A., Oldfield C., Nash L.J., Young K.D.;

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Fri Jun 29 08:04:32 2001

us-09-724-406-16.rsp

Page 7





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: June 28, 2001, 16:08:22 ; Search time 411.58 Seconds  
(without alignments)  
2.893 Million cell updates/sec  
Title: US-09-724-406-16  
Perfect score: 54  
Sequence: 1 QQSNEPWT 9  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SPTREMBL16:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_unclassified:\*

13: sp\_vertebrate:\*

14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	41	75.9	086992
2	39	72.2	09m4t2
3	39	72.2	09m4t2 phaseolus a
4	39	72.2	055592 synechocyst
5	39	72.2	0915d6 brevundimon
6	39	72.2	086089 pseudomonas
7	37	72.2	09p450 xyella fas
8	37	68.5	09v5e3 drosophila
9	37	68.5	08453 caenorhabdi
10	37	68.5	083900 ovine adeno
11	36	66.7	09ne92 leishmania
12	36	66.7	09hb70 homo sapien
13	36	66.7	09wpx20 homo sapien
14	36	66.7	09wpx20 chimpanzee
15	36	66.7	09fmb4 arabidopsis
16	36	66.7	09wpx9 schizosacch
17	36	66.7	09ncn7 trichomonas
18	36	66.7	09stg4 caenorhabdi
19	35	64.8	09j180 mus musculus

# ALIGNMENTS

RESULT 1		ALIGNMENTS	
ID	Q86992	PRELIMINARY;	PRT; 1104 AA.
AC	Q86992;		
DT	01-NOV-1996 (TRENBLrel. 01, Created)		
DT	01-NOV-1996 (TRENBLrel. 01, Last sequence update)		
DE	01-MAR-2001 (TRENBLrel. 16, Last annotation update)		
DE	DNA POLYMERASE (DELTA DNA POLYMERASE PROTEIN)		
GN	DP.		
OS	Spodoptera ascovirus, and Spodoptera frugiperda ascovirus 1.		
OC	Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.		
OX	NCBI_TaxID=43681, 113374;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=Spodoptera ascovirus;		
RA	MEDLINE=96187793; PubMed=8614981;		
RT	Stasiak K., Demattè M.V., Federici B.A., Bigot Y.;		
RT	"Phylogenetic position of the Diadromus pulchellus ascovirus DNA polymerase among viruses with large double-stranded DNA genomes.";		
RL	J. Gen. Virol. 81:3059-3072(2000).		
RL	VIROLOGY 216:146-157(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=Spodoptera frugiperda ascovirus 1;		
RA	MEDLINE=20540044; PubMed=11086137;		
RT	Stasiak K., Demattè M.V., Federici B.A., Bigot Y.;		
RT	"Phylogenetic position of the Diadromus pulchellus ascovirus DNA polymerase among viruses with large double-stranded DNA genomes.";		
RL	J. Gen. Virol. 81:3059-3072(2000).		
CC	-!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE - N		
CC	-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.		
CC	EMBL; U35732; AAC54632.1; -		
DR	EMBL; AJ279828; CAC19170.1; -		
DR	InterPro; IPR000560; -		
DR	InterPro; IPR002084; -		
DR	InterPro; IPR002088; -		
DR	Prints; PF00136; DNA POL.B. 2.		
DR	PROSITE; PS00106; DNAPOLB.		
DR	PROSITE; PS00116; DNA POLYMERASE_B; UNKNOWN1.		
DR	PROSITE; PS00778; HIS-ACID-PHOSPHAT_2; UNKNOWN1.		
DR	PROSITE; PS00904; PPTA; UNKNOWN1.		
DR	SMART; SM00486; POLBc; 1.		

086939 streptomyce  
091cb1 streptomyce  
09s2d5 streptomyce  
086777 streptomyce  
09p456 aspergillus  
099036 trichoderma  
093785 trichoderma  
005618 propionibac  
09nw27 homo sapien  
09hh18 methanosarc  
083095 treponema p  
09wnx1 thermotoga  
09vkv9 drosophila  
09hck3 homo sapien  
091b24 rhodospirill  
09sel6 elaeis guin  
09ssal arabidopsis  
09esc4 mus musculu  
09s86 streptomyce  
09esc5 mus musculu  
091b4 xenopus lae  
09ye11 aeropyrum p  
09rw14 deinococcus  
P72946 synecocyst  
O88869 rattus norv

us-09-724-406-16.rspt

Fri Jun 29 08:04:33 2001

RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 region from map positions 64% to 92% of the genome.;  
 RL DNA Res. 2:153-166(1995).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 Miyajima N., Hiroseawa M., Sugliura M., Nakazaki N., Naruo K., Okumura S.,  
 Hosouchi T., Matsuno A., Muraki A., Watanabe A., Yamada M., Yasuda M.,  
 Shimo S., Takeuchi C., Wada T., Watanabe A.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL: D63999; BAA10098.1;  
 DR InterPro: IPR002692;  
 DR Pfam: PF01804; Penicill-amidase; 1. 9F13B0DFA2278B63 CRC64;  
 DR SEQUENCE 704 AA; 77956 MW; 9F13B0DFA2278B63 CRC64;  
 SQ

Query Match 72.2%; Score 39; DB 2; Length 704;  
 Best Local Similarity 66.7%; Pred. No. 31; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 2;

QY 1 QOSNEPWT 9  
 DB 429 QNSNDPWT 437

RESULT 4  
 Q9L5D6 PRELIMINARY; PRT; 720 AA.

ID Q9L5D6  
 AC Q9L5D6  
 DT 01-OCT-2000 (TREMELrel. 15, Created)  
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
 DE GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE  
 OS Brevundimonas diminuta (Pseudomonas diminuta)  
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
 OC Brevundimonas  
 OX NCBI\_TaxID=293;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-KAC-1;  
 RA Kim D.-W., Kang S.-M., Yoon K.-H.;  
 RT "Isolation of new Pseudomonas diminuta KAC-1 strain producing glutaryl  
 7-aminocephalosporanic acid acylase.";  
 RT Korean J. Microbiol. 37:200-205(1999).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-KAC-1;  
 RC Kim D.-W., Kang S.-M., Yoon K.-H.;  
 RT "Cloning and the nucleotide sequence of a Pseudomonas diminuta KAC-1  
 glutaryl 7-aminocephalosporanic acid acylase gene.";  
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF251710; AAF64242.1;  
 DR InterPro: IPR002692;  
 DR Pfam: PF01804; Penicill-amidase; 1. AD624797845CC39B CRC64;  
 DR SEQUENCE 720 AA; 79779 MW; AD624797845CC39B CRC64;  
 SQ

Query Match 72.2%; Score 39; DB 2; Length 720;  
 Best Local Similarity 66.7%; Pred. No. 32;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEPWT 9  
 DB 439 QNSNDPWT 447

RESULT 5  
 O86089

KW DNA replication; DNA-binding; DNA-directed DNA polymerase.  
 SQ SEQUENCE 1104 AA; 125786 MW; 3E609827CE3E40B CRC64;

Query Match 75.9%; Score 41; DB 14; Length 1104;  
 Best Local Similarity 85.7%; Pred. No. 21; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0;

QY 3 SNEDPWT 9  
 DB 828 SNQDPWT 834

RESULT 2  
 Q9M4T2 PRELIMINARY; PRT; 263 AA.

AC Q9M4T2  
 DT 01-OCT-2000 (TREMELrel. 15, Created)  
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
 DE ARL2.  
 GN Phaseolus acutifolius (teary bean).  
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 OC Fabales; Fabaceae; Papilionoideae; Phaseolus.  
 OX NCBI\_TaxID=33129;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gerhardt I.R., Pappas G., Chrispeels M.J., Grossi de Sa M.F.;  
 RT "Insecticidal arcelin genes of the common bean are subject to  
 divergent selection.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF25724; AAF71744.1;  
 DR InterPro: IPR000985;  
 DR InterPro: IPR001220;  
 DR Pfam: PF00138; lectin\_legA; 1.  
 DR Pfam: PF00139; lectin\_legB; 1.  
 DR SEQUENCE 263 AA; 29025 MW; 36ED84DAFA8ECF9C CRC64;  
 SQ

Query Match 72.2%; Score 39; DB 10; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 11; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;

QY 3 SNEDPW 8  
 DB 63 SNEDPW 68

RESULT 3  
 Q55592 PRELIMINARY; PRT; 704 AA.

ID Q55592  
 AC Q55592;  
 DT 01-NOV-1996 (TREMELrel. 01, Created)  
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
 DE 7-BETA-(4-CARBXYBUTANAMIDO)CEPHALOSPORANIC ACID ACYLASE.  
 GN Siro378.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PCC6803;  
 RA Tabata S.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=96127529; PubMed=8590279;  
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
 Sugliura M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium

ID O86089 PRELIMINARY; PRT; 720 AA.  
 AC O86089;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE CEPHALOSPORIN ACYLASE.  
 GN CAL.  
 OS Pseudomonas sp. 130.  
 OC Bacteria; Proteobacteria.  
 OK NCBI\_TaxID=81841;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=130.  
 RX MEDLINE=99339939; PubMed=10411632;  
 RA Li Y., Chen J., Jiang W., Mao X., Zhao G., Wang E.;  
 RT "In vivo post-translational processing and subunit reconstitution of  
 RL cephalosporin acylase from Pseudomonas sp. 130.";  
 RL Eur. J. Biochem. 262:713-719(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=130;  
 RA Li Y., Zhang Q., Yang Y., Zhao G., Wang E.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF085353; AAC34685.2;  
 DR InterPro: IPR002692;  
 DR Pfam: PF01804; Penicil\_amidase; 1.  
 KW Porin.  
 SQ SEQUENCE 720 AA; 79672 MW; C2EF964F5081D8CB CRC64;

Query Match 72.2%; Score 39; DB 2; Length 720;  
 Best Local Similarity 56.7%; Pred. No. 32;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QOSNEPWT 9  
 | | | | |  
 DB 439 QNSNDPWT 447

RESULT 6  
 Q9PD50 PRELIMINARY; PRT; 2059 AA.  
 ID Q9PD50;  
 AC Q9PD50;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE SURFACE PROTEIN.  
 GN XF1529.  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OK Xylella.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
 RA Coutinho N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.B., Gruber A.,  
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madelira A.M.B.N., Madelira H.M.F., Marino C.L.,  
 RA Marques C.F.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck M.F., Mirra E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,

RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,  
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
 RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,  
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;  
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";  
 RL Nature 406:151-159(2000).  
 DR EMBL: AF003982; AAF84338.1;  
 SQ SEQUENCE 2059 AA; 204035 MW; EPA6A71B5DD24E10 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 2059;  
 Best Local Similarity 75.0%; Pred. No. 96;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QSNEDPWT 3  
 | | | | |  
 DB 68 QCSDDPWT 75

RESULT 7  
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 ID Q9V5E3;  
 AC Q9V5E3;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE PROBABLE SERINE PROTEASE CG12133 (EC 3.4.21.-).  
 GN CG12133.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferrez C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jalali B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Furl V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

us-09-724-406-16.rspt

Fri Jun 29 08:04:33 2001

Best Local Similarity 62.5%; Pred. No. 50;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
"The genome sequence of *Drosophila melanogaster*.";  
Science 287:2185-2195(2000).  
-!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.  
-!- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).  
CC EMBL: AE003831; AAF58868.1; -;  
DR HSP: Q61955; I35469; CG12133.  
DR Flybase; FBgn0033469;  
DR InterPro: IPR001254; -;  
DR InterPro: IPR001314; -;  
DR Pfam: PF00089; trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PROSITE: PS00134; TRYPsin\_HIS; 1.  
DR PROSITE: PS00135; TRYPsin\_SER; 1.  
DR SMART: SM00020; TRYP\_SPC; 1.  
KW Hydrolase; Serine protease.  
SQ SEQUENCE 350 AA; 39380 MW; F922E2AFCD0E960 CRC64;

Query Match 68.5%; Score 37; DB 5; Length 350;  
Best Local Similarity 75.0%; Pred. No. 36;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNEDPWT 9  
DB 69 QSNQFPWT 76

RESULT 8  
ID Q18453 PRELIMINARY; PRT; 483 AA.  
AC Q18453; 1996 (TREMELrel. 01, Created)  
DT 01-NOV-1998 (TREMELrel. 05, Last sequence update)  
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)  
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
DE C34E11.1 PROTEIN.  
GN C34E11.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN SEQUENCE FROM N.A.  
RA McMurray A.;  
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RP MEDLINE-94150718; PubMed-7906398;  
RX Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,  
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,  
Craighton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,  
Smalton N., Smith A., Sonhammer E., Staden K., Sulston J.,  
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;  
"2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.";  
RL Nature 368:32-38(1994).  
DR EMBL: Z67754; CAA91751.1; -;  
DR InterPro: IPR01026; -;  
DR Pfam: PF01417; ENTH; 1.  
DR SMART: SM00273; ENTH; 1.  
SQ SEQUENCE 483 AA; 52797 MW; 7F483D478A16203B CRC64;

Query Match 68.5%; Score 37; DB 5; Length 483;

Best Local Similarity 62.5%; Pred. No. 50;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNEDPW 8  
DB 48 EATNEDEPW 55

RESULT 9  
Q83900 PRELIMINARY; PRT; 515 AA.  
ID Q83900  
AC Q83900; 1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
DE PIIIA PROTEIN.  
OS Ovine adenovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Adenovirus.  
OX NCBI\_TaxID=37367;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-OAV287;  
RX MEDLINE-95297141; PubMed-7778275;  
RA Vratil S., Boyle D., Kocherhans R., Both G.W.;  
"Sequence of ovine adenovirus homologs for 100K hexon assembly, 33K,  
pVIII, and fiber genes: early region E3 is not in the expected  
location.";  
RT Virology 209:400-408(1995).  
RL EMBL: U40839; AAA84974.1; -;  
DR InterPro: IPR003479; -;  
DR Pfam: PF02455; Hex\_IIIa; 1.  
DR PIR: P02455; Hex\_IIIa; 1.  
SQ SEQUENCE 515 AA; 58390 MW; BED9F7C3EC7E8F5B CRC64;

Query Match 68.5%; Score 37; DB 14; Length 515;  
Best Local Similarity 71.4%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSNEDPW 8  
DB 265 RNNEDPW 271

RESULT 10  
Q9NE92 PRELIMINARY; PRT; 2656 AA.  
ID Q9NE92  
AC Q9NE92; 2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
DE HYPOPHOSPHATASE PROTEIN L787.06.  
GN L787.06.  
OS Leishmania major.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-FRIEDLIN;  
RA Robben J., Aert R., Volckaert G., Ivens A.C., Quail M.,  
Rajandream M.A., Barrell B.G.;  
Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-FRIEDLIN;  
RX MEDLINE-98146435; PubMed-9477341;  
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
Smith D.F.;  
"A physical map of the Leishmania major Friedlin genome.";  
RL Genome Res. 8:135-145(1998).  
DR EMBL: AL163492; CAB86690.1; -;  
DR InterPro: IPR001515; -;  
DR PRODOM: PD003823; -; 1.  
SQ SEQUENCE 2656 AA; 288578 MW; 3B281E0713819D0F CRC64;

Query Match 68.5%; Score 37; DB 5; Length 2656;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOSNEDPWT 9  
 Db 1506 QEAESPWT 1514

RESULT 11  
 ID Q9HB70 PRELIMINARY; PRT; 54 AA.  
 AC Q9HB70;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE PNAS-111.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yu W.-O., Chai Y.-B., Sun B.-Z., Zhu F., Liu X.-S., Li Z., Lu F.,  
 RA Yan W., Yang H., Zhao Z.-L.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF275806; AAG23818.1; -;  
 SQ SEQUENCE 54 AA; 6630 MW; 16150F0DFE98A32D CRC64;

Query Match 66.7%; Score 36; DB 4; Length 54;  
 Best Local Similarity 44.4%; Pred. No. 7.9;  
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOSNEDPWT 9  
 Db 9 ERNNQNPWT 17

RESULT 12  
 ID Q9WPN9 PRELIMINARY; PRT; 208 AA.  
 AC Q9WPN9;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.  
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11723;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SVISUN;  
 RA Beer B.E., Bailes E., Goeken R., Dapolito G., Coulibaly C., Norley S.,  
 RA Kurth R., Gautier J.P., Gautier-Hion A., Vallet D., Sharp P.M.,  
 RA Hirsch V.M.;  
 RT "Simian immunodeficiency virus from sun-tailed monkeys (Cercopithecus solatus) - evidence for host-dependent evolution within the C. l'hoesti superspecies";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN REGULATE THE CD4(T4) ANTIGEN. NEF PROTEIN ACCELERATES VIRULENT PROGRESSION OF AIDS BY ITS INTERACTION WITH CELLULAR PROTEINS INVOLVED IN SIGNAL TRANSDUCTION AND HOST CELL ACTIVATION. NEF HAS BEEN SHOWN TO BIND SPECIFICALLY TO A SUBSET OF THE SRC KINASE FAMILY (BY SIMILARITY).  
 DR EMBL; AF131870; AAD39759.1; -;  
 DR InterPro: IPR001556; -;  
 DR Pfam: PF00469; F-protein; 1.  
 KW AIDS; GTP-binding; Myristate.

SQ SEQUENCE 208 AA; 24132 MW; B7C385035D8E1BAF CRC64;

Query Match 66.7%; Score 36; DB 14; Length 208;  
 Best Local Similarity 75.0%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QOSNEDPWT 3  
 Db 165 QGVNEDPW 172

RESULT 13  
 ID Q9NX20 PRELIMINARY; PRT; 251 AA.  
 AC Q9NX20;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE 28.4 KDA PROTEIN.  
 DE 28.4 KDA PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,  
 RA Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,  
 RA Nakamura Y., Sugai T., Sugano S.;  
 RL "NEDO human cDNA sequencing project";  
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PHEOCHROMOCYTOMA;  
 RA Peng Y., Li Y., Tu Y., Xu S., Han Z., Fu G., Chen Z.;  
 RT "A novel gene expressed in human pheochromocytoma";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK000491; BAA91202.1; -;  
 DR EMBL; AF183428; AAG09697.1; -;  
 DR InterPro: IPR000114; -;  
 DR Pfam: PF00252; Ribosomal\_L16; 1.  
 DR PRINTS: PR00060; RIBOSOMALL16.  
 SQ SEQUENCE 251 AA; 28449 MW; 8A42A67DA80A6FEF CRC64;

Query Match 66.7%; Score 36; DB 4; Length 251;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOSNEDPWT 9  
 Db 206 ERNNQNPWT 214

RESULT 14  
 ID Q9FM84 PRELIMINARY; PRT; 252 AA.  
 AC Q9FM84;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE GENOMIC DNA, CHROMOSOME 5, p1 CLONE:MCD7.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=98290546; PubMed=9628582;  
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,  
 RA Tabata S.;

us-09-724-406-16.rspt

Fri Jun 29 08:04:33 2001

"Structural analysis of Arabidopsis thaliana chromosome 5. IV.  
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen  
 RT physically assigned pl and TAC clones."  
 RL DNA Res. 5:41-54(1998).  
 DR EMBL; AB009049; BAB11275.1; -. 5DBFCE1F2213132 CRC64;  
 SQ SEQUENCE 252 AA; 28680 MW; 5DBFCE1F2213132 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 252;  
 Best Local Similarity 62.5%; Pred. No. 39;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QSNEDPWT 9  
 DB 125 RSKDDPWT 132

## RESULT 15

Q9URW7 PRELIMINARY; PRT; 549 AA.  
 AC Q9URW7;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
 DE PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN.  
 GN SPAP696.OIC.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972H-;  
 RA McDougall R.C., Rajandream M.A., Barrell B.G., Brown S., Harris D.;  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AL133359; CAB62421.1; -.  
 DR InterPro; IPR001683; -.  
 DR Pfam; PF00787; PX; 1.  
 DR SMART; SM00312; PX; 1.  
 SQ SEQUENCE 549 AA; 60920 MW; F892A29B80380CD5 CRC64;

Query Match 66.7%; Score 36; DB 3; Length 549;  
 Best Local Similarity 55.6%; Pred. No. 88;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QSNEDPWT 9  
 DB 482 OKTNQDAWT 490

Search completed: June 28, 2001, 16:08:23  
 Job time: 951 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:36 ; Search time 362.28 Seconds  
(without alignments)  
20.918 Million cell updates/sec

Title: US-09-724-406-18  
Perfect score: 674  
Sequence: 1 EVKLVEGGGLVPGGSLRL.....NPHYAMDYWGQGTSTVSS 125

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
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16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	585.5	86.9	124	18 AAW01594	Lead binding Mab 2
2	555.5	82.4	124	17 AAR90831	2B5 heavy chain va
3	553	82.0	140	13 AAR20790	Unprocessed variab
4	553	82.0	141	13 AAR30431	A5B7 antibody heav
5	553	82.0	250	17 AAW06177	Murine A5B7 Fd fr
6	553	82.0	473	18 AAW41415	Human B7.1-murine
7	553	82.0	643	20 AAW82739	Clone PNG4/A5B7VH-
8	553	82.0	647	20 AAW82747	Plasmid pUC19/muA5
9	546.5	81.1	122	16 AAR74942	Immunoglobulin hea
10	545.5	80.9	138	16 AAR74963	Anti-idiotypic anti
11	542.5	80.5	359	20 AAY29913	Human MCP-3 and mu

12	542.5	80.5	361	20 AAY29911	Human IP-10 and mu
13	542.5	80.5	374	20 AAY29916	Artificial synthe
14	521.5	77.4	141	17 AAR92757	Murine anti-human
15	520.5	77.2	392	16 AAR82835	scFv-PP. Syntheti
16	518.5	76.9	122	16 AAR74941	Immunoglobulin hea
17	518.5	76.9	146	16 AAR74962	Anti-idiotypic anti
18	516	76.6	119	20 AAY33425	Mouse antibody MAK
19	515.5	76.5	142	16 AAR92828	CI79Fv-PP variable
20	515	76.4	145	13 AAR22373	CDR-grafted, human
21	515	76.4	146	13 AAR22373	A5B7 gH-2 antibody
22	515	76.4	250	17 AAW06179	Humanised A5B57 Fd
23	513	76.1	119	11 AAR07316	VH domain of antib
24	513	76.1	119	17 AAW14484	Monoclonal antibody
25	513	76.1	119	17 AAR99873	Monoclonal antibody
26	513	76.1	119	21 AAY51368	Mouse monoclonal a
27	512.5	76.0	115	16 AAR82825	Variable heavy reg
28	505	74.9	151	4 AAR30252	Sequence of the le
29	505	74.9	249	13 AAR21262	pScFvN011 encoding
30	499	74.0	146	13 AAR20793	CDR-grafted, human
31	499	74.0	146	13 AAR26150	A5B7 gH-2 antibody
32	493.5	73.2	120	13 AAR27498	WNI 58-9 antibody
33	491.5	72.9	122	14 AAR38610	MCP-3 heavy chain
34	491.5	72.9	122	19 AAW58487	Murine MCP-3 antio
35	491.5	72.9	123	9 AAR80461	Sequence of the va
36	491.5	72.9	222	15 AAR53804	FAB heavy chain fo
37	491.5	72.9	277	14 AAR39336	scFv fragment enco
38	487.5	72.3	121	16 AAR68740	MAB MCP603 heavy
39	485.5	72.0	121	16 AAR68740	Amino acid sequenc
40	484.5	71.9	120	13 AAR27497	WNI 222-5 antibody
41	475.5	70.5	116	14 AAR38609	MCP-3 heavy chain
42	475.5	70.5	141	17 AAR92764	Human/murine chima
43	473.5	70.3	141	17 AAR92766	Human/murine chima
44	471.5	70.0	141	17 AAR92765	Human/murine chima
45	467.5	69.4	141	17 AAR32763	Human/murine chima

ALIGNMENTS

RESULT 1  
AAW01594  
ID AAW01594 standard; Protein; 124 AA.  
XX  
AC AAW01594;  
XX  
DT 22-AUG-1997 (first entry)  
XX  
DE Lead binding MAB 2E7 heavy chain variable region.  
XX  
KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;  
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;  
KW heavy metal.  
XX  
OS Mus musculus.  
XX  
FN WO9639518-A1.  
XX  
PD 12-DEC-1996.  
XX  
PF 05-JUN-1996; 96WO-US09258.  
XX  
PR 10-OCT-1995; 95US-0541373.  
XX  
PR 05-JUN-1995; 95US-0462798.  
XX  
PA (BION-) BIONEBRASKA INC.  
XX  
PI Lopez O, Murray PJ, Wylie DE;  
XX  
DR WPI: 1997-043140/74.  
XX  
DR N-PSDB; AAR58268.  
XX  
PT DNA encoding heavy metal binding polypeptide sequences - used for  
PT detecting, removing, adding or neutralising heavy metals, such as

us-09-724-406-18.rag

Fri Jun 29 08:04:33 2001

PT lead cations

XX Claim 12; Page 91; 125pp; English.

XX The present sequence represents the heavy chain variable region for  
 CC monoclonal antibody (Mab) 2E7, which immunoreacts with a lead cation.  
 CC The sequence was derived from RNA isolated from mouse hybridoma cells.  
 CC The protein can be used for binding heavy metals, such as lead cations.  
 CC It can be used for detecting, removing, adding or neutralising the  
 CC heavy metals in biological and inanimate systems. It can be used in  
 CC e.g. aqueous liquid systems, in biological or environmental systems or  
 CC in such compositions as perfumes, cosmetics, pharmaceuticals, health  
 CC care products, skin treatment products, pesticides, herbicides,  
 CC solvents used in the production of semi-conductor and integrated  
 CC circuit components and production materials for electronic components.  
 CC The products can provide for applications involving minute amounts of  
 CC specific heavy metals.

XX Sequence 124 AA;

Query Match 86.9%; Score 585.5; DB 18; Length 124;

Best Local Similarity 90.4%; Pred. No. 2.3e-44; Indels 1; Gaps 1;

Matches 113; Conservative

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYIMNWVRQPPGKALEWLGFRNKANGYTT 60

Db 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYIMNWVRQPPGKALEWLGFRNKANGYTT 60

QY 61 EFSASVMGRFTISRDDSQSLYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQTS 120

Db 61 EFSASVMGRFTISRDDSQSLYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQTS 119

QY 121 VTVSS 125

Db 120 VTVSS 124

RESULT 2

ID AAR90831 standard; Protein: 124 AA.

XX AC

XX AAR90831;

XX 25-JUN-1996 (first entry)

XX 2B5 heavy chain variable region from pCIB4615.

XX delta endotoxin; Bacillus thuringiensis; western corn rootworm;  
 XX WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;  
 XX antibody.

XX Insecta sp.

XX WO9600783-A1.

XX 11-JAN-1996.

XX 20-JUN-1995; 95WO-TB00497.

XX 28-JUN-1994; 94US-0267641.

XX (CIBA ) CIBA GEIGY AG.

XX Carozzi NB, Koziel MG;

XX WPI; 1996-077494/08.

XX N-PSDB; AAT15727.

XX New monoclonal antibodies which bind insect gut proteins - used  
 PT partic. with toxin moieties for the control of insect pests, partic.  
 PT in plants

XX

PS Claim 8; Page 54-55; 106pp; English.

XX AAR90829-39 are monoclonal antibodies or a binding fragments produced by  
 CC using insect guts, partic. insect brush border membranes (BBMs), esp.  
 CC corn rootworm, as antigen; immunising a donor animal with the antigen;  
 CC isolating immunocompetent B cells from the immunised animal; fusing B  
 CC cells with a tumour cell line; isolating the fused cells, culturing them  
 CC and cloning positive hybrid cells; and screening the hybrid cells for  
 CC prodn. of the required MAb. The MAb bind to the gut of a target insect  
 CC but do not bind to mammalian BBMs. The DNA sequence can be operably  
 CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,  
 CC pseudomonas exotoxin and phytoalexin, etc... The Abs are useful for  
 CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and  
 CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.  
 CC maize.

XX Sequence 124 AA;

Query Match 82.4%; Score 555.5; DB 17; Length 124;

Best Local Similarity 84.4%; Pred. No. 9.9e-42; Indels 7; Gaps 2;

Matches 108; Conservative

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYIMNWVRQPPGKALEWLGFRNKANGYTT 60

Db 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYIMNWVRQPPGKALEWLGFRNKANGYTT 60

QY 61 EFSASVMGRFTISRDDSQSLYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQ 117

Db 61 EFSASVMGRFTISRDDSQSLYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQ 116

QY 118 GTSVTSS 125

Db 117 GTSVTSS 124

RESULT 3

ID AAR20790 standard; Protein: 140 AA.

XX AC

XX AAR20790;

XX 19-MAY-1992 (first entry)

XX Unprocessed variable region of heavy chain of A5B7 antibody.

XX murine monoclonal antibody; Mab; VH domain; humanised antibody; CEA;  
 XX complementarity determining region.

XX Mus musculus.

XX Key Location/Qualifiers

XX Cleavage-site 19..20 /note= "putative signal peptide cleavage site"

XX WO9201059-A.

XX 23-JAN-1992.

XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1990; 90GB-0014932.

XX 21-DEC-1990; 90WO-GB02017.

XX (CELL-) CELLTECH LTD.

XX Adair JR, Bodmer MW, Mountain A, Owens RJ;

XX WPI; 1992-056874/07.

XX N-PSDB; AAQ20984.

XX New CDR-grafted anti carcinoembryonic antigen antibodies - useful  
 PT in plants

XX



PT in therapy and diagnosis of carcinoma

XX Example 1; Fig 1; 70pp; English.

CC The A5B7 MAB is a mouse MAB of the type IgG1-kappa raised against  
CC CEA which had been denatured by heating to 85 degrees C for 35  
CC minutes. The MAB has been extensively studied by Harwood et al.  
CC (Br. J. Cancer, 54, 75-82, 1986). A cDNA library was prepared from  
CC polyA RNA isolated from the A5B7 hybridoma cell line. A probe  
CC complementary to mouse heavy chain constant region was used to  
CC identify clone pBG1 containing the complete leader, variable and  
CC constant regions of the heavy chain. The amino acid sequence  
CC predicted from the sequence encoding the unprocessed variable  
CC region is given here.

XX Sequence 140 AA;

Query Match 82.0%; Score 553; DB 13; Length 140;  
Best Local Similarity 86.4%; Pred. No. 1.9e-41;  
Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYNNWVRQPPGKALEWLGFIKANGYTT 60

Db 20 evklvesggglvqpggsirlscatsgftfdyymnwvrppgkalewlgfignkangytt 79

QY 61 EFSASVMGRFTISRDDSSQSLYLQMTLRAEDSATYYCARDPPYGNPHYVANDYWGQGT 120

Db 80 eysasvkgfrftrskdsgsilylqmntlraedsatyyctrd--rglrlyf--dywgggtt 135

QY 121 VTVSS 125

Db 136 ltvss 140

RESULT 4

AAAR30431  
ID AAR30431 standard; Protein; 141 AA.

AC AAR30431;

DT 03-FEB-1993 (first entry)

DE A5B7 antibody heavy chain sequence.

XX humanised antibody; chimaeeric; carcino-embryonic antigen; therapy;  
KW diagnosis; carcinomas; CDR; IgG; human; murine; ss.  
XX Chimaeric.

XX WO9201059-A.  
XX 23-JAN-1992.

XX 05-JUL-1991; 91WO-GB01108.  
XX 05-JUL-1991; 91WO-GB01108.  
XX 05-JUL-1990; 90GB-0014932.  
XX 21-DEC-1990; 90WO-GB02017.  
XX (CELL-) CELTECH LTD.

XX Adair JR, Bodmer MW, Mountain A, Owens RJ;  
XX WPI: 1992-284316/34.  
XX N-PSDB: AAQ27351.

XX Humanised antibody molecules - comprising murine and human regions,  
PT specific for carcino-embryonic antigen, useful for diagnosis and  
XX therapy

PS Example 1; Figure 1; 71pp; English.

CC This sequence represents the A5B7 monoclonal antibody heavy chain.  
CC It was decoded from the cDNA (AAQ27351). Sequence analysis confirmed  
CC A5B7 to be an IgG1 K antibody.

XX Sequence 141 AA;

Query Match 82.0%; Score 553; DB 13; Length 141;  
Best Local Similarity 86.4%; Pred. No. 1.9e-41;  
Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYNNWVRQPPGKALEWLGFIKANGYTT 60

Db 20 evklvesggglvqpggsirlscatsgftfdyymnwvrppgkalewlgfignkangytt 79

QY 61 EFSASVMGRFTISRDDSSQSLYLQMTLRAEDSATYYCARDPPYGNPHYVANDYWGQGT 120

Db 80 eysasvkgfrftrskdsgsilylqmntlraedsatyyctrd--rglrlyf--dywgggtt 135

QY 121 VTVSS 125

Db 136 ltvss 140

RESULT 5

AAAW06177

ID AAW06177 standard; Protein; 250 AA.

XX AAW06177;

DT 17-FEB-1997 (first entry)

DE Murine A5B7 Fd fragment.

XX ribonuclease; human; bovine; pancreatic; anti-tumour therapy; ADEPT;  
KW mustard-ribonuclease; antibody directed enzyme prodrug therapy;  
KW anti-neoplastic; prodrug; reverse polarity; ion pair interaction;  
KW reduced immunogenicity; non-selective triggering; primer;  
KW polymerase chain reaction; PCR; HP-RNase; Fd; F(ab')<sub>2</sub>.

XX Synthetic.

XX WO9620011-A1.

XX 04-JUL-1996.

XX 21-DEC-1995; 95WO-GB02991.

XX 16-AUG-1995; 95GB-0016810.

XX 23-DEC-1994; 94GB-0026192.

XX (ZENE ) ZENECA LTD.

XX Blakey DC, Boyle FT, Davies DH, Eggelte HJ, Heaton DM;  
XX Hennen JF, Hennequin LFA, Marsham PR, Rabin BR, Slater AM;  
XX Tarragona-Fiol A, Taylorson CJ;

XX WPI: 1996-321650/32.  
XX N-PSDB: AAT42507.

XX Two component system for anti-tumour therapy - comprising targeting  
PT moiety linked to mutated enzyme which can transform an  
XX anti-neoplastic prodrug

XX Example 6; Page 118-119; 182pp; English.

XX A two-component system for anti-tumour therapy comprises a targeting  
CC moiety linked to a mutated enzyme which can transform an anti-neoplastic  
CC prodrug. The system is based on antibody directed enzyme prodrug therapy  
CC (ADEPT) using a non-naturally occurring mutant form of a host enzyme,  
CC pref. human pancreatic ribonuclease (HP-RNase), (see AAT42478-83). The  
CC targeting moiety can be an antibody, in partic. murine monoclonal  
CC antibody A5B7 (which binds to human carcinoembryonic antigen). A5B7 is

Fri Jun 29 08:04:33 2001

CC suitable for targeting colorectal carcinoma. Fragments, esp. F(ab')<sub>2</sub>,  
 CC of the antibody can be conjugated to HP-RNase. A5B7 Fd and L chain  
 CC fragments were isolated by PCR using cDNA isolated from A5B7 hybridoma  
 CC cells. The present sequence is that of the murine A5B7 Fd fragment.

XX Sequence 250 AA;

Query Match 82.0%; Score 553; DB 17; Length 250;  
 Best Local Similarity 86.4%; Pred. No. 3.4e-41;  
 Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVSGLVQPGSLRLSCATSGFTSDYNNVRQPPGKALEWLGFIIRNKANGYTT 60  
 Db 20 EVKLVSGLVQPGSLRLSCATSGFTSDYNNVRQPPGKALEWLGFIIRNKANGYTT 79  
 QY 61 EFSASVMGRTISRDSSQSLYLQMTLRAEDSATYVCARDPPYGNPHYAMDYWGOGTS 120  
 Db 80 EFSASVMGRTISRDSSQSLYLQMTLRAEDSATYVCARDPPYGNPHYAMDYWGOGTS 135  
 QY 121 VIVSS 125  
 Db 136 IIVSS 140

## RESULT 6

AAW41415  
 ID AAW41415 standard; Protein; 473 AA.

XX AAW41415;

XX 02-JUN-1998 (first entry)

XX Human B7.1-murine A5B7 F(ab')<sub>2</sub> fusion protein.

XX Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;  
 XX cancer diagnosis; complementarity determining region.

XX Chimeric - Homo sapiens.

XX Chimeric - Mus sp.

XX WO9742329-A1.

XX 13-NOV-1997.

XX 29-APR-1997; 97WO-GB01165.

XX 14-FEB-1997; 97GB-0003103.

XX 04-MAY-1996; 96GB-0009405.

XX (ZENE) ZENECA LTD.

XX Copley CG, Edge MD, Emery SC;

XX WPI; 1997-558987/51.

XX N-PSDB; AAV17340.

XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for

XX diagnosis and therapy of cancer

XX Reference Example 3; Page 190-193; 208pp; English.

XX This sequence is the human B7.1-murine A5B7 F(ab')<sub>2</sub> fusion protein  
 CC (AB7), and is an example of the antibody of the invention. The antibody  
 CC is an anti-CEA (carcinoembryonic antigen) antibody (preferably  
 CC 806.077 Ab). Host cells or transgenic organisms transformed with DNA  
 CC encoding the antibody, are used to make the antibody or conjugate. The  
 CC conjugate is used in a medicament suitable for intravenous  
 CC administration. The conjugate can be used for cancer therapy, selectively  
 CC killing tumour cells. The conjugate can be used for in vivo or in vitro  
 CC diagnosis of cancer.

XX Sequence 473 AA;

Query Match 82.0%; Score 553; DB 18; Length 473;  
 Best Local Similarity 86.4%; Pred. No. 6.7e-41;  
 Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVSGLVQPGSLRLSCATSGFTSDYNNVRQPPGKALEWLGFIIRNKANGYTT 60  
 Db 243 EVKLVSGLVQPGSLRLSCATSGFTSDYNNVRQPPGKALEWLGFIIRNKANGYTT 302  
 QY 61 EFSASVMGRTISRDSSQSLYLQMTLRAEDSATYVCARDPPYGNPHYAMDYWGOGTS 120  
 Db 303 EFSASVMGRTISRDSSQSLYLQMTLRAEDSATYVCARDPPYGNPHYAMDYWGOGTS 358  
 QY 121 VIVSS 125  
 Db 359 IIVSS 363

## RESULT 7

AAW82739  
 ID AAW82739 standard; Protein; 643 AA.

XX AAW82739;

XX 10-MAY-1999 (first entry)

XX Clone pNG4/A5B7VH-IgG2CH1/CPG2 R6 protein.

XX Conjugate; cell targeting; cytotoxic drug; prodrug therapy system;  
 XX prodrug-converting enzyme; cell surface antigen; treatment; cancer;  
 XX inflammation; rheumatoid arthritis; antibody.

XX Synthetic.

XX WO9851787-A2.

XX 19-NOV-1998.

XX 05-MAY-1998; 98WO-GB01294.

XX 10-MAY-1997; 97GB-0009421.

XX (ZENE) ZENECA LTD.

XX Blakey DC, Emery SC;

XX WPI; 1999-059700/05.

XX N-PSDB; AAV72046.

XX New gene construct expressing conjugate of targeting agent and  
 XX prodrug-converting enzyme - useful for, e.g. targeted production of  
 XX cytotoxic drug in vivo, especially for treatment of cancer

XX Example 1e; Page 68-70; 100pp; English.

XX This sequence is used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a  
 CC cell-targeting group (I) and a heterologous prodrug-converting enzyme  
 CC (II), and (B) is directed to leave the cell for selective localisation at  
 CC a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a  
 CC target site, then administration of (II) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme prodrug therapy  
 CC system.

XX Sequence 643 AA;

Query Match 82.0%; Score 553; DB 20; Length 643;

Best Local Similarity 86.4%; Pred. No. 9.3e-41;

Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGSLRLSCATSGFTFSDYYMNMVROPKALEWLGFIKNGKANGYTT 60  
 |||||  
 Db 20 evklvesggglvqpgslrlscatsgftfdyymnmvropkalewlgfignkangytt 79  
 |||||  
 QY 61 EFSASVMGRTISRDSSQSLYLQMTNLRADTSATYICARDPPYGNPHYYAMDYWGQGT 120  
 |||||  
 Db 80 eysasvgrftisrdksqsllylqmntlraedsatyyctrd--rglrlyf--dywgqgtt 135  
 |||||  
 QY 121 VTVSS 125  
 |||||  
 Db 136 ltvss 140

## RESULT 8

AAW82747  
 ID AAW82747 standard; Protein; 647 AA.

XX AC AAW82747;

DT 10-MAY-1999 (first entry)

DE Plasmid pUC19/muA5B7-RC/CPG2(R6) protein.

XX Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;  
 KW prodrug-converting enzyme; cell surface antigen; treatment; cancer;  
 KW inflammation; rheumatoid arthritis; antibody; prodrug therapy system.

XX Synthetic.

OS Mus sp.

XX FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= signal\_peptide

FT /note= "murine Fd linker"

XX WO9851787-A2.

XX 19-NOV-1998.

XX 05-MAY-1998; 98WO-GB01294.

XX 10-MAY-1997; 97GB-0009421.

XX (ZENE ) ZENECA LTD.

XX Blakey DC, Emery SC;

XX WPT; 1999-059700/05.

XX N-PSDB; AAV72082.

PT New gene construct expressing conjugate of targeting agent and  
 PT prodrug-converting enzyme - useful for, e.g. targeted production of  
 PT cytotoxic drug in vivo, especially for treatment of cancer

PS Example 22; Page 97-98; 100pp; English.

XX This sequence is a used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a  
 CC cell-targeting group (I) and a heterologous prodrug-converting enzyme  
 CC (II), and (B) is directed to leave the cell for selective localisation  
 CC at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a  
 CC target site, then administration of (III) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme prodrug therapy  
 CC system.

XX Sequence 647 AA;

SQ

Query Match 82.08; Score 553; DB 20; Length 647;  
 Best Local Similarity 86.4%; Pred. No. 9.3e-41;  
 Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGSLRLSCATSGFTFSDYYMNMVROPKALEWLGFIKNGKANGYTT 60  
 |||||  
 Db 20 evklvesggglvqpgslrlscatsgftfdyymnmvropkalewlgfignkangytt 79  
 |||||  
 QY 61 EFSASVMGRTISRDSSQSLYLQMTNLRADTSATYICARDPPYGNPHYYAMDYWGQGT 120  
 |||||  
 Db 80 eysasvgrftisrdksqsllylqmntlraedsatyyctrd--rglrlyf--dywgqgtt 135  
 |||||  
 QY 121 VTVSS 125  
 |||||  
 Db 136 ltvss 140

## RESULT 9

AAW74942  
 ID AAR74942 standard; peptide; 122 AA.

XX AC AAR74942;

DT 19-JAN-1996 (first entry)

XX Immunoglobulin heavy chain of anti-idiotypic antibody against human  
 DE anticancer antibody.

XX Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
 KW complementarity determining region.

XX Mus sp.

XX FH Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT Region 50..68

FT /label= CDR2

FT Region 101..111

FT /label= CDR3

XX JP07101999-A.

XX 18-APR-1995.

XX 06-OCT-1993; 93JP-0272950.

XX 06-OCT-1993; 93JP-0272950.

XX (HAGI/) HAGIWARA Y.

XX WPT; 1995-182987/24.

XX Novel anti-idiotypic antibody against an human anticancer monoclonal  
 PT antibody - and DNA sequences encoding the antibody, useful in  
 PT pharmacology, medicine and biochemical fields.

PS Claim 4; Page 2; 28pp; Japanese.

XX AAR74940-R74943 are possible heavy chains of a new anti-idiotypic  
 CC antibody against a human anticancer monoclonal antibody. This antibody  
 CC contains in its heavy chain 3 complementarity determining regions CDR1  
 CC (AAR74929-R74931) CDR2 (AAR74932-R74935) and CDR3 (AAR74936-R74939),  
 CC this is also true of the light chain which has its own CDR1  
 CC (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3  
 CC (AAR74950-R74954). The antibody and DNA encoding it are useful in  
 CC pharmacological, medical and biochemical fields.

XX Sequence 122 AA;

Query Match

81.1%; Score 546.5; DB 16; Length 122;



QY 120 SVTVSS 125  
Db 210 tltvss 215

## RESULT 12

AAAY29911  
ID AAY29911 standard; Protein; 361 AA.

XX AC AAY29911;

XX DT 17-NOV-1999 (first entry)

XX DE Human IP-10 and murine scFv38 fusion protein.

XX KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
XX KW Immune response; HIV; infection.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Synthetic.

XX PN WO9946392-A1.

XX PD 16-SEP-1999.

XX PF 12-MAR-1999; 99WO-US05345.

XX PR 12-MAR-1998; 98US-0077745.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kwak LW, Biragyn A;

XX DR WPI; 1999-551418/46.

XX PT New fusion polypeptides comprising a chemokine and a tumour antigen or

XX PT HIV antigen, used for treating cancers or treating or preventing HIV

XX PT infection -

XX PS Disclosure; Page 115-116; 142pp; English.

XX CC The present invention describes fusion proteins comprising a chemokine

XX CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins

XX CC comprise: (1) human monocyte chemoattractant protein-3 (MCP-3) and human

XX CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human

XX CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1;

XX CC SDF-1 and human Muc-1; (5) human IP-10 and human Muc-1; (4) human

XX CC HIV gp120; (7) human MDC and HIV gp120; and (8) human MCP-3 and

XX CC gp120. The fusion proteins, and nucleotide sequences encoding them, can

XX CC be used for producing an immune response, e.g. an effector T cell immune

XX CC response. They can also be used for treating cancer or treating or

XX CC preventing HIV infection. The fusion proteins and/or nucleotide sequences

XX CC can be used in in vitro diagnostic assays, as well as in screening assays

XX CC for identifying unknown tumour antigen epitopes and fine mapping of

XX CC tumour antigen epitopes. The present sequence represents a fusion protein

XX CC from the present invention.

XX SQ Sequence 361 AA;

Query Match 80.5%; Score 542.5; DB 20; Length 361;  
Best Local Similarity 82.5%; Pred. No. 4.2e-40;  
Matches 104; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYVMNVRPPGKALEWLGFIKNGKGYTT 60

Db 92 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYVMNVRPPGKALEWLGFIKNGKGYTT 151

Qy 61 EFSASVNGRTFISRDSSQSLYLQMTLRAEDSATYICARDPPYGNPHYYA-MDYWGQCT 119

Db 152 EYSASVNGRTFISRDSSQSLYLQMTLRAEDSATYICARDPPYGNPHYYA-MDYWGQCT 211

QY 120 SVTVSS 125  
Db 212 tltvss 217

## RESULT 13

AAAY29916

ID AAY29916 standard; Protein; 374 AA.

XX AC AAY29916;

XX DT 17-NOV-1999 (first entry)

XX DE Artificial synthetic construct protein SEQ ID NO:15.

XX KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
XX KW Immune response; HIV; infection.

XX OS Synthetic.

XX PN WO9946392-A1.

XX PD 16-SEP-1999.

XX PF 12-MAR-1999; 99WO-US05345.

XX PR 12-MAR-1998; 98US-0077745.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kwak LW, Biragyn A;

XX DR WPI; 1999-551418/46.

XX PT New fusion polypeptides comprising a chemokine and a tumour antigen or

XX PT HIV antigen, used for treating cancers or treating or preventing HIV

XX PT infection -

XX PS Disclosure; Page 117-118; 142pp; English.

XX CC The present invention describes fusion proteins comprising a chemokine

XX CC and a tumour antigen or HIV antigen. Specifically claimed fusion

XX CC proteins comprise: (1) human monocyte chemoattractant protein-3 (MCP-3) and

XX CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human

XX CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)

XX CC human SDF-1 and human Muc-1; (5) human IP-10 and human Muc-1; (6) human

XX CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and

XX CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,

XX CC can be used for producing an immune response, e.g. an effector T cell

XX CC immune response. They can also be used for treating cancer or treating

XX CC preventing HIV infection. The fusion proteins and/or nucleotide

XX CC sequences can be used in in vitro diagnostic assays, as well as in

XX CC screening assays for identifying unknown tumour antigen epitopes and fine

XX CC mapping of tumour antigen epitopes. AAY29916 and AA221156 to AA221168 are

XX CC sequences given in the SEQ ID LISTING in the present invention but which

XX CC are not mentioned further within the specification.

XX SQ Sequence 374 AA;

Query Match 80.5%; Score 542.5; DB 20; Length 374;  
Best Local Similarity 82.5%; Pred. No. 4.4e-40;  
Matches 104; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYVMNVRPPGKALEWLGFIKNGKGYTT 60

Db 215 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYVMNVRPPGKALEWLGFIKNGKGYTT 274

Qy 61 EFSASVNGRTFISRDSSQSLYLQMTLRAEDSATYICARDPPYGNPHYYA-MDYWGQCT 119

Db 275 EYSASVNGRTFISRDSSQSLYLQMTLRAEDSATYICARDPPYGNPHYYA-MDYWGQCT 334

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QY 120 SVTVSS 125
Db 335 lltvss 340

RESULT 14
AA92757
ID AAR92757 standard; Protein; 141 AA.
XX AC
XX AC AAR92757;
XX DT
XX DT 17-SEP-1996 (first entry)
XX DE Murine anti-human IL-8 monoclonal Ab variable heavy chain.
XX KW pUC-WS4-VH: variable; heavy chain; WS4; hybridoma; monoclonal;
XX KW antibody; MAb; BALB/c mouse; spleen cell; human; interleukin-8;
XX KW IL-8; myeloma P3X63-Ag8.653 cell; CDR; framework; chimeric
XX KW complementarity determining region; chimaeric; murine;
XX KW inflammation; disease; mediated; low antigenicity.
XX OS Mus musculus.

XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Peptide /label= sig_peptide
XX FT Peptide 20..141
XX FT Peptide /label= mat_peptide
XX FT Region 50..54
XX FT /note= "complementarity determining region 1"
XX FT Region 69..87
XX FT /note= "complementarity determining region 2"
XX FT Region 120..130
XX FT /note= "complementarity determining region 3"
XX FH WO9602576-A1.
XX PD 01-FEB-1996.
XX PF 12-JUL-1995; 95WO-JP01396.
XX PR 14-DEC-1994; 94JP-0310785.
XX PR 13-JUL-1994; 94JP-0161481.
XX PR 24-NOV-1994; 94JP-0289951.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX XX Matsumoto Y, Matsushima K, Sato K, Tsuchiya M, Yamada Y;
XX PI Yamazaki T;
XX XX WPI; 1996-105864/11.
XX DR N-PSDB; AAT16904.
XX PT Reconstituted human antibody recognising human interleukin-8
XX PT containing mouse anti-IL8 antibody variable region sequences, has
XX PT low antigenicity in humans
XX PS Claim 4; Pages 72-73; 125pp; Japanese.
XX CC The present sequence, encoded by pUC-WS4-VH, is the variable heavy
XX CC chain from a WS4 hybridoma monoclonal antibody (MAb). The hybridoma
XX CC was constructed by fusing BALB/c mouse spleen cells, immunised with
XX CC human IL-8, with mouse myeloma P3X63-Ag8.653 cells. Complementarity
XX CC determining region (CDR) DNA from pUC-WS4-VH and its light chain
XX CC equivalent pUC-WS4-VL, was used together with human framework
XX CC region DNA to construct chimaeric H and L region, V region DNA. The
XX CC DNA was then inserted into a HEF vector along with human C-kappa
XX CC and C-gamma-1, C region DNA to produce a vector capable of
XX CC expressing a human/murine chimaeric MAb. The MAb can be used for
XX CC the treatment of inflammatory diseases mediated by IL-8, and as the
XX CC major part of the MAb comes from a human Ab, and only the CDR
XX CC regions are of murine origin, the MAb has the advantage of having
XX CC low antigenicity to the human body when used therapeutically.

```

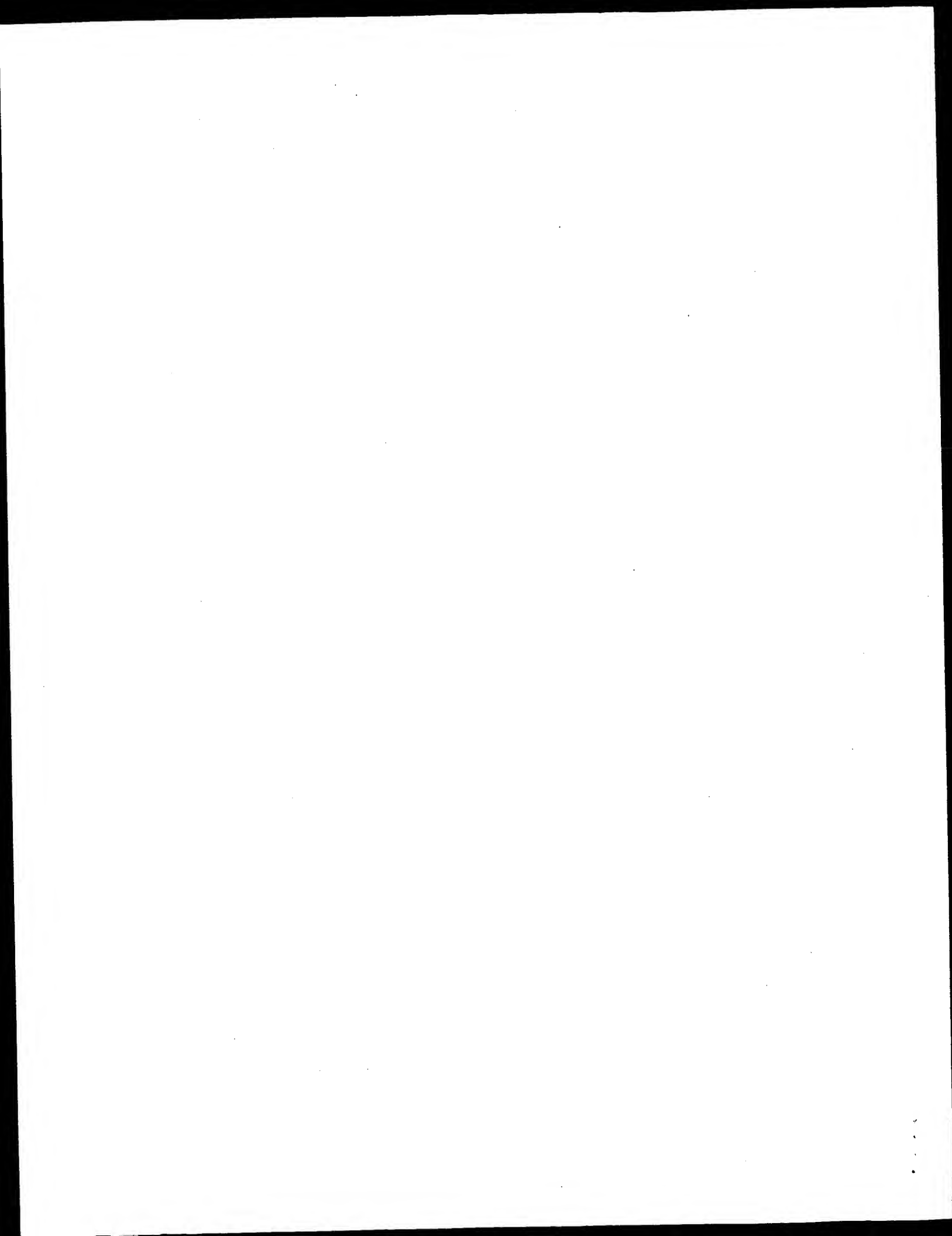
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XX SQ Sequence 141 AA;
Query Match 77.4%; Score 521.5; DB 17; Length 141;
Best Local Similarity 80.2%; Pred. No. 1.1e-38;
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;
QY 1 EVKLIVSGGLVOPGSLRLSCATSGFTSDYMMVROPKALEWLGFIIRNKANGYTT 60
Db 20 EVKLIVSGGLVOPGSLRLSCATSGFTSDYMMVROPKALEWLGFIIRNKANGYTT 79
QY 61 EFSASVMGRETISRDSQSILYLQMTLRAEDSATYVCARDPPYGNPHY-YAMDIWGGGT 119
Db 80 EYSASVAGRTISRDSQSILYLQMTLRAEDSATYVCARE----NYRYDVELAYWGGGT 135
QY 120 SVTVSS 125
Db 136 lltvsa 141

RESULT 15
AAR82835
ID AAR82835 standard; Protein; 392 AA.
XX AC
XX AC AAR82835;
XX DT 09-MAY-1996 (first entry)
XX DE scFv-PP.
XX KW Antibody; human; influenza type A virus; H1N1; H2N2; HA; diagnosis;
XX KW haemagglutinin; variable heavy chain; therapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Protein 23..144
XX FT Protein /note= "variable heavy chain"
XX FT Protein 164..263
XX FT Protein /note= "variable light chain"
XX FT Domain 273..330
XX FT Domain /note= "Fc binding domain-like structure"
XX FT Domain 331..388
XX FT /note= "Fc binding domain-like structure"
XX PN EP675199-A2.
XX PD 04-OCT-1995.
XX PF 14-MAR-1995; 95EP-0301664.
XX PR 30-MAR-1994; 94JP-0082693.
XX PA (TAKI ) TAKARA SHUZO CO LTD.
XX PI Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;
XX WPI; 1995-338286/44.
XX DR N-PSDB; AAT04180.
XX PT Gene encoding variable region of anti-human influenza A type virus
XX PT antibody - useful for prodn. of artificial antibodies
XX PS Example 4; Page 36-38; 42pp; English.
XX CC This sequence represents the scFv-PP fusion polypeptide. This sequence
XX CC is an anti-human influenza A type virus antibody. The antibody
XX CC recognises the stem region of the haemagglutinin (HA) molecule of the
XX CC H1N1 and H2N2 subtypes of human influenza A type virus, and shows
XX CC neutralisation activity against these two subtypes. The antibody shows
XX CC no recognition of the H2N2 subtype. Artificial antibodies (such as this)
XX CC and polypeptides are useful in the diagnosis and treatment of human

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds  
(without alignments)  
18.202 Million cell updates/sec

Title: US-09-724-406-18

Perfect score: 674

Sequence: 1 EVKLVEGGGLVPGGSLRL.....NPHYVMDYWGQGTSTVTVSS 125

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585.5	86.9	124	4	US-08-767-128-38
2	555.5	82.4	124	1	US-08-442-542-6
3	555.5	82.4	124	3	US-08-765-469-6
4	553	82.0	140	2	US-08-449-287-4
5	521.5	77.4	141	3	US-08-765-783A-29
6	521.5	77.4	141	3	US-08-921-100-29
7	521.5	77.4	141	3	US-08-880-142-29
8	521.5	77.4	141	3	US-08-902-201-29
9	517.5	76.8	116	1	US-08-401-908-1
10	515	76.4	146	2	US-08-449-287-12
11	513	76.1	119	1	US-08-459-310-2
12	513	76.1	119	2	US-08-308-494A-9
13	513	76.1	119	4	US-09-280-028-2
14	499	74.0	146	2	US-08-449-287-10
15	498.5	74.0	120	2	US-08-647-144-4
16	491.5	72.9	122	1	US-08-107-6690-6
17	491.5	72.9	122	1	US-08-472-788A-6
18	491.5	72.9	122	2	US-08-082-842A-6
19	491.5	72.9	122	2	US-08-256-790-2
20	481.5	72.9	122	2	US-08-077-2528-2
21	487.5	72.3	121	1	US-09-002-753A-2
22	487.5	72.3	121	4	PCR-US94-06687-2
23	484.5	72.3	121	5	US-08-647-144-2
24	484.5	71.9	120	2	US-08-765-783A-55
25	475.5	70.5	141	2	US-08-921-100-55
26	475.5	70.5	141	3	US-08-880-142-55
27	475.5	70.5	141	3	US-08-902-201-55

28	475.5	70.5	141	3	US-08-902-201-55	Sequence 55, Appl
29	473.5	70.3	141	3	US-08-765-783A-63	Sequence 63, Appl
30	473.5	70.3	141	3	US-08-921-100-63	Sequence 63, Appl
31	473.5	70.3	141	3	US-08-880-142-63	Sequence 63, Appl
32	473.5	70.3	141	3	US-08-902-201-63	Sequence 63, Appl
33	471.5	70.0	141	2	US-08-765-783A-59	Sequence 59, Appl
34	471.5	70.0	141	3	US-08-921-100-59	Sequence 59, Appl
35	471.5	70.0	141	3	US-08-880-142-59	Sequence 59, Appl
36	471.5	70.0	141	3	US-08-902-201-59	Sequence 59, Appl
37	467.5	69.4	141	2	US-08-765-783A-51	Sequence 51, Appl
38	467.5	69.4	141	2	US-08-880-142-51	Sequence 51, Appl
39	467.5	69.4	141	3	US-08-902-201-51	Sequence 51, Appl
40	467.5	69.4	141	3	US-08-921-100-51	Sequence 51, Appl
41	465.5	69.1	141	2	US-08-765-783A-65	Sequence 65, Appl
42	465.5	69.1	141	3	US-08-921-100-65	Sequence 65, Appl
43	465.5	69.1	141	3	US-08-880-142-65	Sequence 65, Appl
44	465.5	69.1	141	3	US-08-902-201-65	Sequence 65, Appl
45	459.5	68.2	113	1	US-07-942-245-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-08-767-128-38  
; Sequence 38, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GOEBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; NUMBER OF INVENTION: NUCLEOTIDES CODING THEREFORE  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079west Center, 90 South Seventh St  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/767,128  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 04-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09258  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/541,373  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/462,798  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaither, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.49USF1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/371-5278  
; TELEFAX: 612/332-9081  
; INFORMATION FOR SEQ ID NO: 38:

us-09-724-406-18.ra

Fri Jun 29 08:04:34 2001

SEQUENCE CHARACTERISTICS:  
 LENGTH: 124 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US-08-767-128-38

Query Match 86.9%; Score 585.5; DB 4; Length 124;  
 Best Local Similarity 90.4%; Pred. No. 3e-51;  
 Matches 113; Conservative 5; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 EVKLVESGGLVQPGGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 Db 1 EVKLVESGGLVQPGGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 QY 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYY---AMDYWGQ 120  
 Db 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARD-YYDYDYAMDYWGQGS 119  
 QY 121 VTVSS 125  
 Db 120 VTVSS 124

RESULT 2  
 US-08-442-542-6  
 ; Sequence 6, Application US/08442542  
 ; Patent No. 5686600  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine B.  
 ; APPLICANT: Kozziel, Michael G.  
 ; TITLE OF INVENTION: Antibodies which Bind to Insect Gut  
 ; TITLE OF INVENTION: Proteins and their Use  
 ; NUMBER OF SEQUENCES: 49  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Ciba-Geigy Corporation  
 ; STREET: 7 Skyline Drive  
 ; CITY: Hawthorne  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10532  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/442.542  
 ; FILING DATE: 16-MAY-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/267,641  
 ; FILING DATE: 28-JUN-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spruill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: CGC 1750  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919-541-8615  
 ; TELEFAX: 919-541-8689  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 124 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-442-542-6

Query Match 82.4%; Score 555.5; DB 1; Length 124;  
 Best Local Similarity 84.4%; Pred. No. 2.8e-48;  
 Matches 108; Conservative 8; Mismatches 5; Indels 7; Gaps 2;  
 QY 1 EVKLVESGGLVQPGGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 Db 1 QVOLQESGGLVQPGGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
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 Db 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARDICYG----YDVGALDIWGQ 116  
 QY 118 GTSVTSS 125  
 Db 117 GTSVTSS 124

RESULT 3  
 US-08-765-469-6  
 ; Sequence 6, Application US/08765469  
 ; Patent No. 6069301  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine B.  
 ; APPLICANT: Kozziel, Michael G.  
 ; TITLE OF INVENTION: Antibodies which Bind to Insect Gut  
 ; TITLE OF INVENTION: Proteins and their Use  
 ; NUMBER OF SEQUENCES: 49  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Ciba-Geigy Corporation  
 ; STREET: 7 Skyline Drive  
 ; CITY: Hawthorne  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10532  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/765,469  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/267,641  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spruill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: CGC 1750  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919-541-8615  
 ; TELEFAX: 919-541-8689  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 124 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-765-469-6

Query Match 82.4%; Score 555.5; DB 3; Length 124;  
 Best Local Similarity 84.4%; Pred. No. 2.8e-48;  
 Matches 108; Conservative 8; Mismatches 5; Indels 7; Gaps 2;  
 QY 1 EVKLVESGGLVQPGGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 Db 1 QVOLQESGGLVQPGGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 QY 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYY---AMDYWGQ 117

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Db 61 EYSASVKGRTISRDSQSLYLQMTLRAEDSATYTCARDICYG-----YDVGALDYWQ 116
QY 118 GTSVTSS 125
Db 117 GTSVTSS 124

RESULT 4
US-08-449-287-4
; Sequence 4, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BOWMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449, 287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-4

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Query Match 82.0%; Score 553; DB 2; Length 140;
Best Local Similarity 86.4%; Pred. No. 5.7e-48;
Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVSGLVQPGGSLRLSCATSGFTSDYNNVWVPPGKALEWLGFIIRNKANGYTT 60
Db 20 EVKLVSGLVQPGGSLRLSCATSGFTSDYNNVWVPPGKALEWLGFIIRNKANGYTT 79
QY 61 EFSASVWGRTISRDSQSLYLQMTLRAEDSATYTCARDPPYGNPHYANDYWGQTS 120

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Db 80 EYSASVKGRTISRDSQSLYLQMTLRAEDSATYTCARD--RGLRFF--DWGQGYT 135
QY 121 VTVSS 125
Db 136 LTVSS 140

RESULT 5
US-08-765-783A-29
; Sequence 29, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yanazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; US-08-765-783A-29

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Query Match 77.4%; Score 521.5; DB 2; Length 141;
Best Local Similarity 80.2%; Pred. No. 7.7e-45;
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVKLVSGLVQPGGSLRLSCATSGFTSDYNNVWVPPGKALEWLGFIIRNKANGYTT 60
Db 20 EVKLVSGLVQPGGSLRLSCATSGFTSDYNNVWVPPGKALEWLGFIIRNKANGYTT 79
QY 61 EFSASVWGRTISRDSQSLYLQMTLRAEDSATYTCARDPPYGNPHY-YANDYWGQCT 119

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us-09-724-406-18.ra1

Fri Jun 29 08:04:34 2001

Db 80 EYSASVKGRTISRDSQSILYLQMTLRGDSATYYCARE-----NRYDVELAYWGQGT 135

QY 120 SVTVSS 125  
Db 136 LVTUSA 141

## RESULT 6

US-08-921-100-29  
; Sequence 29, Application US/08921100  
; Patent No. 6024956  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI  
; APPLICANT: MATSUMOTO, YOSHIHIRO  
; APPLICANT: YAMADA, YOSHIKI  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUCHIYA, MASSAYUKI  
; APPLICANT: YAMAZAKI, TATUMI  
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/921,100  
; FILING DATE: 29-AUG-1997  
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/437,323  
; FILING DATE: 09-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 15580-0001.02

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 141 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-921-100-29

Query Match 77.4%; Score 521.5; DB 3; Length 141;  
Best Local Similarity 80.2%; Pred. No. 7.7e-45;  
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVKLVESGGGLVQPGGSLRLSCATSGFTSDYIMNVVRQPPGKALEWLGFTIRNKANGYTT 60  
Db 20 EVKLVESGGGLVQPGGSLRLSCVTSFTSDYILSVWRQPPGKALEWGLIRNKANGYTR 79

QY 61 EFSASVMGRFTISRDSQSILYLQMTLRGDSATYYCARE-----NRYDVELAYWGQGT 119  
Db 80 EYSASVKGRTISRDSQSILYLQMTLRGDSATYYCARE-----NRYDVELAYWGQGT 135

QY 120 SVTVSS 125  
Db 136 LVTUSA 141

## RESULT 8

US-08-902-201-29  
; Sequence 29, Application US/08902201  
; Patent No. 6068840  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI

## RESULT 7

US-08-880-142-29  
; Sequence 29, Application US/08880142  
; Patent No. 6048972  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI  
; APPLICANT: MATSUMOTO, YOSHIHIRO  
; APPLICANT: YAMADA, YOSHIKI  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUCHIYA, MASSAYUKI  
; APPLICANT: YAMAZAKI, TATUMI  
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/880,142  
; FILING DATE: 20-JUN-1997  
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/345,145  
; FILING DATE: 28-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 15580-0001.20

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 141 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-880-142-29

Query Match 77.4%; Score 521.5; DB 3; Length 141;  
Best Local Similarity 80.2%; Pred. No. 7.7e-45;  
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVKLVESGGGLVQPGGSLRLSCATSGFTSDYIMNVVRQPPGKALEWLGFTIRNKANGYTT 60  
Db 20 EVKLVESGGGLVQPGGSLRLSCVTSFTSDYILSVWRQPPGKALEWGLIRNKANGYTR 79

QY 61 EFSASVMGRFTISRDSQSILYLQMTLRGDSATYYCARE-----NRYDVELAYWGQGT 119  
Db 80 EYSASVKGRTISRDSQSILYLQMTLRGDSATYYCARE-----NRYDVELAYWGQGT 135

QY 120 SVTVSS 125  
Db 136 LVTUSA 141

```

; APPLICANT: MATSUMOTO, YOSHIIRO
; APPLICANT: YAMADA, YOSHIKI
; APPLICANT: SATO, KOH
; APPLICANT: TSUCHIYA, MASSAYUKI
; APPLICANT: YAMAZAKI, TATUMI
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,201
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,328
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-201-29

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Query Match 77.4%; Score 521.5; DB 3; Length 141;
Best Local Similarity 80.2%; Pred. No. 7.7e-45;
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSYNNVVRQPGKALEWLGFTIRNKANGYTT 60
Db 20 EVKLVEGGGLVQPGGSLRLSCATSGFTFSYNNVVRQPGKALEWLGFTIRNKANGYTT 79
QY 61 EFSASVWGRTISRDSQSILYLQNTLRAEDSATYTCARDPPYGNPHY-YAMDYWGQGT 119
Db 80 EYSASVKGRTISRDSQSILYLQNTLRAEDSATYTCARE----NYRDVDELAYWGQGT 135
QY 120 SVTVSS 125
Db 136 LVTVSA 141

RESULT 9
US-08-401-908-1
; Sequence 1, Application US/08401908
; Patent No. 5684-46
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington

```

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; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,908
; FILING DATE: March 10, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-401-908-1

Query Match 76.8%; Score 517.5; DB 1; Length 116;
Best Local Similarity 83.2%; Pred. No. 1.5e-44;
Matches 99; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSYNNVVRQPGKALEWLGFTIRNKANGYTT 60
Db 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSYNNVVRQPGKALEWLGFTIRNKANGYTT 60
QY 61 EFSASVWGRTISRDSQSILYLQNTLRAEDSATYTCARDPPYGNPHY-YAMDYWGQGT 119
Db 61 EYSASVKGRTISRDSQSILYLQNTLRAEDSATYTCARPKCY---FFYANDYWGQGT 116

RESULT 10
US-08-449-287-12
; Sequence 12, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:

```

PRIOR APPLICATION DATA: US 08/100,963  
APPLICATION NUMBER: 03-AUG-1993  
FILING DATE: DE P 422 58 53.7  
APPLICATION NUMBER: 05-AUG-1992  
FILING DATE: ATTORNEY/AGENT INFORMATION:  
NAME: Wadler, Linda A.  
REGISTRATION NUMBER: 33,218  
REFERENCE/DOCKET NUMBER: 02481.1317-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SS-08-459-310-2

[illegible]

RESULT 12  
US-08-308-494A-9  
; Sequence 9, Application US/08308494A  
; Patent No. 5959083  
; GENERAL INFORMATION:  
; APPLICANT: Bosslet, Klaus  
; APPLICANT: Seeman, Gerhard  
; TITLE OF INVENTION: Tetravalent Bispecific Receptors, The  
; TITLE OF INVENTION: Preparation and Use Thereof  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/308,494A  
; FILING DATE: 21-SEP-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/891,739  
; FILING DATE: 01-JUN-1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P4118120.4  
; FILING DATE: 03-JUN-1991  
; ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/154,389  
FILING DATE:  
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT GB91/01108  
FILING DATE: 05-JUL-1991  
PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9014932.9  
FILING DATE: 05-JUL-1990  
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT GB90/02017  
FILING DATE: 21-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 40283/110 CARA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PS-08-449-287-12

Query Match	76.4%	Score 515	DB 2	Length 146
Best Local Similarity	80.8%	Pred. No. 3.5e-44		
Matches 101	Conservative	7	Mismatches 13	Indels 4
Gaps				
QY	1	EYKLVESSGGLVQPGSRLRLSCATSGFTTSDYYNNWVRPPGKALEWLGFIINRKANGYTT	60	
Db	20	EVQLLESGGGLVQPGSRLRLSCATSGFTTDDYYNNWVRQAPGKLEWLGFIINRKANGYTT	79	
QY	61	EFPSASVWGRTLTISRDDSSILYQLQNTLTLRADSAATYYCARDPPYGNPHYAMDYWGQTS	120	
Db	80	EYSASVWGRTLTISRDKSKSTLYLQNTLTQAEADSAIYYCTRD--RGLRFFVF--DYWGQGPL	135	
QY	121	VTVSS	125	
Db	136	VTVSS	140	

RESULT 11  
US-08-459-310-2  
; Sequence 2, Application US/08459310  
; Patent No. 5645817  
; GENERAL INFORMATION:  
; APPLICANT: Seemann, Gerhard  
; APPLICANT: Bosslet, Klaus  
; TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,  
; TITLE OF INVENTION: Their Preparation and Use  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finneqan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,310  
; FILING DATE:  
; CLASSIFICATION: 424

Query Match	76.1%;	Score 513;	DB 4;	Length 119;
Best Local Similarity	82.4%;	Pred. No. 4.4e-44;		
Matches 103; Conservative	7;	Mismatches 9;	Indels 6;	Gaps 3;
QY	1	EVKLVESGGGLVQPGGSLRLSCATSGTFTSDYYMNNYRQP	PKALEWLGFLRNKANGYT	60
Dd		: :		
	1	QVLQESGGGLVQPGGSLRLSCATSG--FSDYYMNNYRQP	PKALEWLGFLSNKNP	58
QY	61	EFSASVMGRFTISRDDQSILYLQMNTLRADSATTCARDPPYGNPHNYAMDYGQGT	S 120	
Dd		: :	:         :	
	59	EYSASVMGRFTISRDNSSQILYLQMNTLRADSATTCARDK--GIRWFYF--DVWGQG	T 114	
QY	121	VTVSS	125	
Dd				
	115	VTVSS	119	

Query Match	74.0%	Score 499;	DB 2;	Length 146;
Best Local Similarity	79.28;	Pred. No. 1.4e-42;		
Matches 99;	Conservative 7;	Mismatches 15;	Indels 4;	Gaps
QY	1	EYKLVESGGGLVQPGGSLRLGCAATGTAFTDDYNNMVVRQPGKALEWLGFTIRNKANGYTT	60	
Db	20	EYQLVESGGGLVQPGGSLRLGCAATGTAFTDDYNNMVVRQPGKALEWLGFTIRNKANGYTT	79	
QY	61	EYSASVWGRETISRDDQSGLIYQMNTLRADSSATYYCARDPYPGNPHYAMDYWGOGTS	120	
Db	80	EYSASVKGRTISRDKSKSTLYLQMGGLQAEVSATYYCTRD--RGLRFYF--DYWGOGTL	135	
QY	121	VTVSS	125	
Db	136	VTVSS	140	

Search completed: June 28, 2001, 16:01:14  
Job time: 522 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:44 ; Search time 234.85 Seconds  
(without alignments)  
40.544 Million cell updates/sec

Title: US-09-724-406-18  
Perfect score: 674  
Sequence: 1 EVKLVEGGGLVQPGGSLRL.....NPHYAMDYWGQTSVTSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	580	86.1	119	2 D30540	Ig heavy chain V r
2	574	85.2	123	2 S32186	Ig heavy chain V r
3	550.5	81.7	118	2 E30540	Ig heavy chain V r
4	542.5	80.5	145	2 S03844	Ig heavy chain V r
5	537.5	79.7	126	2 S16280	Ig heavy chain pre
6	530	78.6	124	2 PT0388	Ig heavy chain (38
7	528	78.3	122	1 AVMSX2	Ig heavy chain V r
8	522	77.4	117	1 AVMS47	Ig heavy chain V r
9	520.5	77.2	114	2 PH1027	Ig heavy chain V r
10	519.5	77.1	121	2 PT0391	Ig heavy chain V r
11	517.5	76.8	122	2 S20642	Ig heavy chain V r
12	513.5	76.2	124	2 H30539	Ig heavy chain V r
13	512	76.0	120	2 PT0393	Ig heavy chain V r
14	512	76.0	124	2 G30540	Ig heavy chain V r
15	510.5	75.7	124	2 G30539	Ig heavy chain V r
16	510	75.7	122	2 PT0392	Ig heavy chain V r
17	510	75.7	123	2 PT0354	Ig heavy chain V r
18	509.5	75.6	118	2 PT0355	Ig heavy chain V r
19	509.5	75.6	123	2 PT0386	Ig heavy chain V r
20	509	75.5	123	1 AVMSH6	Ig heavy chain V r
21	508.5	75.4	124	2 E30539	Ig heavy chain V r
22	508.5	75.4	124	2 F30539	Ig heavy chain V r
23	508	75.4	124	2 PT0389	Ig heavy chain V r
24	507.5	75.3	121	2 E30502	Ig heavy chain V r
25	507.5	75.3	123	2 PT0384	Ig heavy chain V r
26	505.5	75.0	124	2 A30539	Ig heavy chain V r
27	505	74.9	123	1 AVMS75	Ig heavy chain V r
28	504	74.8	119	2 S24517	Ig heavy chain V r
29	503	74.6	123	2 B30540	Ig heavy chain V r

30 503 74.6 123 2 I30538  
31 502 74.5 125 2 PT0353  
32 499.5 74.1 124 1 AVMS51  
33 497.5 73.8 123 2 PT0383  
34 497 73.7 123 1 AVMS14  
35 496.5 73.7 115 2 S20706  
36 496.5 73.7 123 2 PT0387  
37 496 73.6 140 2 S32805  
38 495.5 73.5 123 2 PT0385  
39 495.5 73.5 124 2 A30515  
40 495 73.4 123 1 AVMSH8  
41 495 73.4 144 1 AVMS67  
42 493 73.1 123 2 B30556  
43 492 73.0 119 2 S24520  
44 492 73.0 121 2 PT0352  
45 491.5 72.9 122 1 AVMS63

## ALIGNMENTS

RESULT 1  
D30540  
Ig heavy chain V region (174.3F4) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996  
C:Accession: D30540  
R:Clafalin, J.L.; Berry, J.  
J. Immunol. 141, 4012-4019, 1988  
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus p  
A:Reference number: A30534; MUID:89035545  
A:Accession: D30540  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
A:Molecule type: mRNA  
A:Residues: 1-119 <CL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 580; DB 2; Length 119;  
Best Local Similarity 89.6%; Pred. No. 2.2e-45;  
Matches 112; Conservative 4; Mismatches 3; Indels 6; Gaps 1;  
QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFRNKANGYTT 60  
Db 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFRNKANGYTT 60  
QY 61 EFSASVMGRETISRDDSSILYLQMTLRADTSATYTCARDPPYGNPHYAMDYWGQTS 120  
Db 61 EYSASVKGRTT...SRDNSQSILYLQMTLRADTSATYTCARD...DYDAMDYWGQTS 114  
QY 121 VTVSS 125  
Db 115 VTVSS 119

RESULT 2  
S32186  
Ig heavy chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S32186  
R:Izui, S.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S32185  
A:Accession: S32186  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <IZU>  
A:Cross-references: EMBL:X70093; NID:g288249; PIDN:CAA49698.1; PID:g288250  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Fri Jun 29 08:04:35 2001

us-09-724-406-18.rpr

F;15-100/Product: Ig heavy chain (38C13) (fragment) #status predicted <MAT>  
 F;20-119/Domain: V region (38C13) <VRE>  
 F;34-119/Domain: immunoglobulin homology <IMM>  
 F;120-130/Domain: D region <DRE>  
 F;131-145/Domain: J region (J2) (fragment) <JRE>

Query Match 85.2%; Score 574; DB 2; Length 123;  
 Best Local Similarity 88.8%; Pred. No. 7.8e-45;  
 Matches 111; Conservative 4; Mismatches 8; Indels 2; Gaps 1;  
 QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 QY 61 EFSASVMGRFTISRDDQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 120  
 DB 61 EFSASVMGRFTISRDDQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 118  
 QY 121 VTVSS 125  
 DB 119 VTVSS 123

RESULT 3  
 E30540  
 Ig heavy chain V region (252.8G3) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996  
 C:Accession: E30540  
 R:Clafin, J.L.; Berry, J.  
 J. Immunol. 141, 4012-4019, 1988  
 A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae  
 A:Reference number: A30534; MUID:89035545  
 A:Accession: E30540  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <CLA>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 550.5; DB 2; Length 118;  
 Best Local Similarity 84.8%; Pred. No. 9.6e-43;  
 Matches 106; Conservative 5; Mismatches 7; Indels 7; Gaps 1;  
 QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 QY 61 EFSASVMGRFTISRDDQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 120  
 DB 61 EFSASVMGRFTISRDDQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 113  
 QY 121 VTVSS 125  
 DB 114 VTVSS 118

RESULT 4  
 S0384  
 Ig heavy chain precursor V-D-J region (38C13) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 23-Jul-1999  
 C:Accession: J0061; S0384  
 R:Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.  
 J. Exp. Med. 168, 1607-1620, 1988  
 A:Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explanation of the V-D-J region  
 A:Reference number: J0061; MUID:89035985  
 A:Accession: J0061  
 A:Molecule type: mRNA  
 A:Residues: 1-145 <CAR>  
 A:Cross-References: EMBL:X14096; NID:g52528; PIDN:CAA32258.1; PID:g52529  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;1-19/Domain: signal sequence #status predicted <SIG>

Query Match 80.5%; Score 542.5; DB 2; Length 145;  
 Best Local Similarity 82.5%; Pred. No. 6.3e-42;  
 Matches 104; Conservative 7; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 DB 20 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 79  
 QY 61 EFSASVMGRFTISRDDQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 119  
 DB 80 EFSASVMGRFTISRDDQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 139  
 QY 120 SVTVSS 125  
 DB 140 TLTVSS 145

RESULT 5  
 SI6280  
 Ig heavy chain (38C13) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
 C:Accession: SI6280  
 R:Thieleman, K.; Rothbard, J.B.; Levy, S.; Levy, R.  
 J. Exp. Med. 162, 19-34, 1985  
 A:Title: Syngeneic antidiotypic immune responses to a B cell lymphoma. Comparison between the heavy chain of the anti-idiotypic antibody and the heavy chain of the lymphoma  
 A:Reference number: SI6280; MUID:85236147  
 A:Accession: SI6280  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-126 <DEX>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 537.5; DB 2; Length 126;  
 Best Local Similarity 81.0%; Pred. No. 1.5e-41;  
 Matches 102; Conservative 9; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYMNWVRQPPGKALEWLGFIIRNKANGYTT 60  
 QY 61 EFSASVMGRFTISRDDQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 119  
 DB 61 EFSASVMGRFTISRDDQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 120  
 QY 120 SVTVSS 125  
 DB 121 TLTVSS 126

RESULT 6  
 PT0388  
 Ig heavy chain V region (SI07/VH11 group 3-23) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: PT0388  
 R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.  
 J. Exp. Med. 173, 731-741, 1991  
 A:Title: Characterization of somatically mutated SI07 VH11-encoded anti-DNA autoantibody  
 A:Reference number: PT0376; MUID:91147903  
 A:Accession: PT0388  
 A:Molecule type: DNA  
 A:Residues: 1-124 <BEH>

Best Local Similarity 81.6%; Score 326; DB 1; Length 122;  
Matches 102; Conservative 8; Mismatches 11; Indels 4; Gaps

Query Match	77.28; Score 520.5; DB 2; Length 114;
-------------	---------------------------------------

	Matches	98;	Conservative	7;	Mismatches	14;	Indels	6;	Gaps	1;
QY	1	EVKLVESGGGLVQPGGSLRLSCATSGFTFSDYYMMNWVRQPPKALELWLGFI	RNKANGYTT	60						
st	1	EVKLVESGGGLVQPGGSLRLSCATSGFTFSDYYMMNWVRQPPKALELWLGFI	RNKANGYTT	60						

Db 61 EYSASYKGRFVVSRDTSQISILYLQMNALRAEDTAIYCCARD-IYGSSYYWYFDVWGAGTT 119

Qy 121 VTVSS 125

Db 120 VTVSS 124

Search completed: June 28, 2001, 15:58:44  
Job time: 372 sec

Query Match 76.0%; Score 512; DB 2; Length 125;  
Best Local Similarity 76.8%; Pred. No. 2.9e+39;  
Matches 96; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

**RESULT** 15

RESULT 15  
G30539  
Ig heavy chain V region (224..7E7) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996  
C:Accession: G30539  
R:Clafalin, J.L.; Berry, J.  
J:Immunol. 141, 4012-4019, 1988  
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae  
A:Reference number: A30534; MUID:89035545  
A:Accession: G30539  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-124 <C1A>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match	75.7%	Score 510.5;	DB 2;	Length 124;
Best Local Similarity	77.6%;	Pred. No. 4e-39;		
Matches	97;	Conservative	9;	Mismatches 18;
				Indels 1;
				Gaps 1;

1 EVKLVESGGGLVPGGSLRLSCATSGFTSDYIMNWVRPPGKALEWLGFIIRNKANGYTT 60  

1 EVKLVESGGGLVPGGSLRLSCTTSGFTSDYIMEWVRPPGKRLEWTAAGRKNADYTT 60  

61 EFSASVMGRFTISRDDSQSILYLQMNTLRAEDSATYYCARDPPYGNPHYVAMDYWGQGT'S 120

us-09-724-406-18.rpr

Fri Jun 29 08:04:35 2001

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:37 ; Search time 105.36 Seconds  
(without alignments)  
40.641 Million cell updates/sec

Title: US-09-724-406-18  
Perfect score: 674  
Sequence: 1 EVKLVESGGGLVQPGSLRL.....NPHYAMDYWGQTSVTSS 125

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues  
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	522	77.4	117	1 HV17_MOUSE	P01786 mus musculus
2	509	75.5	123	1 HV22_MOUSE	P01791 mus musculus
3	507	75.2	123	1 HV19_MOUSE	P01788 mus musculus
4	505	74.9	123	1 HV18_MOUSE	P01787 mus musculus
5	497	73.7	123	1 HV25_MOUSE	P01794 mus musculus
6	495	73.4	123	1 HV23_MOUSE	P01792 mus musculus
7	495	73.4	144	1 HV26_MOUSE	P01795 mus musculus
8	491.5	72.9	122	1 HV20_MOUSE	P01789 mus musculus
9	490.5	72.8	122	1 HV21_MOUSE	P01790 mus musculus
10	485	72.0	123	1 HV24_MOUSE	P01793 mus musculus
11	431	63.9	142	1 HV01_RAT	P01805 rattus norv
12	424.5	63.0	122	1 HV3G_HUMAN	P01768 homo sapien
13	411	61.0	115	1 HV32_MOUSE	P01801 mus musculus
14	409.5	60.8	136	1 HV16_MOUSE	P01783 mus musculus
15	406	60.2	113	1 HV30_MOUSE	P01804 mus musculus
16	401.5	59.6	111	1 HV35_MOUSE	P01796 mus musculus
17	401	59.5	113	1 HV27_MOUSE	P01800 mus musculus
18	399	59.2	113	1 HV31_MOUSE	P01797 mus musculus
19	397	58.9	115	1 HV33_MOUSE	P01798 mus musculus
20	395	58.6	113	1 HV28_MOUSE	P01802 mus musculus
21	393	58.3	113	1 HV29_MOUSE	P01799 mus musculus
22	392	58.2	117	1 HV42_MOUSE	P01796 mus musculus
23	391	58.0	121	1 HV3J_HUMAN	P01771 homo sapien
24	384	57.0	115	1 HV3F_HUMAN	P01767 homo sapien
25	381	56.5	115	1 HV3D_HUMAN	P01765 homo sapien
26	380	56.4	120	1 HV3E_HUMAN	P01766 homo sapien
27	377.5	56.0	119	1 HV3N_HUMAN	P01775 homo sapien
28	377	55.9	113	1 HV34_MOUSE	P01803 mus musculus
29	375.5	55.7	114	1 HV3B_HUMAN	P01763 homo sapien
30	375.5	55.7	119	1 HV3M_HUMAN	P01774 homo sapien
31	375.5	55.7	122	1 HV3A_HUMAN	P01762 homo sapien
32	374.5	55.6	119	1 HV40_MOUSE	P01810 mus musculus
33	374.5	55.6	126	1 HV3K_HUMAN	P01772 homo sapien

34	372.5	55.3	119	1 HV37_MOUSE	P01807 mus musculus
35	370.5	55.0	122	1 HV3H_HUMAN	P01769 homo sapien
36	369.5	54.8	119	1 HV38_MOUSE	P01808 mus musculus
37	366.5	54.4	116	1 HV3T_HUMAN	P01781 homo sapien
38	362.5	53.8	116	1 HV05_CARAU	P19181 carassius a
39	357	53.0	117	1 HV3C_HUMAN	P01764 homo sapien
40	357	53.0	118	1 HV39_MOUSE	P01809 mus musculus
41	355	52.7	117	1 HV41_MOUSE	P01811 mus musculus
42	355	52.7	119	1 HV3I_HUMAN	P01770 homo sapien
43	351.5	52.2	117	1 HV3O_HUMAN	P01776 homo sapien
44	348.5	51.7	114	1 HV01_CANFA	P01784 canis famil
45	348.5	51.7	119	1 HV3P_HUMAN	P01777 homo sapien

## ALIGNMENTS

RESULT 1					
HV17_MOUSE					
ID	HV17_MOUSE	STANDARD;	PRT;	117 AA.	
AC	P01786;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG HEAVY CHAIN V REGION MOPC 47A.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RA	MEDLINE=80049769; PubMed=115869;				
RA	Robinson E.A., Appella E.;				
RT	*Amino acid sequence of a mouse myeloma immunoglobulin heavy chain				
RT	(MOPC 47 A) with a 100-residue deletion.*;				
RL	J. Biol. Chem. 254:11418-11430(1979).				
CC	-I- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA				
CC	PROTEIN THAT CONTAINS ONE LIGHT AND ONE HEAVY CHAIN PER MOLECULE,				
CC	LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA				
CC	MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A				
CC	LIGHT-HEAVY CHAIN DISULFIDE BOND.				
DR	PIR; A02069; AIMS47.				
DR	HSSP; P01789; 2MCP.				
DR	InterPro; IPR003006; .				
DR	Protein; PF00047; Ig; 1.				
KW	Immunoglobulin V region.				
FT	NON_TER 117 117				
SQ	SEQUENCE 117 AA; 12975 MW; 0C74BE8BB154BDF4 CRC64;				
Query Match 77.4%; Score 522; DB 1; Length 117;					
Best Local Similarity 80.0%; Pred. No. 1.7e-46;					
Matches 100; Conservative 9; Mismatches 8; Indels 8; Gaps 2;					
QY	1 EVKLVESGGGLVQPGSLRLSCATSGFTSYMMVWVQPPGKALEWLGFTIRNKGYYT 60				
Db	1 EVKLVESGGGLVQPGSLRLSCATSGFTTDDYISWVQPPGKALEWLGFTIRNKGYYT 60				
QY	61 EFSASVMGRFTISRDDSSILYLQMTLRAEDSATFYCARDPPYGNPHYAMDYWGQTS 120				
Db	61 EYSA-VKGRFTISRBSZGILYLQMTLRAQDSATFYCARD-----ITFEATWGZGTL 112				
QY	121 VTVSS 125				
Db	113 VTVSS 117				
RESULT 2					
HV22_MOUSE					
ID	HV22_MOUSE	STANDARD;	PRT;	123 AA.	
AC	P01791;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				

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DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCM6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMS75.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;

Query Match 75.5%; Score 509; DB 1; Length 123;
Best Local Similarity 79.2%; Pred. No. 3.8e-45;
Matches 99; Conservative 7; Mismatches 17; Indels 2; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGIRNKANGYTT 60
DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGIRNKANGYTT 60

QY 61 EFSASVNGRFTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQTS 120
DB 61 EYSASVKGRIIVSRDTSQSILYLQMTLRAEDTAIYYCARD-YIDYPRWY-FDVWGAGTT 118

QY 121 VTVSS 125
DB 119 VTVSS 123

RESULT 3
HV19_MOUSE
ID HV19_MOUSE STANDARD; PRT; 123 AA.
AC P01788;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX Barstad P.;
RA Thesis (1975), California Institute of Technology / Pasadena, U.S.A.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMS75.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;

Query Match 75.2%; Score 507; DB 1; Length 123;
Best Local Similarity 78.4%; Pred. No. 6.1e-45;
Matches 98; Conservative 9; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGIRNKANGYTT 60

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DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGIRNKANGYTT 60
QY 61 EFSASVNGRFTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQTS 120
DB 61 EYSASVKGRIIVSRDTSQSILYLQMTLRAEDTAIYYCARD-YIGBSYWY-FDVWGAGTT 118
QY 121 VTVSS 125
DB 119 VTVSS 123

RESULT 4
HV18_MOUSE
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 15).
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RP SEQUENCE FROM N.A. (H107).
RX MEDLINE=8019926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH.";
RL Cell 19:981-992(1980).
RN [3]
RP SEQUENCE (S107).
RX MEDLINE=76110488; PubMed=813561;
RA Rudikoff S., Barstad P., Potter M., Hood L.;
RL Unpublished results, cited by:
RL Hood L., Campbell J.H., Elgin S.C.R.;
RL Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -!- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
CC -!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMS75.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 74.9%; Score 505; DB 1; Length 123;
Best Local Similarity 78.4%; Pred. No. 9.7e-45;
Matches 98; Conservative 9; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGIRNKANGYTT 60
DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGIRNKANGYTT 60
QY 61 EFSASVNGRFTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQTS 120

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Db 61 EYSASVKGREIVSRDTSQSLYLQNNALRAEDTAIIYCARD-YYGSSYWF-FDWMGAGTT 118  
 QY 121 VTVSS 125  
 Db 119 VTVSS 123

RESULT 5  
 HV25\_MOUSE  
 ID HV25\_MOUSE STANDARD; PRT; 123 AA.  
 AC P01794;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION HPGC14.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

Query Match 73.7%; Score 497; DB 1; Length 123;  
 Best Local Similarity 76.8%; Pred. No. 6.3e-44;  
 Matches 96; Conservative 9; Mismatches 18; Indels 2; Gaps 1;  
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than  
 their IgM counterparts.";  
 RL Nature 291:29-34(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS PHOSPHORYLCHOLINE.

DR PIR; A02070; AVMS75.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; ig; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT NON\_TER 123 123  
 SQ SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;

Query Match 73.7%; Score 497; DB 1; Length 123;  
 Best Local Similarity 76.8%; Pred. No. 6.3e-44;  
 Matches 96; Conservative 9; Mismatches 18; Indels 2; Gaps 1;  
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than  
 their IgM counterparts.";  
 RL Nature 291:29-34(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS PHOSPHORYLCHOLINE.

DR PIR; A02070; AVMS75.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; ig; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT NON\_TER 123 123  
 SQ SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;

RESULT 6  
 HV23\_MOUSE  
 ID HV23\_MOUSE STANDARD; PRT; 123 AA.  
 AC P01792;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION HPGC8.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

Query Match 73.7%; Score 497; DB 1; Length 123;  
 Best Local Similarity 76.8%; Pred. No. 6.3e-44;  
 Matches 96; Conservative 9; Mismatches 18; Indels 2; Gaps 1;  
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than  
 their IgM counterparts.";  
 RL Nature 291:29-34(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS PHOSPHORYLCHOLINE.

RL Nature 291:29-34(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS PHOSPHORYLCHOLINE.  
 CC PIR; A02070; AVMS75.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; ig; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT NON\_TER 123 123  
 SQ SEQUENCE 123 AA; 13879 MW; 4559D3106CAF7D8D CRC64;

Query Match 73.4%; Score 495; DB 1; Length 123;  
 Best Local Similarity 76.8%; Pred. No. 1e-43;  
 Matches 96; Conservative 7; Mismatches 20; Indels 2; Gaps 1;  
 QY 1 EVKLVESSGGLVQPGGSLRLSCATSGFTFSFYNNVVRQPPGKALEWLGFIIRNKANGYTT 60  
 Db 1 EVKLVESSGGLVQPGGSLRLSCATSGFTFSFYNNVVRQPPGKALEWLGFIIRNKANGYTT 60

QY 61 EFSASVMGRFTISRDSQSILYLQNNALRAEDTAIIYCARDPPYGNPHYAMDYWGQGTS 120  
 Db 61 EFSASVMGRFTISRDSQSILYLQNNALRAEDTAIIYCARDPPYGNPHYAMDYWGQGTS 120  
 QY 121 VTVSS 125  
 Db 119 VTVSS 123

## RESULT 7

HV26\_MOUSE  
 ID HV26\_MOUSE STANDARD; PRT; 144 AA.  
 AC P01795;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION M167 PRECURSOR.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=93358330; PubMed=6101208;  
 RA Kim S., Davis M., Sinn E., Patten P., Hood L.;  
 RT "Antibody diversity: somatic hypermutation of rearranged VH genes.";  
 RL Cell 27:573-581(1981).  
 RN [2]  
 RP SEQUENCE OF 20-142  
 RX MEDLINE=76222762; PubMed=819932;  
 RA Rudikoff S., Potter M.;  
 RT "Size differences among immunoglobulin heavy chains from  
 phosphorylcholine-binding proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN  
 THAT BINDS PHOSPHORYLCHOLINE.

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 CC EMBL; J00516; AAC18867.1; -.  
 DR PIR; A02071; AVMS67.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; ig; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 CHAIN 20 144 IG HEAVY CHAIN V REGION M167.

FT	STRAND	3	7
FT	STRAND	11	12
FT	TURN	14	15
FT	STRAND	17	25
FT	HELIX	29	31

1 EVKLVESGGGLVQPGGSLRLSCATSGFTFSDYIMNWRQPPGKALEWLGFTRNKANGYTT 60

1 EVKLVESGGGLVQPGGSLRLSCATSGFTFSDYMEWVRQSPGKRLEWIAASRNKANDYTT 60

Query Watch	72.0%	Score 485;	DB 1;	Length 123;
Best Local Similarity	75.2%	Pred. No. 1.1e-42;		
Matches 94;	Conservative 8;	Mismatches 21;	Indels 2;	Gaps 1;
QY	1	EVKLVESGGLVQPGGSLRLSCATSGTTFSDYYMNVWRQPPGKALELWGLFIRNKANGVTT	60	
Db	1	EVKLVESGGLVQPGGSLRLSCATSGTTFSDYYMNVWRQPPGKALELWGLFIRNKANGVTT	60	
QY	61	EFSASVNGRFTISRDDQSILYLQMNTRLRAEDSATYYCARDPPYGNPHYAMDYWGQGTS	120	
Db	61	EFSASVNGRFTISRDDQSILYLQMNTRLRAEDSATYYCARDPPYGNPHYAMDYWGQGTS	120	
QY	121	VTVSS	125	
Db	119	VTVSS	123	

RESULT	11
ID	HV01_RAT
AC	P01805;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DE	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG HEAVY CHAIN V REGION IR2 PRECURSOR.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;	[1]
SEQUENCE FROM N.A.	
MEDLINE=83064537; PubMed=6292865;	
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;	

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RT      "structure and evolution of the heavy chain from rat immunoglobulin
RT      E.";
RL      Nucleic Acids Res. 10:6041-6049(1982).
CC      -1- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGF-SECRETING
CC      IMMUNOCYTONA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
DR      PIR; A02075; EVRTR2.
DR      HSSP; P01789; 2MCP.
DR      InterPro; IPR003006; -.
DR      Pfam; PF00047; Ig; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL 1 19
FT      CHAIN 20 142
FT      NON_TER 142 142
FT      SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;
SQ

Query Match      63.9%; Score 431; DB 1; Length 142;
Best Local Similarity 66.4%; Pred. NO. 3.9e-37;
Matches 83; Conservative 13; Mismatches 27; Indels 2; Gaps

1 EVKLVEGGGVLPQGGSLRLSCATSGFTFSDDYMNVRPPGKALEWLGFIRNKANGYTT 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
20 EVKLEESGGGVLPQGMVKLSLCATSGFTFSDDYMWVVRQAPGKLEWVAEIRNKANNVA 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 EFSASVMGRFTISRDDSSQSLYILQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGS 121
   : : : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
80 YYGSLKGRFTLSRDDSKSVILYLMNNIRSEDTGIYCSRG--YGGYSENWVYWGQGT 133
   : : : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 VTVSS 125
   |||||
138 VTSS 142
   |||||

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RESULT	12	
HV3C_HUMAN		
ID	HV3C_HUMAN	STANDARD;
AC	P01768;	PRT; 122 AA.
DT	21-JUL-1986	(Rel. 01, Created)
DT	21-JUL-1986	(Rel. 01, Last sequence update)
DT	21-JUL-1999	(Rel. 38, Last annotation update)
DE	IG HEAVY CHAIN V-III REGION CAM.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Verte	
OX	Mammalia; Eutheria; Primates; Catarrhini; Hom	
NCBI_TaxID=9606;		
[1]		
RP	SEQUENCE.	
RP	MEDLINE=81013859; PubMed=6774332;	
RA	Lehman D.W., Putnam F.W.;	
RT	"Amino acid sequence of the variable region o	
RT	location of a possible JH segment.";	
RT	Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(19	
CC	-!- MISCELLANEOUS; THIS MU CHAIN WAS ISOLATED	
CC	PATIENT WITH MACROGLOBULINEMIA.	
CC	PIR; A02051; M3HUAM.	
DR	HSP; P01772; 2IG2.	
DR	InterPro; IPR003006; -	
DR	Pfam; PF00047; Ig: 1.	
KW	Immunoglobulin V region.	
FT	MOD_RES 1	
FT	NON_TER 122 122	
FT	SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C	
Q		PYRROLIDONE CARBO

	Query Match	Best Local Similarity	Score	424..5;	DB 1;	Length	122;
	Matches	83;	Conservative	17;	Mismatches	21;	Indels
							Gaps
QY	1	EYKLVESGGGLVPGGSLRLSCA	SGTFS	GYNNWV	PPGKALEWLF	GI	RKANGYTT
		:   :     : :					60
Db	1	QVELVESGGGVVZPGRSILRLSCA	SGTFS	NYAMHW	PPPGKGLSEAVI		58
		:   :     : :					
QY	61	EPFSASVGRGRTISRDDSGSILY	LQMTLR	RAEDSATYTC	ARDPP		119
		:   :     : :					

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.:: || ||||||:-: |||||:-: |||||:-: ||:-: ||:-: |||||
59 YVASVKGRTISRDESKBTLYLQNSLRABETAVYICARDRPLYGB--YRAFNYWGQGTT 116
          |||||
120 SVTVSS 125
      |||||
117 LVTWSS 122

RESULT 13
HV32_MOUSE STANDARD; PRT; 115 AA.
C D C HV32_MOUSE
P01801;
T T 21-JUL-1986 (Rel. 01, Created)
T T 21-JUL-1986 (Rel. 01, Last sequence update)
T T 21-JUL-1986 (Rel. 01, Last annotation update)
E E 15-JUL-1999 (Rel. 38, Last annotation update)
I G HEAVY CHAIN V-III REGION J606.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE.
MEDLINE=82099361; PubMed=6798111;
Johnson N., Slankard J., Paul L., Hood L.;
"The complete v domain amino acid sequences of two myeloma inulin-binding proteins";
J. Immunol. 128:302-307(1982).
BL -1 MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
PIR; C92811; AVMS06.
InterPro: IPR003006; -.
Pfam: PF00047; Ig_1.
Immunoglobulin V region.
DISULFID 22 98 BY SIMILARITY.
NON TER 115 115
SEQUENCE 115 AA; 12810 MW; B67AD6G38A12IA5F CRC64;

Query Match 61.0%; Score 411; DB 1; Length 115;
Best Local Similarity 63.2%; Pred. No. 3.3e-35;
Matches 79; Conservative 12; Mismatches 24; Indels 10; Gaps

QY 1 EVKLVEGGGLVPQGSRLSCATSGFTSDSYNNWVRPPPKALEWLGFIRNKANGYT 60
    ||||| ||||| ::||| :||| :||| :||| :||| :||| :||| :||| :|||
Ddb 1 EVKLESGGLVPQGSMLCSVGSTFSNWNWVRQPKEGLEWAIEIKSNNTAT 60
    ||||| ||||| ::||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 61 EFSAVSVMGRITISRDQSQTLYLOMTLRADSATTYYCARDPPYPHYNAMYDGQGT 120
    ||||| ||||| ::||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 HYASVKGRITISRDSKSQSVYLQNNLRAEDTGIIYCCT-----GFAYWGQGT 110
    |||||

QY 121 VTWSS 125
      |||||
Db 111 VTWSA 115

RESULT 14
HV16_MOUSE STANDARD; PRT; 136 AA.
ID ID HV16_MOUSE
AC AC P01783;
DT DT 21-JUL-1986 (Rel. 01, Created)
DT DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE DE 15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=81234548; PubMed=6788376;
Botwell A.L.M.; Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Ra Baltimore D.;
The variable region contribution to the NPb family of
```

CC BINDS INULIN.  
 DR PIR: A90400: AVMSB7.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; 19; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 22 98  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

BY SIMILARITY.

Query Match 60.2%; Score 406; DB 1; Length 113;  
 Best Local Similarity 63.4%; Pred. No. 1e-34;  
 Matches 78; Conservative 13; Mismatches 22; Indels 10; Gaps 1;

QY 1 EVKLVESGGGLVQPGGSLRLSCLATSGGTFTSDYNNWVVRQPPGKALEWLGFIIRNKANGYTT 60  
 DB 1 EVKLEESGGGLVQPGGSKLSCVAGGTFTSNWNNWVRQSPKGLWVAEIRLKSHTYAT 60  
 QY 61 EFSASVMGRTISRDDSSILYLMNTLRADSATYICARDPPYGNPHYYAMDYWGQTS 120  
 DB 61 HYAESVKGRTISRDDSKSSVYLMNNLRADETAIYYCST-----CFAYWGQGT 110  
 QY 121 VTV 123  
 DB 111 VTV 113

Search completed: June 28, 2001, 15:54:37  
 Job time: 125 sec





Db 59 YYADSVKGRFTISRDNKNTLYLQMSLRADTAFTVYICARD-----LNYWGQGTGL 108  
 QY 121 VTVSS 125  
 Db 109 VTVSS 113

RESULT 2  
 Q9UL91 ID Q9UL91 PRELIMINARY; PRT; 118 AA.  
 AC Q9UL91;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98271139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AF035023; AAD56259.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR NON\_TER 1  
 FT NON\_TER 118  
 FT SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 59.4%; Score 400.5; DB 4; Length 118;  
 Best Local Similarity 65.3%; Pred. No. 1.9e-35;  
 Matches 81; Conservative 12; Mismatches 24; Indels 7; Gaps 2;

QY 1 EVKLVEGGGLVOPGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60  
 :::  
 Db 1 EVQLVESGGGLVOPGSGSLRLSCAASGFTFSYMNVRQAPGKLEWVSGI--ITI 58  
 :::  
 QY 61 EFASVNGRFTISRDNKNTLYLQMSLRADTAFTVYICARDPPYGNPHYAMDYWGQGT 120  
 :::  
 Db 59 YYADSVKGRFTISRDNKNTLYLQMSLRADTAFTVYICAR-----GDSSEAFDIWGQGT 113  
 :::  
 QY 121 VTVSS 124  
 Db 114 VTVSS 117

RESULT 3  
 Q9HCC1 ID Q9HCC1 PRELIMINARY; PRT; 112 AA.  
 AC Q9HCC1;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE SINGLE CHAIN FV FRAGMENT (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;  
 RT "An antibody fragment 2A3 specific for native lysozyme: Isolation from a  
 RT human synthetic phage display library and characterization.";

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB049915; BAB16829.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 112  
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 59.1%; Score 398.5; DB 4; Length 112;  
 Best Local Similarity 64.5%; Pred. No. 2.9e-35;  
 Matches 78; Conservative 16; Mismatches 18; Indels 9; Gaps 2;

QY 1 EVKLVEGGGLVOPGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60  
 :::  
 Db 1 EVQLVESGGGVPRGSLRLSCAASGFTFDYGMVSRQAPGKLEWVSGI--NNGSGT 58  
 :::  
 QY 61 EFASVNGRFTISRDNKNTLYLQMSLRADTAFTVYICARDPPYGNPHYAMDYWGQGT 120  
 :::  
 Db 59 GYADSVKGRFTISRDNKNTLYLQMSLRADTAFTVYICAR-----RRYALDYWGQGT 111  
 :::  
 QY 121 V 121  
 Db 112 V 112

RESULT 4  
 Q9UL72 ID Q9UL72 PRELIMINARY; PRT; 118 AA.  
 AC Q9UL72;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98271139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AF035042; AAD56278.1; -.  
 DR HSP: P01772; 2FBA.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR NON\_TER 1  
 FT NON\_TER 118  
 FT SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 58.8%; Score 396.5; DB 4; Length 118;  
 Best Local Similarity 65.6%; Pred. No. 5e-35;  
 Matches 82; Conservative 13; Mismatches 23; Indels 7; Gaps 3;

QY 1 EVKLVEGGGLVOPGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60  
 :::  
 Db 1 EVQLVESGGGLVOPGSGSLRLSCAASGFTVSSNMVVRQAPGKLEWVSGVSVTSGSSV-- 58  
 :::  
 QY 61 EFASVNGRFTISRDNKNTLYLQMSLRADTAFTVYICARDPPYGNPHYAMDYWGQGT 120  
 :::  
 Db 59 -YADSVKGRFTISRDNKNTLYLQMSLRADTAFTVYICAR--RFGS---FLFDYWGQGT 113  
 :::  
 QY 121 VTVSS 125  
 Db 114 VTVSS 118



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RESULT 5
Q9Y509 ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE V3 PROTEIN (FRAGMENT).
GN V3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; S80860; RAD14339.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT SEQUENCE -47 AA; 15768 MW; 8489FCAA7BC925C CRC64;
SQ

Query Match 58.8%; Score 396.5; DB 4; Length 147;
Best Local Similarity 62.5%; Pred. No. 6.6e-35;
Matches 80; Conservative 17; Mismatches 26; Indels 5; Gaps 3;

QY 1 EVKLVEGGGLVPGGSLRLSCATSGFTSDYMNWVRPPGKALEWLGFIIRNKANGYTT 60
Db 1 QVHLVSGGVVPGGSLRSCASGFTFTYGMVWVRPPGKLEWLGFIIRNKANGYTT 58
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPYGNP--HYVA-MDYWGO 117
Db 59 YVAGSVKGRFTISRDNKNTLYLQMTSLRVEDTAVYICAKDGNVDSVGYVYAGIDYWGO 118
QY 118 GTSVTYSS 125
Db 119 GTLVTYSS 126

RESULT 6
Q9UL88 ID Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
SQ

Query Match 57.7%; Score 389; DB 4; Length 121;
Best Local Similarity 63.2%; Pred. No. 3.3e-34;
Matches 79; Conservative 14; Mismatches 28; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVPGGSLRLSCATSGFTSDYMNWVRPPGKALEWLGFIIRNKANGYTT 60
Db 1 EVQLVESGGGVVPGGSLRFLCAASGFTFDGYAMHWVRQAPGKLEWVSLI--SGDGST 58
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGO 120
Db 59 YVAGSVKGRFTISRDNKNTLYLQMTSLRVEDTAVYICAKDGNVDSVGYVYAGIDYWGO 118
QY 121 VTYSS 125

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DR EMBL; AF035026; AAD56262.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 58.6%; Score 395; DB 4; Length 131;
Best Local Similarity 58.8%; Pred. No. 8.3e-35;
Matches 77; Conservative 20; Mismatches 28; Indels 6; Gaps 1;

QY 1 EVKLVEGGGLVPGGSLRLSCATSGFTSDYMNWVRPPGKALEWLGFIIRNKANGYTT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSKAMSWVRQAPGKLEWVGRISKTGGTT 60
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPY-----GNPHYAMDY 114
Db 61 DYAAVPKGRFTISRDSKNTLYLRMSLTKTDTAVYYCTGTMIIWITTSKRTSFEY 120
QY 115 WGQTSVTYSS 125
Db 121 WGQGLTVTVSS 131

RESULT 7
Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
SQ

Query Match 57.7%; Score 389; DB 4; Length 121;
Best Local Similarity 63.2%; Pred. No. 3.3e-34;
Matches 79; Conservative 14; Mismatches 28; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVPGGSLRLSCATSGFTSDYMNWVRPPGKALEWLGFIIRNKANGYTT 60
Db 1 EVQLVESGGGVVPGGSLRFLCAASGFTFDGYAMHWVRQAPGKLEWVSLI--SGDGST 58
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGO 120
Db 59 YVAGSVKGRFTISRDNKNTLYLQMTSLRVEDTAVYICAKDGNVDSVGYVYAGIDYWGO 118
QY 121 VTYSS 125

```



```

RESULT 11
Q9QYF0
AC Q9QYF0 PRELIMINARY; PRT; 298 AA.
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CN 8 SCFV.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinohara N.; Demura T.; Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinohara N.; Demura T.; Fukuda H.;
RL "Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
method.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036341; BAA88633.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGv; 1.
SQ SEQUENCE 298 AA; 31867 MW; EOF96B8A17004317 CRC64;

Query Match 53.0%; Score 357.5; DB 11; Length 298;
Best Local Similarity 56.0%; Pred. No. 2.3e-30;
Matches 70; Conservative 23; Mismatches 25; Indels 7; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYYMNVVRQPPGKALEWLGFIKNGYTT 60
Db 40 QVKLQSGGGLVQPGGSLRLSCAASGFSRYWMSVVRQAPGKLGWLGFIKNGYTT 97
QY 61 EFSASVGMGRTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGT 120
Db 98 NTPSLKDFEISRNKNTLYLQMSKVRSEDALYYCARASYVGH-----SAYWGQGT 152
QY 121 VTSS 125
Db 153 VTSS 157

RESULT 12
Q9GYZ2
AC Q9GYZ2 PRELIMINARY; PRT; 119 AA.
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MONOCLONAL ANTI-IDIDOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OC Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeldida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T.; Feng Z.Q.; Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

```

```

DR EMBL; AF282622; AAG01452.1; -.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 50.1%; Score 338; DB 5; Length 119;
Best Local Similarity 52.8%; Pred. No. 9.3e-29;
Matches 66; Conservative 22; Mismatches 31; Indels 6; Gaps 4;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYYMNVVRQPPGKALEWLGFIKNGYTT 60
Db 1 QVQLVESGAERKPGASVRVSCASGYFTFGYYMNVVRQAPGKLGWLGFIKNGYTT 58
QY 61 EFSASVGMGRTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGT 120
Db 59 NYNOKERDRTVMTDKSFSTAYMDLRLSLRADSANVYCAR---YYDDH-YCLDYWGQGT 114
QY 121 VTSS 125
Db 115 VTSS 119

RESULT 13
Q9ULB6
AC Q9ULB6 PRELIMINARY; PRT; 95 AA.
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y.; Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL; AB035268; BAA87067.1; -.
DR HSSP; P01772; 2FH4.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; -Gv; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 50.0%; Score 337; DB 4; Length 95;
Best Local Similarity 68.0%; Pred. No. 9e-29;
Matches 66; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 2 VKLVEGGGLVQPGGSLRLSCATSGFTFSDYYMNVVRQPPGKALEWLGFIKNGYTT 61
Db 1 VOLEESGGGLVQPGGSLRLSCAASGFTFSYWMNVVRQAPGKLGWLGFIKNGYTT 58
QY 62 FSAASVGMGRTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGT 98
Db 59 YVDSVGMGRTISRDNKSLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGT 95

RESULT 14
Q9UL92
AC Q9UL92 PRELIMINARY; PRT; 124 AA.
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

```

```
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035022; AAD56258.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
```

```
Query Match 49.9%; Score 336.5; DB 4; Length 124;
Best Local Similarity 50.8%; Pred. No. 1.4e-28;
Matches 64; Conservative 26; Mismatches 33; Indels 3; Gaps 2;

QY 1 EVKLVEGGGLVQPGSLRLSCATSGFTFSYIMNMVVRQPPGKALEWLGFIIRNKANGYTT 60
DB 1 EVQLQSGGPELVKPGASVKMSCKASGYTFTDYIMKWKQSHGKSLIEWIGDI-NPNNG-GT 58

QY 61 EFSASVMGRFTISRDDQSILYLQMNLTIRAEASATYYCARDPPYGNPHYYAMDYWGQGT 120
DB 59 SYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKY----YF--DYWGQGT 112

QY 121 VTVSS 125
DB 113 LTVSS 117
```

Search completed: June 28, 2001, 16:08:23  
Job time: 951 sec

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RESULT 15
Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225171; CAB65236.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;
```

Query Match 49.6%; Score 334; DB 11; Length 117;  
Best Local Similarity 52.8%; Pred. No. 2.4e-28;  
Matches 66; Conservative 23; Mismatches 28; Indels 8; Gaps 4;

0

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:36 ; Search time 362.28 Seconds  
(without alignments)  
0.837 Million cell updates/sec

Title: US-09-724-406-20  
Perfect score: 31  
Sequence: 1 DYVMN 5

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11:	/SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
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13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15:	/SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18:	/SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19:	/SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	31	100.0	5	16	AA1980
2	31	100.0	5	20	AA1981
3	31	100.0	5	21	AA1982
4	31	100.0	111	20	AA1983
5	31	100.0	119	11	AA1984
6	31	100.0	119	15	AA1985
7	31	100.0	119	11	AA1986
8	31	100.0	119	17	AA1987
9	31	100.0	119	17	AA1988
10	31	100.0	119	21	AA1989
11	31	100.0	122	16	AA1990

12	31	100.0	122	16	AA1991
13	31	100.0	138	16	AA1992
14	31	100.0	140	13	AA1993
15	31	100.0	141	13	AA1994
16	31	100.0	146	13	AA1995
17	31	100.0	146	13	AA1996
18	31	100.0	146	13	AA1997
19	31	100.0	146	13	AA1998
20	31	100.0	146	13	AA1999
21	31	100.0	146	16	AA2000
22	31	100.0	250	17	AA2001
23	31	100.0	250	17	AA2002
24	31	100.0	473	18	AA2003
25	31	100.0	643	20	AA2004
26	28	90.3	647	20	AA2005
27	28	90.3	100	18	AA2006
28	28	90.3	234	21	AA2007
29	28	90.3	248	21	AA2008
30	28	90.3	253	21	AA2009
31	28	90.3	317	21	AA2010
32	28	90.3	327	21	AA2011
33	28	90.3	344	21	AA2012
34	28	90.3	414	18	AA2013
35	28	90.3	416	18	AA2014
36	28	90.3	499	16	AA2015
37	28	90.3	499	16	AA2016
38	28	90.3	511	21	AA2017
39	28	90.3	567	16	AA2018
40	28	90.3	703	16	AA2019
41	28	90.3	708	16	AA2020
42	28	90.3	736	20	AA2021
43	28	90.3	736	21	AA2022
44	28	90.3	753	16	AA2023
45	28	90.3	753	16	AA2024

## ALIGNMENTS

RESULT 1

AA19930

ID AA19930 standard; peptide; 5 AA.

AC AA19930;

XX

DT 19-JAN-1996 (first entry)

XX

DE H-CDR-1 of anti-idiotypic antibody against human anticancer antibody.

XX

KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;

KW complementarity determining region.

OS Mus sp.

XX

PN JP07101999-A.

XX

PD 18-APR-1995.

XX

PF 06-OCT-1993; 93JP-0272950.

XX

PR 06-OCT-1993; 93JP-0272950.

XX

PA (HAGI/) HAGIWARA Y.

XX

DR WPI; 1995-182987/24.

XX

PT Novel anti-idiotypic antibody against an human anticancer monoclonal

PT antibody - and DNA sequences encoding the antibody, useful in

XX pharmacology, medicine and biochemical fields.

PS Claim 1; Page 2; 28pp; Japanese.

XX

CC A new anti-idiotypic antibody against a human anticancer monoclonal

Immunoglobulin hea  
Anti-idiotypic anti  
Unprocessed variab  
A5B7 antibody heav  
CDR-grafted, human  
CDR-grafted, human  
A5B7 gH-2 antibody  
Anti-idiotypic anti  
Humanised A5B57 Fd  
Murine A5B57 Fd fr  
Human B7.1-murine  
Clone PMG4/A5B7VH-  
Plasmid pUC19/muA5  
H. pylori cell env  
Zea mays protein f  
Zea mays protein f  
Zea mays protein f  
Zea mays protein f  
Zea mays protein f  
H. pylori ORF 02ae  
H. pylori ORF 07ce  
Rat cell cycle pro  
Human cell cycle p  
Human cancer assoc  
Bovine foetal hear  
Human placental en  
Rovine foetal hear  
Human PRO403 prote  
Human PRO403 prote  
Endothelin convert  
Human endothelin c  
Bovine endothelin

ns



Query Match 100.0%; Score 31; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
| | | | |  
Db 1 dyymn 5

RESULT 4  
AAW89172  
ID AAW89172 standard; peptide; 111 AA.  
AC AAW89172;  
XX 25-MAR-1999 (first entry)  
DT Anti-p53 monoclonal antibody 248 variable heavy chain sequence.  
XX  
DE  
XX  
KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;  
KW Immune response; tumour associated antigen; metastatic cancer.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
XX WO9856416-A.  
PN  
XX  
PD 17-DEC-1998.  
XX  
XX 09-JUN-1998; 98WO-IL00266.  
PF  
XX  
PR 09-JUN-1997; 97IL-0121041.  
XX  
XX (YEDA ) YEDA RES & DEV CO LTD.  
PA  
XX  
XX Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;  
PI Wolkowicz R;  
PI  
XX  
DR WPI; 1999-070296/06.  
XX  
PT Use of a monoclonal antibody to a tumour-associated antigen - to  
PT induce anti-tumour immunity or elicit an increased immune response  
PT to the antigen  
XX  
PS Example 3; Fig 3: 47pp; English.  
XX

CC The present invention describes the use of an immunogen (A) to induce  
CC anti-tumour immunity; to elicit an increased immune response to tumour  
CC associated antigen (TAA) and/or to induce an immune response to mutant  
CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody  
CC (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR  
CC (complementarity determining region) on the heavy or light chain of Mab  
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the  
CC variable (V) region of Mab, in a gene delivery vehicle. The present  
CC sequence represents the variable heavy chain sequence from anti-p53 Mab  
CC 248. Also described is a method for generating sequence-specific,  
CC anti-DNA antibodies (Ab) by immunising a mammal with a Mab directed to a  
CC domain containing a DNA-binding site of a DNA-binding protein. (A) is  
CC used to treat a wide variety of primary and metastatic cancers,  
CC particularly those where p53 is involved. Ab are used for diagnosis (e.g  
CC to determine critical sequences in animal or plant breeding); to  
CC identify bacteria and other parasites; to determine parentage; in  
CC forensic science; to isolate specific genes for DNA vaccination; in  
CC sequencing and cloning; also possibly for activation of selected  
CC therapeutic genes in plants, animals and humans. (A) induce an effective  
CC anti-tumour response without causing harm to the patient. The method  
CC uses (A) to generate anti-TAA by exploiting the anti-idiotype network.  
XX  
SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 20; Length 111;  
Best Local Similarity 100.0%; Pred. No. 23;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYYMN 5  
| | | | |  
Db 28 dyymn 32

RESULT 5  
AAR07316  
ID AAR07316 standard; protein; 119 AA.  
XX  
AC AAR07316;  
XX  
DT 22-JAN-1991 (first entry)  
XX  
DE VH domain of antibody A against tumour-associated antigens.  
XX  
XX Tumour-associated antigen; murine monoclonal antibody A;  
KW granulocyte compartment; carcinoma; colon; pancreas; lung; mammary;  
KW diagnosis.  
XX  
OS Mus musculus.  
XX  
XX EP388914-A.  
PN  
XX  
PD 26-SEP-1990.  
XX  
XX 21-MAR-1990; 90EP-0105322.  
PF  
XX  
PR 24-MAR-1989; 89DE-3909799.  
XX  
XX (BEHW ) BEHRINGWERKE AG.  
XX  
XX Bosslet K, Seemann G, Sedlacek HH;  
PI WPI; 1990-291873/39.  
DR N-PSDB; AAQ06212.  
XX  
PT Monoclonal antibodies to tumour associated antigens - used for  
PT diagnosis of malignant tumours etc.  
XX  
PS Disclosure; Page 11; 18pp; German.  
XX  
CC Antibody A is produced as described in EP-141079 and binds to cells  
CC of the granulocyte compartment and to colonic, pancreatic and  
CC certain pulmonary and mammary carcinomas. They are useful in tumour  
CC diagnosis and therapy.  
CC See also AAQ06213 for VK of Mab A, AAQ07314-15 for Mab B, and  
CC AAQ06227-30 for Mab C and D.  
XX  
SQ Sequence 119 AA;

Query Match 100.0%; Score 31; DB 11; Length 119;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYYMN 5  
| | | | |  
Db 29 dyymn 33

RESULT 6  
AAR47221  
ID AAR47221 standard; Protein; 119 AA.  
XX  
AC AAR47221;  
XX  
DT 04-AUG-1994 (first entry)  
XX  
DE Antibody heavy chain used in construction of humanised antibody.  
XX Antibody; light chain; heavy chain; monoclonal; humanised;  
KW

Fri Jun 29 08:04:42 2001

us-09-724-406-20.rag

KW diagnosis; detection; therapy; inflammation; tumour; metastasis;  
 KW lymphoma; carcinoma.

XX Chimeric: Mus musculus.  
 OS Chimeric: Homo sapiens.

XX DE4225853-A.  
 XX 10-FEB-1994.

XX 05-AUG-1992; 92DE-4225853.

XX 05-AUG-1992; 92DE-4225853.

XX (BEHW ) BEHRINGWERKE AG.

XX Bosslet K, Seemann G;

XX WPI; 1994-049745/07.

XX N-PSDB; AAQ56145.

XX Humanised antibody chains - derived from mouse monoclonal antibody  
 PT and humanised antibodies useful for diagnosis or therapy of  
 PT inflammations and tumours

XX Claim 2; Page 10; 12pp; German.

XX This antibody heavy chain is derived from the mouse monoclonal  
 CC antibody BW 250/183. After mutagenesis of the coding sequence,  
 CC the resulting protein sequence was used in the construction of a  
 CC humanised antibody directed against nonspecific crossreacting  
 CC antigen NCA 95 and carcinoembryonic antigen (CEA). The antibody  
 CC may be used for diagnosis and/or therapy of inflammations and  
 CC tumours which metastasise to bone marrow, especially lymphomas and  
 CC mammary, prostatic and small cell carcinomas.

XX Sequence 119 AA;

Query Match 100.0%; Score 31; DB 15; Length 119;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 29 dyyrn 33

RESULT 7

AAW14484

ID AAW14484 standard; Protein; 119 AA.

XX AAW14484;

XX 28-JAN-1997 (first entry)

XX Monoclonal antibody A VH.

XX heavy; light chain; monoclonal antibody; antigen 3; marker; melanoma;  
 KW permanent human tumour cell line; tumour-associated antigen; epitope;  
 KW gastrointestinal tumour; pancreatic carcinoma; diagnostic; therapeutic;  
 KW antigen 11; Vibrio cholera; neuraminidase-resistant; ganglioside GD2.

XX Synthetic.

XX EP727436-A1.

XX 21-AUG-1996.

XX 21-MAR-1990; 90EP-0105322.

XX 24-MAR-1989; 89DE-3909799.

PA (BEHW ) BEHRINGWERKE AG.

XX Auerbach B, Bosslet K, Sedlacek H, Seemann G;

XX WPI; 1996-372836/38.

XX N-PSDB; AAT63501.

XX Monoclonal antibody to tumour-associated antigen - useful as  
 PT gastrointestinal tumour marker

XX Claim 1; Page 11; 19pp; German.

XX AAW14484-85 are the heavy and light chains (respectively) of monoclonal  
 CC antibody (Mab) A. Mab A recognises antigen 3 of a permanent human tumour  
 CC cell line. This tumour-associated antigenic epitope occurs at high  
 CC concn. in the serum of patients with gastrointestinal tumours, e.g.  
 CC pancreatic carcinoma, and is thus useful as a tumour marker for  
 CC diagnostic or therapeutic purposes. Mabs B, C and D (see AAW14486-91) are  
 CC mentioned in the specification, but are not part of the claims. Mab B  
 CC recognises antigen 11 of permanent human tumour cell line. Mab C also  
 CC recognises an epitope of a tumour-associated antigen occurring at high  
 CC concn. in the serum of patients with gastrointestinal tumours. Mab D  
 CC recognises a Vibrio cholera neuraminidase-resistant epitope of  
 CC ganglioside GD2, from a human melanoma cell line.

XX Sequence 119 AA;

Query Match 100.0%; Score 31; DB 17; Length 119;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 29 dyyrn 33

RESULT 8

AAR99873

ID AAR99873 standard; Protein; 119 AA.

XX AAR99873;

XX 28-JAN-1997 (first entry)

XX Monoclonal antibody A VH.

XX Monoclonal antibody; Mab; epitope; tumour-associated antigen;  
 KW marker; antigen.

XX Synthetic.

XX EP727435-A1.

XX 21-AUG-1996.

XX 21-MAR-1990; 90EP-0105322.

XX 24-MAR-1989; 89DE-3909799.

XX (BEHW ) BEHRINGWERKE AG.

XX Auerbach B, Bosslet K, Sedlacek H, Seemann G;

XX WPI; 1996-372835/38.

XX N-PSDB; AAT36661.

XX Monoclonal antibody to tumour-associated antigen - useful as  
 PT gastrointestinal tumour marker

XX Disclosure; Page 11; 19pp; German.

XX Mab C (AAT36659-T36660) is a monoclonal antibody that recognises an

CC epitope of a tumour-associated antigen occurring at high concn. in  
 CC the serum of patients with gastrointestinal tumours, e.g. pancreatic  
 CC carcinoma, and is thus useful as a tumour marker for diagnostic or  
 CC therapeutic purposes.  
 CC MABs A, B and D are mentioned in the specification, but are not  
 CC part of the claims.  
 CC MAB A (AAT36661-T36662) recognises antigen 3 of permanent human  
 CC tumour cell line.  
 CC MAB B (AAT36663-T36664) recognises antigen 11 of permanent human  
 CC tumour cell line.  
 CC MAB D (AAT36665-T36666) recognises a Vibrio cholera neuraminidase-  
 CC resistant epitope of ganglioside GD2, from a human melanoma cell  
 CC line.  
 XX  
 SQ Sequence 119 AA;

Query Match 100.0%; Score 31; DB 17; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYYMN 5  
 |||||  
 Db 29 dyyrn 33

RESULT 9  
 AAY33425  
 ID AAY33425 standard; Protein; 119 AA.  
 XX  
 AC AAY33425;  
 XX  
 DT 13-DEC-1999 (first entry)  
 DE  
 DE Mouse antibody MAK heavy chain VH region protein fragment.  
 XX  
 KW Murine; antibody; MAK; heavy chain; VH region; alpha emitter; therapy;  
 KW beta emitter; radioimmunoconjugate; hematopoietic disease; solid tumor;  
 KW metastasis; inflammatory disease; chemotherapy; irradiation.  
 XX  
 OS Mus sp.  
 XX  
 PN DE19813687-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PF 27-MAR-1998; 98DE-1013687.  
 XX  
 PR 27-MAR-1998; 98DE-1013687.  
 XX  
 PA (BENE/) BENES I F.  
 PA (BOSS/) BOSSLET K.  
 XX  
 PI Benes IF, Bosslet K, Maecke HR;  
 XX  
 WPI; 1999-541798/46.  
 DR N-PSDB; AA223369.  
 XX  
 PT New radioimmunoconjugate, useful for treating hematopoietic diseases,  
 PT solid tumors and their metastases and inflammatory diseases -  
 XX  
 PS Example 1; Page 6-7; 12pp; German.  
 XX

This invention describes a novel radioimmunoconjugate comprising an alpha  
 or beta emitter other than iodine, coupled to an antibody without using a  
 complexing agent. The conjugate is especially useful for therapy of  
 hematopoietic diseases, as well as solid tumors and their metastases and  
 inflammatory diseases, optionally in combination with chemotherapy.  
 preferably as a substitute for high-dose chemotherapy and/or total  
 body irradiation. The conjugate is more stable than prior art directly  
 coupled conjugates and does not elicit an immune response to a  
 complexing agent. This sequence represents a fragment of the murine MAK  
 antibody heavy chain VH region which is used in the method of the

CC invention.  
 XX  
 SQ Sequence 119 AA;

Query Match 100.0%; Score 31; DB 20; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYYMN 5  
 |||||  
 Db 29 dyyrn 33

RESULT 10  
 AAY51368  
 ID AAY51368 standard; Protein; 119 AA.  
 XX  
 AC AAY51368;  
 XX  
 DT 27-APR-2000 (first entry)  
 DE  
 DE Mouse monoclonal antibody VH chain protein fragment.  
 XX  
 KW Variable region; heavy chain; monoclonal antibody; VH region; murine;  
 KW radioimmunoconjugate; anticancer; cytostatic; antineoplastic; tumor;  
 KW chemotherapy; radiotherapy; treatment; hematopoietic disease; carcinoma;  
 KW metastasis; inflammatory disease; leukemia; pemphigus; bone marrow.  
 XX  
 OS Mus sp.  
 XX  
 PN EP972528-A2.  
 XX  
 PD 19-JAN-2000.  
 XX  
 PF 25-MAR-1999; 99EP-0106013.  
 XX  
 PR 27-MAR-1998; 98DE-1013687.  
 PR 15-MAR-1999; 99DE-1011329.  
 XX  
 PA (BENE/) BENES I F.  
 PA (BOSS/) BOSSLET K.  
 XX  
 PI Benes IF, Bosslet K;  
 XX  
 WPI; 2000-138524/13.  
 DR N-PSDB; AA288540.  
 XX

Radioimmunoconjugates useful for treating hematopoietic diseases, solid  
 tumors, tumor metastases and inflammatory diseases comprise an alpha or  
 beta emitter coupled to an antibody -  
 XX  
 PS Example 1; Page 11-12; 18pp; German.  
 XX

This invention describes novel radioimmunoconjugates (I), in which an  
 alpha or beta emitter (II and III) is stably coupled to an antibody (IV)  
 without using a complexing agent, provided that the radioisotope is not  
 iodine. The conjugate of the invention have anticancer, cytostatic and  
 antineoplastic activity. (I) are useful, either alone or in combination  
 with chemotherapy or radiotherapy, for treating hematopoietic diseases,  
 solid tumors, tumor metastases and inflammatory diseases, especially  
 malignant hematopoietic diseases such as acute and chronic myeloid  
 leukemias, malignant pemphigus (optionally in combination with bone  
 marrow transplantation), or preferably bone marrow metastases. (I) are  
 particularly useful for treating carcinomas of the prostate, lung,  
 pancreas, stomach, liver, colon, rectum, kidney, testicle, ovary, muscle,  
 bone, bladder, throat, nose and ear, lymphomas, bone marrow depletion  
 prior to transplantation, or for treating diseases in which bone marrow  
 conditioning is carried out. (I) may be used in combination with known  
 ligands specific for lymphocyte antigens such as CD19, CD20, CD22, HLL2  
 and HLA DR 10beta. (I) elicit no immune response to complexing agents.  
 This sequence represents the variable region heavy chain fragment of a  
 mouse monoclonal antibody which is used to illustrate the method of the

CC invention.  
XX Sequence 119 AA;  
SQ

Query Match 100.0%; Score 31; DB 21; Length 119;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5  
Db 29 dyymn 33

## RESULT 11

AAR74941  
ID AAR74941 standard; peptide; 122 AA.

AC AAR74941;

DT 19-JAN-1996 (first entry)

XX Immunoglobulin heavy chain of anti-idiotypic antibody against human  
DE anticancer antibody.

XX Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
KW complementarity determining region.

XX Mus sp.

XX Key Location/Qualifiers  
FH Region 31..35  
FT /label= CDR1  
FT Region 50..68  
FT /label= CDR2  
FT Region 101..111  
FT /label= CDR3

PN JP07101999-A.

XX 18-APR-1995.

XX 06-OCT-1993; 93JP-0272950.

XX 06-OCT-1993; 93JP-0272950.

XX (HAGI/) HAGIWARA Y.

XX WPI; 1995-182987/24.

XX Novel anti-idiotypic antibody against a human anticancer monoclonal  
PT antibody - and DNA sequences encoding the antibody, useful in  
PT pharmacology, medicine and biochemical fields.

XX Claim 3; Page 2; 28pp; Japanese.

XX AAR74940-R74943 are possible heavy chains of a new anti-idiotypic  
CC antibody against a human anticancer monoclonal antibody. This antibody  
CC contains in its heavy chain 3 complementarity determining regions CDR1  
CC (AAR74929-R74931) CDR2 (AAR74932-R74935) and CDR3 (AAR74936-R74939),  
CC this is also true of the light chain which has its own CDR1  
CC (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3  
CC (AAR74950-R74954). The antibody and DNA encoding it are useful in  
CC pharmacological, medical and biochemical fields.

XX Sequence 122 AA;

Query Match 100.0%; Score 31; DB 16; Length 122;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 31 dyymn 35

## RESULT 12

AAR74942  
ID AAR74942 standard; peptide; 122 AA.

AC AAR74942;

DT 19-JAN-1996 (first entry)

XX Immunoglobulin heavy chain of anti-idiotypic antibody against human  
DE anticancer antibody.

XX Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
KW complementarity determining region.

XX Mus sp.

XX Key Location/Qualifiers  
FH Region 31..35  
FT /label= CDR1  
FT Region 50..68  
FT /label= CDR2  
FT Region 101..111  
FT /label= CDR3

PN JP07101999-A.

XX 18-APR-1995.

XX 06-OCT-1993; 93JP-0272950.

XX 06-OCT-1993; 93JP-0272950.

XX (HAGI/) HAGIWARA Y.

XX WPI; 1995-182987/24.

XX Novel anti-idiotypic antibody against a human anticancer monoclonal  
PT antibody - and DNA sequences encoding the antibody, useful in  
PT pharmacology, medicine and biochemical fields.

XX Claim 4; Page 2; 28pp; Japanese.

XX AAR74940-R74943 are possible heavy chains of a new anti-idiotypic  
CC antibody against a human anticancer monoclonal antibody. This antibody  
CC contains in its heavy chain 3 complementarity determining regions CDR1  
CC (AAR74929-R74931) CDR2 (AAR74932-R74935) and CDR3 (AAR74936-R74939),  
CC this is also true of the light chain which has its own CDR1  
CC (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3  
CC (AAR74950-R74954). The antibody and DNA encoding it are useful in  
CC pharmacological, medical and biochemical fields.

XX Sequence 122 AA;

Query Match 100.0%; Score 31; DB 16; Length 122;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 31 dyymn 35

## RESULT 13

AAR74963  
ID AAR74963 standard; Protein; 138 AA.

XX AAR74963;

Qy 1 DYYMN 5

DT 02-FEB-1995 (first entry)  
 XX Anti-idiotypic antibody Idio27 clone 27GA5.  
 DE Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
 XX complementarity determining region.  
 KW Mus sp.  
 XX Key Location/Qualifiers  
 FH Peptide 1..10  
 FT /label= signal\_peptide  
 XX JP07101999-A.  
 XX 18-APR-1995.  
 PD 06-OCT-1993; 93JP-0272950.  
 PF 06-OCT-1993; 93JP-0272950.  
 XX (HAGI/) HAGIWARA Y.  
 XX WPI: 1995-182987/24.  
 DR N-PSDB; AAQ90428.  
 XX Novel anti-idiotypic antibody against an human anticancer monoclonal  
 PT antibody - and DNA sequences encoding the antibody, useful in  
 PT pharmacology, medicine and biochemical fields.  
 XX Example 5; Page 16; 28pp; Japanese.  
 XX AAR74960-R74969 are clones of the anti-idiotypic antibodies Idio3,  
 CC Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoclonal  
 CC antibody. These antibodies and DNA encoding them are useful in  
 CC pharmacological, medical and biochemical fields of research.  
 XX Sequence 138 AA;  
 SQ

Query Match 100.0%; Score 31; DB 16; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYYMN 5  
 DB 41 dyyrn 45

RESULT 14  
 AAR20790  
 ID AAR20790 standard; Protein; 140 AA.  
 AC AAR20790;  
 XX 19-MAY-1992 (first entry)  
 DE Unprocessed variable region of heavy chain of A5B7 antibody.  
 XX murine monoclonal antibody; MAb; VH domain; humanised antibody; CEA;  
 KW complementarity determining region.  
 XX Mus musculus.  
 OS Key Location/Qualifiers  
 FH Cleavage-site 19..20  
 FT /note= "putative signal peptide cleavage site"  
 XX WO9201059-A.  
 PN 23-JAN-1992.  
 PD 05-JUL-1991; 91WO-GB01108.  
 XX Humanised antibody molecules - comprising murine and human regions,  
 PF

XX 05-JUL-1991; 91WO-GB01108.  
 PR 05-JUL-1990; 90GB-0014932.  
 PR 21-DEC-1990; 90WO-GB02017.  
 XX (CELL-) CELLTech LTD.  
 PA Adair JR, Bodmer MW, Mountain A, Owens RJ;  
 PI WPI: 1992-056874/07.  
 DR N-PSDB; AAQ20984.  
 XX New CDR-grafted anti carcinoembryonic antigen antibodies - useful  
 PT in therapy and diagnosis of carcinoma  
 XX Example 1; Fig 1; 70pp; English.  
 XX The A5B7 MAB is a mouse MAB of the type IgG1-kappa raised against  
 CC CEA which had been denatured by heating to 85 degrees C for 35  
 CC minutes. The MAB has been extensively studied by Harwood et al.  
 CC (Br. J. Cancer, 54, 75-82, 1986). A cDNA library was prepared from  
 CC polyA RNA isolated from the A5B7 hybridoma cell line. A probe  
 CC complementary to mouse heavy chain constant region was used to  
 CC identify clone pBGI containing the complete leader, variable and  
 CC constant regions of the heavy chain. The amino acid sequence  
 CC predicted from the sequence encoding the unprocessed variable  
 CC region is given here.  
 XX Sequence 140 AA;  
 SQ

Query Match 100.0%; Score 31; DB 13; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYYMN 5  
 DB 50 dyyrn 54

RESULT 15  
 AAR30431  
 ID AAR30431 standard; Protein; 141 AA.  
 AC AAR30431;  
 XX 03-FEB-1993 (first entry)  
 DE A5B7 antibody heavy chain sequence.  
 XX humanised antibody; chimaeric; carcino-embryonic antigen; therapy;  
 KW diagnosis; carcinomas; CDR; IgG; human; murine; ss.  
 XX Chimaeric.  
 OS WO9201059-A.  
 PN 23-JAN-1992.  
 PD 05-JUL-1991; 91WO-GB01108.  
 XX 05-JUL-1991; 91WO-GB01108.  
 PR 05-JUL-1990; 90GB-0014932.  
 PR 21-DEC-1990; 90WO-GB02017.  
 XX (CELL-) CELLTech LTD.  
 PA Adair JR, Bodmer MW, Mountain A, Owens RJ;  
 PI WPI: 1992-284316/34.  
 DR N-PSDB; AAQ27351.  
 XX Humanised antibody molecules - comprising murine and human regions,  
 PF

Fri Jun 29 08:04:42 2001

PT specific for carcino-embryonic antigen, useful for diagnosis and  
 PR therapy  
 XX  
 PS  
 XX Example 1; Figure 1; 71pp; English.  
 XX  
 CC This sequence represents the A5B7 monoclonal antibody heavy chain.  
 CC It was decoded from the cDNA (AAQ27351). Sequence analysis confirmed  
 CC A5B7 to be an IgG1 K antibody.  
 XX  
 SQ Sequence 141 AA;

Query Match 100.0%; Score 31; DB 13; Length 141;  
 Best Local Similarity 100.0%; Pred. NO. 30;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5  
 |||||  
 Db 50 dyymn 54

Search completed: June 28, 2001, 16:14:37  
 Job time: 1325 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds  
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Title: US-09-724-406-20  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep.\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	5	1	US-08-318-970B-2
2	31	100.0	5	4	US-09-280-028-6
3	31	100.0	119	1	US-08-459-310-2
4	31	100.0	119	1	US-08-459-310-12
5	31	100.0	119	2	US-08-308-494A-9
6	31	100.0	119	4	US-09-280-028-2
7	31	100.0	128	1	US-08-202-047-21
8	31	100.0	128	3	US-08-964-690-21
9	31	100.0	140	2	US-08-449-287-4
10	31	100.0	146	2	US-08-449-287-10
11	31	100.0	146	2	US-08-449-287-12
12	28	90.3	30	3	US-08-433-522A-22
13	28	90.3	30	3	US-09-135-166-22
14	28	90.3	31	3	US-08-433-522A-23
15	28	90.3	31	3	US-09-135-166-23
16	28	90.3	499	5	PCT-US95-01806-2
17	28	90.3	499	5	PCT-US95-01806-4
18	28	90.3	567	3	US-08-646-273-19
19	28	90.3	703	3	US-08-646-273-25
20	28	90.3	703	3	US-08-646-273-36
21	28	90.3	753	3	US-08-646-273-36
22	28	90.3	754	3	US-08-646-273-30
23	28	90.3	758	1	US-08-289-112-2
24	28	90.3	772	1	US-08-258-639A-2
25	28	90.3	772	2	US-08-900-931-2
26	28	90.3	772	5	PCT-US95-07391A-2
27	28	90.3	787	1	US-08-574-763-2

28	28	90.3	792	3	US-08-433-522A-8	Sequence 8, Appli
29	28	90.3	792	3	US-09-135-166-8	Sequence 8, Appli
30	28	90.3	793	3	US-08-433-522A-10	Sequence 10, Appli
31	28	90.3	793	3	US-09-135-166-10	Sequence 10, Appli
32	28	90.3	797	3	US-08-433-522A-2	Sequence 2, Appli
33	28	90.3	797	3	US-08-433-522A-4	Sequence 4, Appli
34	28	90.3	797	3	US-08-433-522A-6	Sequence 6, Appli
35	28	90.3	797	3	US-09-135-166-2	Sequence 2, Appli
36	28	90.3	797	3	US-09-135-166-4	Sequence 4, Appli
37	28	90.3	797	3	US-09-135-166-6	Sequence 6, Appli
38	27	87.1	138	3	US-08-603-024-2	Sequence 2, Appli
39	27	87.1	139	1	US-08-253-877C-8	Sequence 8, Appli
40	27	87.1	139	1	US-08-253-877C-19	Sequence 19, Appli
41	27	87.1	139	2	US-08-452-164A-8	Sequence 8, Appli
42	27	87.1	139	2	US-08-452-164A-19	Sequence 19, Appli
43	27	87.1	139	3	US-08-603-024-18	Sequence 18, Appli
44	27	87.1	246	1	US-08-257-341-7	Sequence 7, Appli
45	27	87.1	252	1	US-08-461-838-4	Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
US-08-318-970B-2  
; Sequence 2, Application US/08318970B  
; Patent No. 5589573  
; GENERAL INFORMATION:  
; APPLICANT: Hideaki HAGIWARA, et al.  
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY  
; NUMBER OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Office of Sherman and Shalloway  
; STREET: 413 N. Washington Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor  
; OPERATING SYSTEM: MS DOS 3.3  
; SOFTWARE: Word Perfect, Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,970B  
; FILING DATE: October 6, 1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Richard A. Steinberg  
; REGISTRATION NUMBER: 26,588  
; REFERENCE/DOCKET NUMBER: S-2371  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 549-2282  
; TELEFAX: (703) 836-0106  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: H-CDRI-2  
; OTHER INFORMATION: hypervariable region

US-08-318-970B-2  
Query Match 100.0%; Score 31; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYYMN 5





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QY      1 DYMN 5
Db      29 DYMN 33

RESULT 5
US-08-308-494A-9
; Sequence 9, Application US/08308494A
; Patent No. 595083
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
; TITLE OF INVENTION: Preparation and Use Thereof
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,494A
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,739
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4118120.4
; FILING DATE: 03-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 05552-1186-02000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-308-494A-9

Query Match 100.0%; Score 31; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYMN 5
Db      29 DYMN 33

RESULT 6
US-09-280-028-2
; Sequence 2, Application US/09280028
; Patent No. 6241961
; GENERAL INFORMATION:
; APPLICANT: BENES, IVAN FRIEDRICH
; APPLICANT: BOSSLET, KLAUS

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; TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND
; FILE REFERENCE: BENES
; CURRENT APPLICATION NUMBER: US/09/280,028
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 199 11 329.7
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: 198 13 687.0
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-280-028-2

Query Match 100.0%; Score 31; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYMN 5
Db      29 DYMN 33

RESULT 7
US-08-202-047-21
; Sequence 21, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1...28

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OTHER INFORMATION: /label= MOUSE_IIA
US-08-202-047-21

Query Match      100.0%; Score 31; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
Db 31 DYYMN 35

RESULT 8
US-08-964-690-21
; Sequence 21, Application US/08964690
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to p-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,690
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= MOUSE_IIA
US-08-964-690-21

Query Match      100.0%; Score 31; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
Db 31 DYYMN 35

OTHER INFORMATION: /label= MOUSE_IIA
US-08-202-047-21

Query Match      100.0%; Score 31; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
Db 31 DYYMN 35

RESULT 9
US-08-449-287-4
; Sequence 4, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-4

Query Match      100.0%; Score 31; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
Db 50 DYYMN 54

OTHER INFORMATION: /label= MOUSE_IIA
US-08-202-047-21

Query Match      100.0%; Score 31; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
Db 31 DYYMN 35

RESULT 10
US-08-449-287-10
; Sequence 10, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
```

```

; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-10

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Query Match 100.0%; Score 31; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 DYYMN 5
Db 50 DYYMN 54

```

```

RESULT 11
US-08-449-287-12
; Sequence 12, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner

```

```

; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-12

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Query Match 100.0%; Score 31; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYYMN 5
Db 50 DYYMN 54

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RESULT 12
US-08-433-522A-22
; Sequence 22, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/433,522A  
; FILING DATE: 12-SEP-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEWART, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-433-522A-22

Query Match 90.3%; Score 28; DB 3; Length 30;  
Best Local Similarity 80.0%; Pred. No. 15;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
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DB 26 DYYLN 30

RESULT 13  
US-09-135-166-22  
; Sequence 22, Application US/09135166  
; Patent No. 6083743  
; GENERAL INFORMATION:  
; APPLICANT: CHONG, Pele  
; APPLICANT: THOMAS, Wayne  
; APPLICANT: YANG, Yan Ping  
; APPLICANT: LOOSMORE, Sheena  
; APPLICANT: SIA, Dwo Yuan Charles  
; APPLICANT: KLEIN, Michel  
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6TH Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 12-SEP-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEWART, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-135-166-22

Query Match 90.3%; Score 28; DB 3; Length 30;  
Best Local Similarity 80.0%; Pred. No. 15;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
|||:|  
DB 26 DYYLN 30

RESULT 14  
US-08-433-522A-23  
; Sequence 23, Application US/08433522A  
; Patent No. 6013514  
; GENERAL INFORMATION:  
; APPLICANT: CHONG, Pele  
; APPLICANT: THOMAS, Wayne  
; APPLICANT: YANG, Yan Ping  
; APPLICANT: LOOSMORE, Sheena  
; APPLICANT: SIA, Dwo Yuan Charles  
; APPLICANT: KLEIN, Michel  
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6TH Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/433,522A  
; FILING DATE: 12-SEP-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEWART, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-433-522A-23

Query Match 90.3%; Score 28; DB 3; Length 31;  
Best Local Similarity 80.0%; Pred. No. 15;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
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DB 6 DYYLN 10

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US-09-135-166-23

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; Sequence 23, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-135-166-23

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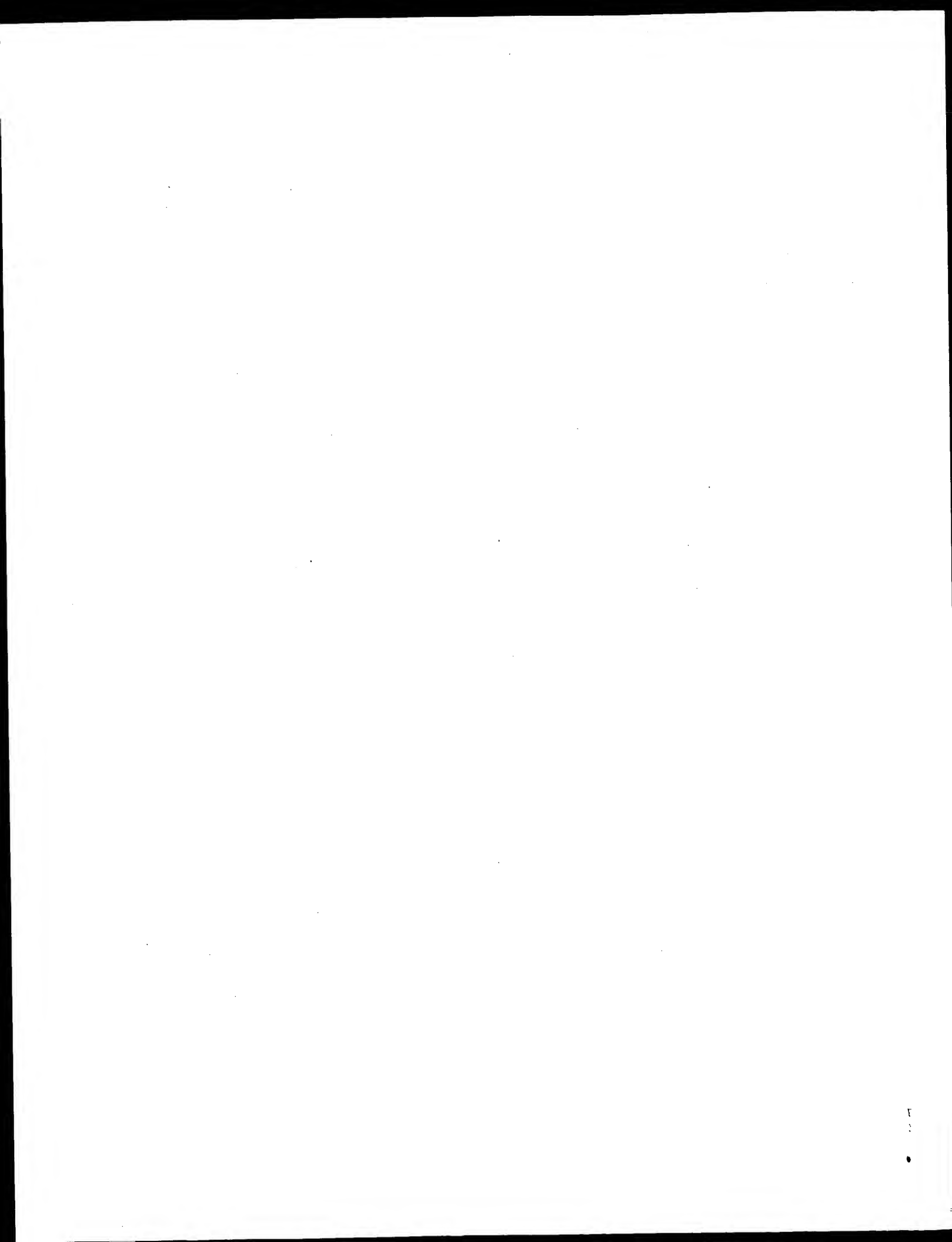
Query Match      90.3%; Score 28; DB 3; Length 31;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYYMN 5
DB 6 DYYLN 10

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Search completed: June 28, 2001, 16:01:14
Job time: 522 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: June 28, 2001, 15:58:44 ; Search time 234.85 Seconds  
(without alignments)  
1.622 Million cell updates/sec

Title: US-09-724-406-20

Perfect score: 31

Sequence: 1 DRYM 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query No.	Score	%			ID	Description
			Match	Length	DB		
1	31	100.0	34	2	S46469	Ig heavy chain V r	
2	31	100.0	71	2	PH1167	Ig heavy chain V r	
3	31	100.0	109	2	PH0973	Ig heavy chain V r	
4	31	100.0	112	2	S09957	Ig heavy chain V-D	
5	31	100.0	113	2	PH0974	Ig heavy chain V r	
6	31	100.0	114	2	PH1027	Ig heavy chain V r	
7	31	100.0	118	1	MHMS38	Ig heavy chain V r	
8	31	100.0	121	2	E30502	Ig heavy chain V r	
9	31	100.0	122	2	S20642	Ig heavy chain V r	
10	31	100.0	124	2	PT0388	Ig heavy chain V r	
11	31	100.0	263	2	C64339	Ig heavy chain V r	
12	31	100.0	672	2	E72391	Ig heavy chain V r	
13	28	90.3	107	2	PL0241	hypothetical prote	
14	28	90.3	107	2	S05516	beta-D-galactosida	
15	28	90.3	132	2	H96708	Ig heavy chain V r	
16	28	90.3	149	2	D82889	hypothetical prote	
17	28	90.3	221	2	T32048	hypothetical prote	
18	28	90.3	223	1	A41965	type I restriction	
19	28	90.3	223	1	H85686	hypothetical prote	
20	28	90.3	224	1	R85686	transcription regu	
21	28	90.3	250	2	S28474	transcription regu	
22	28	90.3	271	2	F82346	transcription regu	
23	28	90.3	282	2	T06973	lipopolysaccharide	
24	28	90.3	286	1	JQ2154	probable protochlo	
25	28	90.3	286	2	S25620	frxC protein - Ple	
26	28	90.3	290	2	S73108	frxC protein - Syn	
27	28	90.3	294	2	E86900	proteochlorophyllid	
28	28	90.3	311	2	S76833	proteochlorophyllid	
29	28	90.3	341	2	T25051	hypothetical prote	

## ALIGNMENTS

RESULT 1

S46469

Ig heavy chain V region (DA-5) - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Jun-2000

C:Accession: S46469

R:Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluweila, L.; Nature Genet. 7: 162-168, 1994

A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the te

A:Reference number: S46460; MUID:95004581

A:Accession: S46469

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-34 <COO>

A:Cross-references: EMBL:229981; NID:505463; PIDN:CAA82871.1; PID:91335180

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 34;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYM 5

Db 4 DRYM 8

RESULT 2

PH1167

Ig heavy chain V region (clone 14C.2B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH1167

R:Schitteck, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A:Reference number: PH1105; MUID:92364545

A:Accession: PH1167

A:Molecule type: DNA

A:Residues: 1-71 <SCH>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 71;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYM 5

|||||

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type II DNA modifi  
hypothetical prote  
hypothetical prote  
conserved hypotet  
cytochrome P450tyr  
udp-n-acetylmuram  
L2 protein - human  
CDC20 protein homo  
probable cell divi  
probable cell divi  
cobalamin biosynth  
probable ABC-type  
hypothetical prote  
penicillin-binding  
hypothetical prote

30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45  
28 28 28 28 28 28 28 28 28 28 28 28 28 28 28 28  
90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3 90.3  
2 C64321 2 F71955 2 T32311 2 D83351 2 C83351 2 T01018 2 D71812 2 S36388 2 T41719 2 A56021 2 B56021 2 G69140 2 C64903 2 D85726 2 C64044 2 T25802

Fri Jun 29 08:04:44 2001

us-09-724-406-20.rpr

Db 4 DYYMN 8

RESULT 3

PH0973

Ig heavy chain V region (clone 17s-cl) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH0973

R:Trillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell autoantibodies

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0973

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-109 <TIL>

A:Experimental source: B cell, strain [NZB x NZWJF1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 9;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35

RESULT 4

S09957

Ig heavy chain V-D-J region (106-10E) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 23-Jul-1999

C:Accession: S09957

R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990

A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies

A:Reference number: S09955; MUID:90269328

A:Accession: S09957

A:Molecule type: mRNA

A:Residues: 1-112 <REL>

A:Cross-references: EMBL:X51845; NID:g55244; PIDN:CAA36138.1; PID:g930213

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35

RESULT 5

PH0974

Ig heavy chain V region (clone 165.60) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH0974

R:Trillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell autoantibodies

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0974

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-113 <TIL>

A:Experimental source: B cell, strain [NZB x NZWJF1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35

RESULT 6

PH1027

Ig heavy chain V region (clone 163-c2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH1027

R:Trillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell autoantibodies

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1027

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-114 <TIL>

A:Experimental source: B cell, strain [NZB x NZWJF1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 9.4;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35

RESULT 7

MHMS38

Ig heavy chain V region (AC38 205.12) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 30-May-1997

C:Accession: A02040

R:Dildrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.

EMBO J. 3, 517-523, 1984

A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocyte

A:Reference number: A91000; MUID:84182519

A:Accession: A02040

A:Molecule type: protein

A:Residues: 1-118 <DIL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-98/Region: V segment

F:15-98/Domain: immunoglobulin homology <IMM>

F:99-104/Region: D segment

F:105-118/Region: J segment

F:22-96/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 118;

Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35



Db 31 DYYMN 35

## RESULT 8

Ig heavy chain V region (D42) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Nov-1988 #sequence\_revision 03-Nov-1988 #text\_change 23-Jul-1999

C:Accession: E30502

R:Ellat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice

A:Reference number: A30502; MUID:88315787

A:Accession: E30502

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-121 &lt;EIL&gt;

A:Cross-references: GB:M21909; NID:gl95587; PIDN:AAA38360.1; PID:gl95588

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 121;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 31 DYYMN 35

## RESULT 9

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S20642

R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react

A:Reference number: S20639

A:Accession: S20642

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-122 &lt;LOS&gt;

A:Cross-references: EMBL:X64997; NID:g52604; PIDN:CAA46130.1; PID:g52605

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 122;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 31 DYYMN 35

## RESULT 10

PT0388

Ig heavy chain V region (S107/VH11 group 3-23) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PT0388

R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

J. Exp. Med. 173, 731-741, 1991

A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi

A:Reference number: PT0376; MUID:91147903

A:Accession: PT0388

A:Molecule type: DNA

A:Residues: 1-124 &lt;BEH&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 124;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 31 DYYMN 35

## RESULT 11

C64339

hypothetical protein MJ0314 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: C64339

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc

A:Reference number: A64300; MUID:96337999

A:Accession: C64339

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-263 &lt;BUL&gt;

A:Cross-references: GB:U67486; GB:L77117; NID:gl591031; PIDN:AAB98310.1; PID:gl591034

C:Genetics:

A:Map position: FOR293581-294372

A:Start codon: TTG

## Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 263;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 184 DYYMN 188

## RESULT 12

E72391

beta-D-galactosidase - Thermotoga maritima (strain MS88)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C:Accession: E72391

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic

garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316

A:Accession: E72391

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-672 &lt;ARN&gt;

A:Cross-references: GB:AE001713; GB:AE000512; NID:g4980809; PIDN:AAD35398.1; PID:g498

A:Experimental source: strain MS88

C:Genetics:

A:Gene: TM0310

C:Superfamily: Bacillus beta-galactosidase

## Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 672;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-724-406-20.rpr

Fri Jun 29 08:04:44 2001

C:Accession: H96708  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malfi, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719  
 A:Accession: H96708  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-132 <STO>  
 A:Cross-references: GB:AE005173; NID:g6553937; PIDN:AAF16601.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: T26J14.5  
 A:Map position: 1

Query Match 90.3%; Score 28; DB 2; Length 132;  
 Best Local Similarity 80.0%; Pred. No. 47;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYVMN 5  
 |||:  
 Db 39 DYVLN 43

Search completed: June 28, 2001, 15:58:45  
 Job time: 373 sec

QY 1 DYVMN 5  
 |||:  
 Db 561 DYVMN 565

RESULT 13  
 PL0241  
 Ig heavy chain V region (anti-DNA, S1VH) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C:Accession: PL0241  
 R:Shomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A:Reference number: PL0231; MUID:90111618  
 A:Accession: PL0241  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <SHL>  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:1-18/Region: framework 1  
 F:3-86/Domain: Immunoglobulin homology <IMM>  
 F:19-23/Region: complementarity-determining 1  
 F:24-37/Region: framework 2  
 F:38-54/Region: complementarity-determining 2  
 F:55-86/Region: framework 3  
 F:87-97/Region: complementarity-determining 3  
 F:98-107/Region: framework 4

Query Match 90.3%; Score 28; DB 2; Length 107;  
 Best Local Similarity 80.0%; Pred. No. 38;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVMN 5  
 |||:  
 Db 19 DYVLN 23

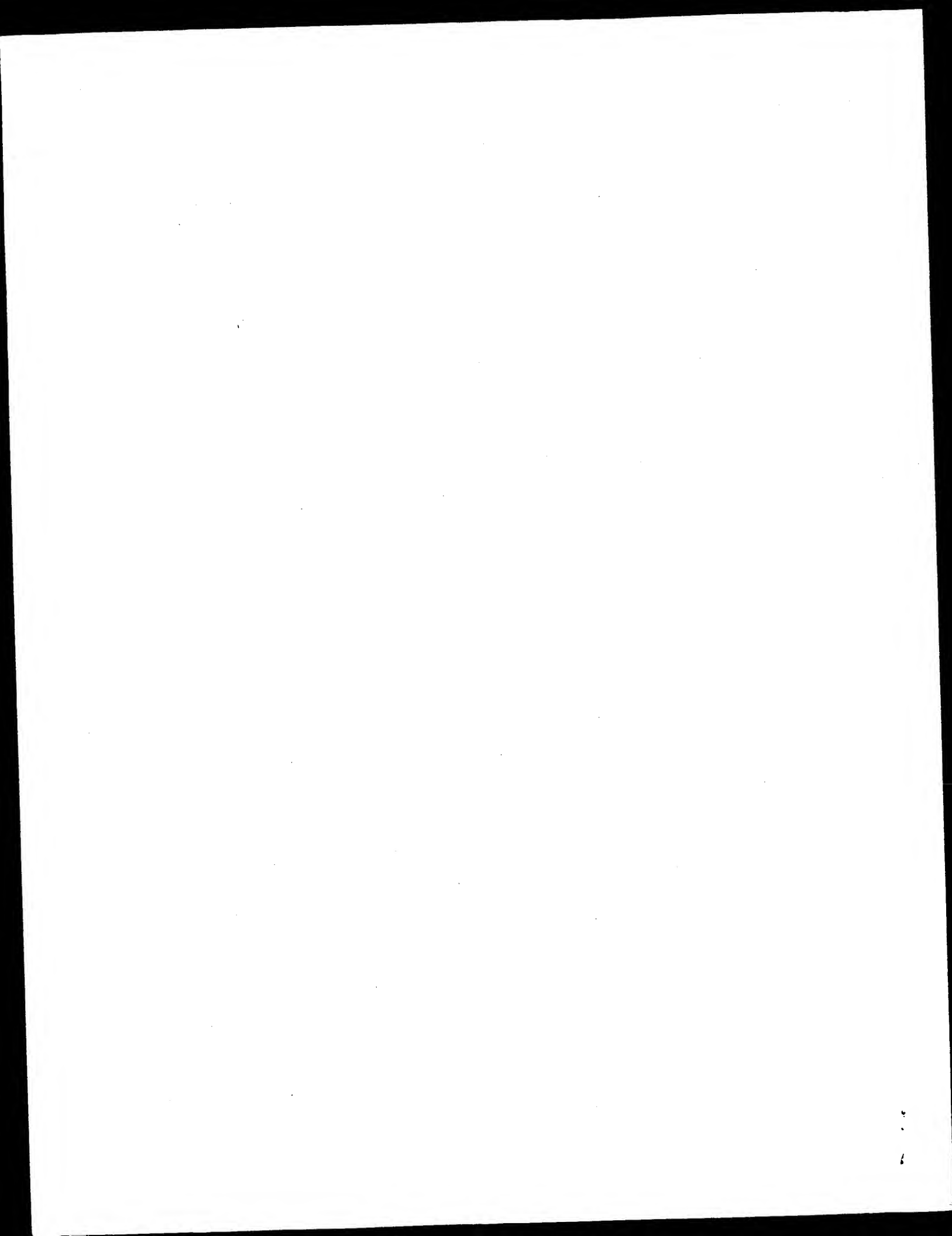
RESULT 14  
 S50516  
 Hypothetical protein YEL073c - yeast (Saccharomyces cerevisiae)  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: S50516  
 R:Dietrich, F.S.  
 submitted to the EMBL Data Library, December 1994  
 A:Description: The sequence of S. cerevisiae cosmid 9669, 8334, 8199, and lambda clone A:Reference number: S50434  
 A:Accession: S50516  
 A:Molecule type: DNA  
 A:Residues: 1-107 <DIE>  
 A:Cross-references: EMBL:U18795; NID:g603241; PID:g603245; GSPDB:GN00005; MIPS:YEL073c  
 C:Genetics:  
 A:Gene: MIPS:YEL073c  
 A:Map position: 5L

Query Match 90.3%; Score 28; DB 2; Length 107;  
 Best Local Similarity 80.0%; Pred. No. 38;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVMN 5  
 |||:  
 Db 39 DYVLN 43

RESULT 15  
 H96708  
 Hypothetical protein T26J14.5 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:37 ; Search time 105.36 Seconds  
(\*without alignments)  
1.626 Million cell updates/sec

Title: US-09-724-406-20  
Perfect score: 31  
Sequence: 1 DYMN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	100.0	118	1 HV51_MOUSE	P06330 mus musculus
2	31	100.0	263	1 Y314_METJA	Q57762 methanococcus
3	28	90.3	107	1 YE13_YEAST	P39974 saccharomyc
4	28	90.3	223	1 PHOP_ECOLI	P23836 escherichia
5	28	90.3	224	1 PHOP_SALTY	P14146 salmonella
6	28	90.3	282	1 CHLL_CVAPA	P48110 cyanophora
7	28	90.3	286	1 CHLL_PLEBO	Q00237 plectonema
8	28	90.3	286	1 CHLL_SNP7	P54207 synecococcus
9	28	90.3	288	1 CHLL_SNP3	P28373 synecocyst
10	28	90.3	290	1 CHLL_PORPU	P51187 porphyra pu
11	28	90.3	350	1 Y170_METJA	Q57634 methanococc
12	28	90.3	447	1 MURE_HELPJ	O921c6 helicobacte
13	28	90.3	456	1 VL2_HPVO7	P36745 human papil
14	28	90.3	561	1 YDPA_ECOLI	P31826 escherichia
15	28	90.3	617	1 ILVD_BUCAP	O51887 buchnera ap
16	28	90.3	651	1 PBP2_HAEIN	P44469 haemophilus
17	28	90.3	739	1 DD15_CAEEL	Q20875 caenorhabdi
18	28	90.3	754	1 ECE1_BOVIN	P42891 bos taurus
19	28	90.3	754	1 ECE1_CAVPO	P42893 cavia porce
20	28	90.3	762	1 ECE1_RAT	P42893 rattus norv
21	28	90.3	765	1 ECE2_HUMAN	O60344 homo sapien
22	28	90.3	766	1 SAK1_SCHPO	P43833 schizosacch
23	28	90.3	770	1 ECE1_HUMAN	P42892 homo sapien
24	28	90.3	787	1 ECE2_BOVIN	Q10711 bos taurus
25	28	90.3	791	1 LOW_CAMJE	O69300 campylobact
26	28	90.3	793	1 D153_HAEIN	O32629 haemophilus
27	28	90.3	795	1 D152_HAEIN	P44935 haemophilus
28	28	90.3	797	1 D151_HAEIN	P46024 haemophilus
29	28	90.3	1104	1 N1R_EMENI	P22944 emericella
30	28	90.3	1165	1 CHS3_YEAST	P29465 saccharomyc
31	28	90.3	1718	1 RPO_SHVX	O04575 shallot vir
32	27	87.1	213	1 SODF_HELPJ	O92ke6 helicobacte
33	27	87.1	213	1 SODF_HELPJ	P43312 helicobacte

34 27 87.1 300 1 PAL\_VESMC P51528 vespula mac  
35 27 87.1 336 1 PAL\_VESVU P49369 vespula vul  
36 27 87.1 338 1 GALE\_HAEIN P24325 haemophilus  
37 27 87.1 345 1 T2CL\_HERAU P25258 herpetosiph  
38 27 87.1 371 1 RIBD\_BACAM P70814 b riboflavi  
39 27 87.1 410 1 PKR\_METFE P20971 methanother  
40 27 87.1 426 1 VA20\_VACCC P20995 vaccinia vi  
41 27 87.1 426 1 VA20\_VAVR P33843 variola vir  
42 27 87.1 470 1 NRAM\_IAHAL Q07575 influenza a  
43 27 87.1 470 1 NRAM\_IAHAL Q07576 influenza a  
44 27 87.1 470 1 NRAM\_IAHKL P08326 influenza a  
45 27 87.1 470 1 NRAM\_IAHNO Q07580 influenza a

## ALIGNMENTS

RESULT 1  
HV51\_MOUSE  
ID HV51\_MOUSE STANDARD; PRT; 118 AA.  
AC P06330;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION AC38 205.12.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=84182515; PubMed=6201362;  
RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;  
RT "A V region determinant (idiotope) expressed at high frequency in B  
lymphocytes is encoded by a large set of antibody structural genes.";  
RL EMBL J. 3:517-523(1984).  
DR PIR: A02040; MHWS38.  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; ig; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 98 V SEGMENT.  
FT DOMAIN 99 104 D SEGMENT.  
FT DOMAIN 105 118 J SEGMENT.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON\_TER 118 118  
SQ SEQUENCE 118 AA; 12934 MW; 94F7BE4C762A018 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMN 5  
|||||  
Db 31 DYMN 35

RESULT 2  
Y314\_METJA  
ID Y314\_METJA STANDARD; PRT; 263 AA.  
AC Q57762;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HYPOTHETICAL PROTEIN MJ0314.  
GN MJ0314.  
OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;  
OC Methanococcus.  
OX NCBI\_TaxID=2190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RA MEDLINE-96337999; PubMed-8688087;  
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus  
RA jannaschii";  
RA Science 273:1058-1073(1996).  
CC -1- SIMILARITY: SOME, TO M.JANNASCHII MJ0398.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U67486; AAB98310.1; -  
DR TIGR: MJ0314; -  
KW Hypothetical protein.  
SQ SEQUENCE 263 AA; 30804 MW; A7520A3BBE0CC5CD CRC64;  
  
Query Match 100.0%; Score 31; DB 1; Length 263;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYMN 5  
DB 184 DYMN 188  
  
RESULT 3  
YE13\_YEAST STANDARD; PRT; 107 AA.  
AC P39974;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE HYPOTHETICAL 12.0 KDA PROTEIN IN DLD3 5' REGION.  
GN YEL073C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C / AB972;  
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,  
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,  
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,  
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,  
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,  
RA Petef F.X., Roberts D., Sehl P., Schramm S., Shogen T., Smith V.,  
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;  
RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
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CC  
CC EMBL; U18795; AAB65014.1; -  
DR SGD; S0000799; YEL073C.  
KW Hypothetical protein.

SQ SEQUENCE 107 AA; 11960 MW; F5FBA3246A328ABF CRC64;  
  
Query Match 90.3%; Score 28; DB 1; Length 107;  
Best Local Similarity 80.0%; Pred. No. 16;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYMN 5  
DB 39 DYTN 43  
  
RESULT 4  
PHOP\_ECOLI STANDARD; PRT; 223 AA.  
ID PHOP\_ECOLI  
AC P23836;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE TRANSCRIPTIONAL REGULATORY PROTEIN PHOP.  
GN PHOP.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE-92105017; PubMed-1729240;  
RA Kasahara M., Nakata A., Shinagawa H.;  
RT "Molecular analysis of the Escherichia coli phoP-phoQ operon";  
RL J. Bacteriol. 174:492-498(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-92105016; PubMed-1530848;  
RA Groisman E.A., Heffron F., Solomon F.;  
RT "Molecular genetic analysis of the Escherichia coli phoP locus";  
RL J. Bacteriol. 174:486-491(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE-97426617; PubMed-9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shaoy Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1453-1474(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE-97061202; PubMed-8905232;  
RA Oshima T., Aliba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horiuchi T.;  
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 12.7-28.0 min region on the linkage map";  
RL DNA Res. 3:137-155(1996).  
RN [5]  
RP SEQUENCE OF 1-50 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE-92104952; PubMed-1729205;  
RA He B., Smith J.M., Zalkin H.;  
RT "Escherichia coli purB gene: cloning, nucleotide sequence, and  
RT regulation by purR";  
RL J. Bacteriol. 174:130-136(1992).  
RN [6]  
RP SEQUENCE OF 1-24 FROM N.A.  
RC STRAIN=K12;  
RX Green S.M., Drabble W.T.;

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RT Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PHOQ/PHOP
CC INVOLVED IN THE REGULATION OF ACID PHOSPHATASE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -!- PTM: PHOSPHORYLATED BY PHOQ (PROBABLE).
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90393; BAA14390.1; -
DR EMBL; M81433; AAA24377.1; -
DR EMBL; AE000213; AAC74214.1; -
DR EMBL; D90748; BAA35952.1; -
DR EMBL; D90749; BAA35961.1; -
DR EMBL; M74924; BAA92732.1; -
DR EMBL; X59307; CAA41997.1; -
DR PIR; A41965; A41965.
DR PIR; A41966; A41966.
DR PIR; S19213; S19213.
DR HSSP; Q56312; 4TMY.
DR EC02DBASE; C025.3; 6TH EDITION.
DR EcoGene; EG10731; phop.
DR InterPro; IPR001789; -.
DR InterPro; IPR001867; -.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00486; trans_reg_C; 1.
DR Sensory transduction; Phosphorylation; Transcription regulation;
KW DNA-binding; Activator.
FT MOD_RES 51 51 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 223 AA; 25535 MW; 2EFF27E3923D43BF CRC64;

Query Match 90.38; Score 28; DB 1; Length 223;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
Db 37 DYLEN 41

RESULT 5
PHOP_SALTY STANDARD; PRT; 224 AA.
AC P1A146;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VIRULENCE TRANSCRIPTIONAL REGULATORY PROTEIN PHOP.
GN PHOP.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10428;
RX MEDLINE=89296942; PubMed=2544889;
RA Miller S.I., Kukral A.M., Mekalanos J.J.;
RT "A two-component regulatory system (phoP phoQ) controls Salmonella
RT typhimurium virulence."
RL Proc. Natl. Acad. Sci. U.S.A. 86:5054-5058(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89386683; PubMed=2674945;
RA Groisman E.A., Chiao E., Lipps C.J., Heffron F.;

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RT "Salmonella typhimurium phoP virulence gene is a transcriptional
RT regulator."
RL Proc. Natl. Acad. Sci. U.S.A. 86:7077-7081(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SL1344;
RA Cano D.A., Martinez-Moya M., Casadesus J., Groisman E.A.,
RA Garcia-del Portillo F.;
RT "Attenuation of Salmonella proliferation within host cells mediated by
RT pathogen virulence regulators."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PHOQ/PHOP
CC WHICH REGULATES THE EXPRESSION OF GENES INVOLVED IN VIRULENCE AND
CC MACROPHAGE SURVIVAL OF S.TYPHIMURIUM. MAY ACTIVATE PROMOTERS FOR
CC PAG GENES.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -!- PTM: PHOSPHORYLATED BY PHOQ (PROBABLE).
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
CC -----
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CC -----
DR EMBL; M24424; AAA27188.1; -
DR EMBL; M25241; AAA27187.1; -
DR EMBL; AJ272210; CAB75591.1; -
DR PIR; A32932; RGEBFT.
DR HSSP; P03025; 1CDD.
DR StyGene; SGI0293; phop.
DR InterPro; IPR001789; -.
DR InterPro; IPR001867; -.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00486; trans_reg_C; 1.
DR Sensory transduction; Phosphorylation; Transcription regulation;
KW DNA-binding; Activator; Virulence.
FT MOD_RES 52 52 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 224 AA; 25633 MW; 3A90B2FDC328C7B2 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 224;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
Db 38 DYLEN 42

RESULT 6
CHLL_CYAPA STANDARD; PRT; 282 AA.
AC P48110;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PROTOCHLOROPHYLLIDE REDUCTASE IRON-SULFUR ATP-BINDING PROTEIN.
GN CHLL OR FRXC.
OS Cyanophora paradoxa.
OG Cyanelle.
OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
OX NCBI_TaxID=2762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LB555 / PRINGSHEIM;
RA Stirewalt V.L., Michalowski C.B., Luffelhardt W., Bohnert H.J.,
RA Bryant D.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN AN ELECTRON TRANSPORT

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CC SYSTEM USED IN CHLOROPHYLL BIOSYNTHESIS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.  
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 CC -----  
 CC EMBL; U30821; AAA81316.1; -.  
 CC HSSP; P00459; INIP.  
 CC Mendel; 7873; CYAPA:chlL;1.  
 CC InterPro; IPR000392; -.  
 CC Pfam; PF00142; fer4\_NifH; 1.  
 CC PRINTS; PR00091; NITROGNASEII.  
 CC PROSITE; PS00692; NIFH\_FRXC\_2; 1.  
 CC PROSITE; PS00746; NIFH\_FRXC\_1; 1.  
 CC Photosynthesis; Chlorophyll biosynthesis; Cyanelle; ATP-binding;  
 KW Iron-sulfur; 4Fe-4S.  
 FT NP\_BIND 7 14 ATP (POTENTIAL).  
 FT METAL 95 95 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 FT METAL 129 129 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 SQ SEQUENCE 286 AA; 30847 MW; BC5072D21AE28684 CRC64;  
 Query Match 90.3%; Score 28; DB 1; Length 282;  
 Best Local Similarity 80.0%; Pred. No. 46;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYMMN 5  
 Db 234 DYLN 238  
 RESULT 7  
 CHLL\_PLEBO STANDARD; PRT; 286 AA.  
 ID CHLL\_PLEBO  
 AC Q00237;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PROTOCHLOROPHYLLIDE REDUCTASE IRON-SULFUR ATP-BINDING PROTEIN.  
 GN CHLL OR FRXC.  
 OS Plectonema boryanum.  
 OC Bacteria; Cyanobacteria; Oscillatoriales; Plectonema.  
 OX NCBI\_TaxID=1184;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-IAM M-101;  
 RA Fujita Y., Takahashi Y., Shonai F., Ogura Y., Matsubara H.;  
 RT "Cloning, nucleotide sequences and differential expression of the nifh  
 RT and nifh-like (frxc) genes from the filamentous nitrogen-fixing  
 RT cyanobacterium Plectonema boryanum";  
 RL Plant Cell Physiol. 32:1093-1106(1991).  
 CC -!- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN AN ELECTRON TRANSPORT  
 CC SYSTEM USED IN CHLOROPHYLL BIOSYNTHESIS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.  
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 CC -----  
 CC EMBL; D00665; BAA00565.1; -.  
 CC PIR; JQ2154; JQ2154.  
 CC PIR; S36671; S36671.

DR HSSP; P00459; IN2C.  
 DR InterPro; IPR000392; -.  
 DR Pfam; PF00142; fer4\_NifH; 1.  
 DR PRINTS; PR00091; NITROGNASEII.  
 DR PROSITE; PS00692; NIFH\_FRXC\_2; 1.  
 DR PROSITE; PS00746; NIFH\_FRXC\_1; 1.  
 KW Photosynthesis; Chlorophyll biosynthesis; ATP-binding; Iron-sulfur;  
 KW 4Fe-4S.  
 FT NP\_BIND 7 14 ATP (BY SIMILARITY).  
 FT METAL 95 95 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 FT METAL 129 129 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 SQ SEQUENCE 286 AA; 31220 MW; 9E74CE7F4C47EC01 CRC64;  
 Query Match 90.3%; Score 28; DB 1; Length 286;  
 Best Local Similarity 80.0%; Pred. No. 47;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYMMN 5  
 Db 234 DYLN 238  
 RESULT 8  
 CHLL\_SYNP7 STANDARD; PRT; 286 AA.  
 ID CHLL\_SYNP7  
 AC P54207;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PROTOCHLOROPHYLLIDE REDUCTASE IRON-SULFUR ATP-BINDING PROTEIN.  
 GN CHLL OR FRXC.  
 OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OX NCBI\_TaxID=1140;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lieman-Hurwitz J., Ronen-Tarazi M., Gabai C., Hassidim M., Schwarz R.,  
 RA Kaplan A.;  
 RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN AN ELECTRON TRANSPORT  
 CC SYSTEM USED IN CHLOROPHYLL BIOSYNTHESIS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.  
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 CC -----  
 CC EMBL; X67694; CAA47923.1; -.  
 CC HSSP; P00459; IN2C.  
 CC InterPro; IPR000392; -.  
 CC Pfam; PF00142; fer4\_NifH; 1.  
 CC PRINTS; PR00091; NITROGNASEII.  
 CC PROSITE; PS00692; NIFH\_FRXC\_2; 1.  
 CC PROSITE; PS00746; NIFH\_FRXC\_1; 1.  
 KW Photosynthesis; Chlorophyll biosynthesis; ATP-binding; Iron-sulfur;  
 KW 4Fe-4S.  
 FT NP\_BIND 7 14 ATP (POTENTIAL).  
 FT METAL 95 95 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 FT METAL 129 129 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 SQ SEQUENCE 286 AA; 31117 MW; 651121F5CD60A803 CRC64;  
 Query Match 90.3%; Score 28; DB 1; Length 286;  
 Best Local Similarity 80.0%; Pred. No. 47;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYMMN 5



Db 234 DYVLN 238  
|||||  
RESULT 9  
CHLL\_SYNY3  
ID CHLL\_SYNY3 STANDARD; PRT; 288 AA.  
AC P28373; 055241; P74632;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE PROTOCHLOROPHYLLIDE REDUCTASE IRON-SULFUR ATP-BINDING PROTEIN.  
GN CHLL OR FRXC OR SLR0749.  
OS Synechocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92330029; PubMed=1368342;  
RA Ogura Y., Takemura M., Oda K., Yamato K., Ohta E., Fukuzawa H.,  
RA Ohshima K.;  
RT "Cloning and nucleotide sequence of a frxC-ORF469 gene cluster of  
RT Synechocystis PCC6803: conservation with liverwort chloroplast frxC-  
RT ORF465 and nif operon."  
RL Biosci. Biotechnol. Biochem. 56:788-793(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97061201; PubMed=8905231;  
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,  
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,  
RA Yamada M., Yasuda M., Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions."  
RL DNA Res. 3:109-136(1996).  
CC -!- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN AN ELECTRON TRANSPORT  
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.  
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CC -----  
CC EMBL; D10474; BAA01275.1;  
CC EMBL; D10474; BAA01274.1; ALT\_INIT.  
CC EMBL; D90916; BAA18745.1; ALT\_INIT.  
CC PIR; J06000; J06000.  
CC HSSP; P00459; IN2C.  
CC InterPro; IPR000392;  
CC Pfam; PF00142; fer4\_NifH; 1.  
CC PRINTS; PR00091; NITROGNASEII.  
CC PROSITE; PS00692; NIFH\_FRXC\_2; 1.  
CC PROSITE; PS00746; NIFH\_FRXC\_1; 1.  
CC Photosynthesis; Chlorophyll biosynthesis; ATP-binding; Iron-sulfur;  
KW 4Fe-4S.  
FT NP\_BIND 9 16 ATP (POTENTIAL).  
FT METAL 97 97 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
FT METAL 131 131 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
FT CONFLICT 159 159 K -> N (IN REF. 2).  
SQ SEQUENCE 288 AA; 31480 MW; 5D1D0C71029B5EFF CRC64;  
  
Query Match 90.3%; Score 28; DB 1; Length 288;  
Best Local Similarity 80.0%; Pred. No. 48;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYTMN 5  
|||||  
Db 236 DYVLN 240  
  
RESULT 10  
CHLL\_PORPU  
ID CHLL\_PORPU STANDARD; PRT; 290 AA.  
AC P51187;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE PROTOCHLOROPHYLLIDE REDUCTASE IRON-SULFUR ATP-BINDING PROTEIN.  
GN CHLL.  
OS Porphyra purpurea.  
OC Chloroplast.  
OX Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
OX NCBI\_TaxID=2787;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=AVONPORT;  
RA Reith M.E., Munholland J.;  
RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast  
RT genome."  
RL Plant Mol. Biol. Rep. 13:333-335(1995).  
CC -!- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN AN ELECTRON TRANSPORT  
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.  
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CC -----  
CC EMBL; U38804; AAC08073.1;  
CC HSSP; P00459; IN2C.  
CC Mendel; 10275; PORpu; chlL; 1.  
CC InterPro; IPR000392;  
CC Pfam; PF00142; fer4\_NifH; 1.  
CC PRINTS; PR00091; NITROGNASEII.  
CC PROSITE; PS00692; NIFH\_FRXC\_2; 1.  
CC PROSITE; PS00746; NIFH\_FRXC\_1; 1.  
CC Photosynthesis; Chlorophyll biosynthesis; Chloroplast; ATP-binding;  
KW Iron-sulfur; 4Fe-4S.  
FT NP\_BIND 7 14 ATP (POTENTIAL).  
FT METAL 95 95 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
FT METAL 129 129 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
SQ SEQUENCE 290 AA; 31690 MW; 3D265E3ADD3C9CAA CRC64;  
  
Query Match 90.3%; Score 28; DB 1; Length 290;  
Best Local Similarity 80.0%; Pred. No. 48;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYTMN 5  
|||||  
Db 234 DYVLN 238  
  
RESULT 11  
Y170\_METJA  
ID Y170\_METJA STANDARD; PRT; 350 AA.  
AC Q57634;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HYPOTHETICAL PROTEIN MJ0170.  
GN MJ0170.  
OS Methanococcus jannaschii.

```
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervilave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE UPF0003 FAMILY.
CC
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CC
CC EMBL: U67474; AAB98155.1; -.
CC TIGR: MJ0170; -.
CC InterPro: IPR001880; -.
CC Pfam: PF00924; UPF0003; 1.
CC PROSITE: PS01246; UPF0003; 1.
CC Hypothetical protein; Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 130 150 POTENTIAL.
SQ SEQUENCE 350 AA; 39953 MW; 4EA0E5025086E7DF CRC64;

Query Match 90.3%; Score 28; DB 1; Length 350;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVMN 5
DB 313 DYILN 317

RESULT 12
MURE_HELPJ
ID MURE_HELPJ STANDARD; PRT; 447 AA.
AC Q92JG6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE UDP-N-ACETYLURAMIDYL-L-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
DE (EC 6.3.2.13) (UDP-N-ACETYLURAMIDYL-L-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
DE DIAMINOPIMELATE-ADDING ENZYME) (UDP-MURNAC-TRIPETIDE SYNTHETASE).
GN MURE OR JHP1387.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
```

```
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLURAMIDYL-L-ALANYL-D-
CC GLUTAMATE + MESO-2,6-DIAMINOPIMELATE --> ADP + ORTHOPHOSPHATE
CC + UDP-N-ACETYLURAMIDYL-L-ALANYL-D-GLUTAMYL-MESO-2,6-
CC DIAMINOPIMELATE.
CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE MURCDF FAMILY.
CC
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CC
CC EMBL: AF001561; AAD06968.1; -.
CC InterPro: IPR000713; -.
CC Pfam: PF01225; Mur_ligase; 1.
CC Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
KW ATP-binding.
FT NP_BIND 74 80 ATP (POTENTIAL).
SQ SEQUENCE 447 AA; 50660 MW; 639AB9D18F3740BD CRC64;

Query Match 90.3%; Score 28; DB 1; Length 447;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVMN 5
DB 439 DYILN 443

RESULT 13
VL2_HPV07
ID VL2_HPV07 STANDARD; PRT; 456 AA.
AC P36745;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MINOR CAPSID PROTEIN L2.
GN L2.
OS Human papillomavirus type 7.
OC Viruses; GSDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX NCBI_TaxID=10620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Dellus H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC
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CC
CC EMBL: X74463; CAA52480.1; -.
CC FTR: S36588; S36588.
CC InterPro: IPR000784; -.
CC Pfam: PF00513; late-protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 456 AA; 48994 MW; 87C493D2C85E4FEB CRC64;
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Query Match 90.3%; Score 28; DB 1; Length 456;  
Best Local Similarity 80.0%; Pred. No. 78;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
| | | | |  
DB 437 DYYLN 441

RESULT 14  
YDDA\_ECOLI  
ID YDDA\_ECOLI STANDARD; PRT; 561 AA.  
AC P31826; P76133; P76876;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN POOL-HIPA  
DE INTERGENIC REGION (CDS102).  
GN YDDA.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick J.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,  
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,  
RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,  
RA Oshima T., Saito N., Sampel K., Seki Y., Sivasubraman S.,  
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,  
RA Yamamoto Y., Horiuchi T.;  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 306-561 FROM N.A.  
RC STRAIN=K12;  
RX Turlin E., Gasser F., Biville F.;  
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY  
(ABC TRANSPORTERS).  
CC  
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CC  
CC EMBL: AE000246; AAC74569.1;  
DR EMBL: X71917; CAA50732.1; ALT\_INIT.  
DR EMBL: D90791; BAA15167.1; ALT\_INIT.  
DR EMBL: D90792; BAA15170.1;  
DR PIR: S33468; S33468.  
DR EcoGene: EG11742; ydda.  
DR InterPro: IPR001617;  
DR Pfam: PF00005; ABC\_tran; 1.  
DR PROSITE: PS00211; ABC\_TRANSPORTER; 1.

KW Hypothetical protein; ATP-binding; Transport; Transmembrane.  
FT TRANSMEM 4 24 POTENTIAL.  
FT TRANSMEM 32 52 POTENTIAL.  
FT TRANSMEM 71 91 POTENTIAL.  
FT TRANSMEM 152 172 POTENTIAL.  
FT TRANSMEM 188 208 POTENTIAL.  
FT TRANSMEM 291 311 POTENTIAL.  
FT NP\_BIND 400 407 ATP (POTENTIAL).  
SQ SEQUENCE 561 AA; 64984 MW; 92B47426294413F5 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 561;  
Best Local Similarity 80.0%; Pred. No. 97;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
| | | | |  
DB 109 DYYLN 113

RESULT 15  
ILVD\_BUCAP  
ID ILVD\_BUCAP STANDARD; PRT; 617 AA.  
AC O51887;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE DIHYDROXY-ACID DEHYDRATASE (EC 4.2.1.9) (DAD).  
GN ILVD.  
OS Buchnera aphidicola (subsp. Schizaphis graminum).  
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
OX NCBI\_TaxID=98794;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98184963; PubMed=9516544;  
RA Clark M.A., Baumann L., Baumann P.;  
RT "Sequence analysis of a 34.7-kb DNA segment from the genome of  
RT Buchnera aphidicola (endosymbiont of aphids) containing groEL, dnaA,  
RT the atp operon, gldA, and rho.";  
RL Curr. Microbiol. 36:158-163(1998).  
CC -1- CATALYTIC ACTIVITY: 2,3-DIHYDROXY-3-METHYLBUTANOATE - 3-METHYL-2-  
CC OXOBUTANOATE + H(2)O.  
CC -1- COFACTOR: BINDS A 2FE-2S CLUSTER (POTENTIAL).  
CC -1- PATHWAY: FOURTH STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.  
CC -1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.  
CC  
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CC  
CC EMBL: AF008210; AAC38125.1;  
DR InterPro: IPR000581;  
DR Pfam: PF00920; ILVD\_EDD; 1.  
DR PROSITE: PS00886; ILVD\_EDD\_1; 1.  
DR PROSITE: PS00887; ILVD\_EDD\_2; 1.  
KW Branched-chain amino acid biosynthesis; Lyase; Iron-sulfur.  
FT METAL 122 122 IRON-SULFUR (2FE-2S) (POTENTIAL).  
FT METAL 195 195 IRON-SULFUR (2FE-2S) (POTENTIAL).  
SQ SEQUENCE 617 AA; 67859 MW; 59A52ECD8DFC9381 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 617;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
| | | | |  
DB 245 DYYLN 249

Fri Jun 29 08:04:44 2001

us-09-724-406-20.rsp

Page 8

Search completed: June 28, 2001, 15:54:37  
Job time: 125 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:23 ; Search time 411.58 seconds  
(without alignments)  
1.607 Million cell updates/sec

Title: US-09-724-406-20  
Perfect score: 31  
Sequence: 1 DYWN 5

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: sp.archaea.\*
- 2: sp.bacteria.\*
- 3: sp.fungi.\*
- 4: sp.human.\*
- 5: sp.invertebrate.\*
- 6: sp.mammal.\*
- 7: sp.mhc.\*
- 8: sp.organelle.\*
- 9: sp.phage.\*
- 10: sp.plant.\*
- 11: sp.rodent.\*
- 12: sp.unclassified.\*
- 13: sp.vertebrate.\*
- 14: sp.virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	370	5	O97252
2	31	100.0	672	2	O9WYE6
3	28	90.3	87	2	O9R605
4	28	90.3	87	2	O9R604
5	28	90.3	128	8	O9R604
6	28	90.3	149	2	O9R604
7	28	90.3	170	5	O9R604
8	28	90.3	221	5	O9R604
9	28	90.3	250	2	O9R604
10	28	90.3	271	2	O9R604
11	28	90.3	312	2	O9R604
12	28	90.3	327	10	O9R604
13	28	90.3	341	5	O9R604
14	28	90.3	390	2	O9R604
15	28	90.3	399	5	O9R604
16	28	90.3	405	2	O9R604
17	28	90.3	411	2	O9R604
18	28	90.3	437	10	O9R604
19	28	90.3	483	2	O9R604

20	28	90.3	488	3	P78972
21	28	90.3	499	4	Q12834
22	28	90.3	499	4	Q9UQI9
23	28	90.3	499	11	O70380
24	28	90.3	499	11	Q62623
25	28	90.3	499	11	Q9J766
26	28	90.3	507	13	O9J289
27	28	90.3	522	5	O61588
28	28	90.3	526	5	Q24044
29	28	90.3	533	1	O26418
30	28	90.3	662	5	P91331
31	28	90.3	752	13	Q9DCN6
32	28	90.3	758	6	Q28868
33	28	90.3	758	6	Q28010
34	28	90.3	772	2	Q46080
35	28	90.3	792	2	O32625
36	28	90.3	848	5	O16796
37	28	90.3	1056	5	O9VIG4
38	28	90.3	1105	5	O9VX44
39	28	90.3	1169	5	O9VX45
40	28	90.3	1212	5	O9UOL0
41	28	90.3	1306	2	O9L8Z1
42	28	90.3	1543	14	O09498
43	28	90.3	1550	14	O55601
44	28	90.3	2013	5	O96216
45	28	90.3	2380	5	O96266

ALIGNMENTS

RESULT 1  
O97252 ID O97252 PRELIMINARY; PRT; 370 AA.  
AC O97252;  
DT 01-MAY-1999 (TRENBLrel. 10, Created)  
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE PFC0310C PROTEIN.  
GN PFC0310C.  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3D7;  
RA Churcher C., Bowman S., Lawson D., Quail M., Barrell B.;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL034558; CAB39018.1;  
DR HSSP; P19245; IYF  
DR InterPro; IPR001907;  
DR Pfam; PF00574; CLP\_protease; 1.  
DR PRINTS; PR00127; CLP\_PROTEASEP.  
DR PROSITE; PS00382; CLP\_PROTEASE\_HIS; UNKNOWN\_1.  
SQ SEQUENCE 370 AA; 43321 MW; 3DE959328D14CE87 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 370;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYWN 5  
|||||  
Db 338 DYWN 342

RESULT 2  
O9WYE6 ID O9WYE6 PRELIMINARY; PRT; 672 AA.  
AC O9WYE6;  
DT 01-NOV-1999 (TRENBLrel. 12, Created)  
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ADAPTIVE RESPONSE REGULATOR PHOP (FRAGMENT).
Yersinia enterocolitica.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
NCBI_TaxID=630;
SEQUENCE FROM N.A.
MEDLINE=93146391; PubMed=1490612;
Wren B.W., Colby S.M., Cubberley R.R., Pallen M.J.;
"Generate PCR primers for the amplification of fragments from genes
encoding response regulators from a range of pathogenic bacteria.";
FEMS Microbiol. Lett. 78:287-291(1992).
InterPro; IPR001789; -.
DR Pfam; PF00072; response_reg; 1.
DR SMART; SM00448; REC; 1.
DR SEQUENCE 87 AA; 9779 MW; B72EF38907A383AB CRC64;

Query Match          90.3%; Score 28; DB 2; Length 87;
Best Local Similarity 80.0%; Pred. No. 79;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
Db 29 DYYLN 33

RESULT 5
Q9G8V4 PRELIMINARY; PRT; 128 AA.
ID Q9G8V4 AC Q9G8V4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DT SUBCINATE:CYTOCHROME C OXIDOREDUCTASE SUBUNIT 3 (EC 1.3.5.1).
DE GN SDH3.
OS Rhodomonas salina.
OG Mitochondrion.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBI_TaxID=52970;
[1]
SEQUENCE FROM N.A.
RA Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
"Algae with secondary chloroplasts have mitochondria that originate
from the host";
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF288090; AAG17743.1; -.
DR Oxidoreductase; Mitochondrion.
KW SEQUENCE 128 AA; 15436 MW; EB257D5ACA007C43 CRC64;
SEQUENCE 128 AA; 15436 MW; EB257D5ACA007C43 CRC64;

Query Match          90.3%; Score 28; DB 8; Length 128;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
Db 49 DYYLN 53

RESULT 6
Q9PQ44 PRELIMINARY; PRT; 149 AA.
ID Q9PQ44 AC Q9PQ44
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DT TYPE I RESTRICTION ENZYME S PROTEIN (FRAGMENT).
DE GN HSDS-4.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;

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OC Mycoplasmataceae; Ureaplasma.  
 RN NCBI\_TaxID=134821;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SEROVAR 3;  
 RA MEDLINE=20500219; PubMed=11048724;  
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,  
 RA Cassell G.H.;  
 RT "The complete sequence of the mucosal pathogen Ureaplasma  
 RT urealyticum";  
 RL Nature 407:757-762(2000).  
 DR EMBL; AE002141; AAF30858.1; -;  
 DR InterPro; IPR000055; -;  
 DR InterPro; IPR000267; -;  
 DR Pfam; PF01420; Methylase\_S; 1.  
 DR PROSITE; PS00144; ASN\_GLN\_ASE\_1; UNKNOWN\_1.  
 SQ SEQUENCE 149 AA; 17702 MW; 4CA516DE2DCE1382 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 149;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5  
 Db 120 DYLN 124  
 |||:|

RESULT 7  
 Q9NBF9 PRELIMINARY; PRT; 170 AA.  
 ID Q9NBF9  
 AC Q9NBF9  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).  
 GN TPI-1.  
 OS Philodina roseola.  
 OC Eukaryota; Metazoa; Rotifera; Bdelloidea; Philodinida; Philodinidae;  
 OC Philodina.  
 OX NCBI\_TaxID=96448;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=20280140; PubMed=10817991;  
 RA Welch D.M., Meselson M.;  
 RT "Evidence for the evolution of bdelloid rotifers without sexual  
 RT reproduction or genetic exchange";  
 RL Science 288:1211-1215(2000).  
 RN SEQUENCE FROM N.A.  
 RP Mark Welch D.B., Meselson M.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE - DIHYDROXY-  
 CC ACETONE PHOSPHATE (BY SIMILARITY).  
 CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: TO OTHER TRIOSEPHOSPHATE ISOMERASES.  
 DR EMBL; AF249994; AAF79171.1; -;  
 DR InterPro; IPR000652; -;  
 DR Pfam; PF00121; TIM; 1.  
 DR PROSITE; PS00171; TIM; 1.  
 KW Fatty acid biosynthesis; Gluconeogenesis; Glycolysis; Isomerase;  
 FT NON\_TER 170 170  
 FT Pentose shunt.  
 SQ SEQUENCE 170 AA; 19016 MW; 1F4B758674AB5073 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 170;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 39 DYLN 43  
 |||:|

RESULT 8  
 Q16690 PRELIMINARY; PRT; 221 AA.  
 ID Q16690  
 AC Q16690  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE K07E8.9 PROTEIN.  
 GN K07E8.9  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BRISTOL N2;  
 RC MEDLINE=94150718; PubMed=7906398;  
 RX Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Wilfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lighning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,  
 RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans";  
 RL Nature 368:32-38(1994).  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BRISTOL N2;  
 RC SEQUENCE FROM N.A.  
 RP Jones K., Kramer J.;  
 RN Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BRISTOL N2;  
 RC Waterston R.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF016678; AAB66154.1; -;  
 DR InterPro; IPR003003; -;  
 DR Pfam; PF01604; 7tm\_5; 1.  
 SQ SEQUENCE 221 AA; 24956 MW; B94C56624D5D51F3 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 221;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5  
 Db 11 DYLN 15  
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RESULT 9  
 Q06956 PRELIMINARY; PRT; 250 AA.  
 ID Q06956  
 AC Q06956  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE RFBI PROTEIN.  
 GN RFBI.  
 OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=666;  
 RN SEQUENCE FROM N.A.  
 RP

RC STRAIN-017 / BIOTYPE EL TOR / SEROTYPE OGAWA;  
RX MEDLINE=92212870; PubMed=1372980;  
RA Stroher U.H., Karageorgos L.E., Morona R., Manning P.A.;  
RT "Serotype conversion in *Vibrio cholerae* O1";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2566-2570(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=017;  
RX MEDLINE=95309704; PubMed=7540582;  
RA Manning P.A., Stroher U.H., Karageorgos L.E., Morona R.;  
RT "Putative O-antigen transport genes within the rfb region of *Vibrio*  
RT *cholerae* O1 are homologous to those for capsule transport.";  
RL Gene 158:1-7(1995).  
CC -1- FUNCTION: MAY PLAY A ROLE IN LIPOPOLYSACCHARIDE TRANSPORT.  
DR EMBL; X59554; CAA42140.1; -;  
DR InterPro; IPR001687; -;  
DR InterPro; IPR003439; -;  
DR InterPro; IPR003593; -;  
DR Pfam; PF000005; ABC\_tran; 1.  
DR SMART; SM00382; AAA; 1.  
KW Polysaccharide transport; Transport.  
SQ SEQUENCE 250 AA; 27563 MW; 9DBD9499D57D3677 CRC64;  
  
Query Match 90.3%; Score 28; DB 2; Length 250;  
Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYYMN 5  
Db 242 DYLN 246  
|||:  
RESULT 10  
Q9KVA2 PRELIMINARY; PRT; 271 AA.  
ID Q9KVA2  
AC Q9KVA2;  
DT 01-OCT-2000 (TREMREL. 15, Created)  
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE LIPOPOLYSACCHARIDE/O-ANTIGEN TRANSPORT PROTEIN.  
GN VC0247.  
OS *Vibrio cholerae*.  
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EL TOR N16961 / SEROTYPE O1;  
RX MEDLINE=20406833; PubMed=10952301;  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Peterson J.D., Umayam L.A.,  
RA Dodson R.J., Haft D.H., Hickey E.K., Tettelin H., Richardson D.,  
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,  
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
RA Fraser C.M.;  
RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*  
RT *cholerae*";  
RL Nature 406:477-483(2000).  
DR EMBL; AE004113; AAF93423.1; -;  
DR TIGR; VC0247; -;  
DR InterPro; IPR001687; -;  
DR InterPro; IPR003439; -;  
DR InterPro; IPR003593; -;  
DR Pfam; PF000005; ABC\_tran; 1.  
DR SMART; SM00382; AAA; 1.  
SQ SEQUENCE 271 AA; 29959 MW; DDB640A1E831AB93 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 271;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
Db 263 DYLN 267  
|||:  
RESULT 11  
O86289 PRELIMINARY; PRT; 312 AA.  
ID O86289  
AC O86289;  
DT 01-NOV-1998 (TREMREL. 08, Created)  
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)  
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)  
DE REGULATORY PROTEIN.  
GN CLYR.  
OS *Leuconostoc mesenteroides*.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;  
OC *Leuconostoc*.  
OX NCBI\_TaxID=1245;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=195;  
RX MEDLINE=98117048; PubMed=9457870;  
RA Bekal S., van Beeumen J., Samyn B., Garmyn D., Henini S., Divies C.,  
RA Prevost H.;  
RT "Purification of *Leuconostoc mesenteroides* citrate lyase and cloning  
RT and characterization of the citCDEFG gene cluster.";  
RL J. Bacteriol. 180:647-654(1998).  
DR EMBL; Y10621; CAA71637.1; -;  
SQ SEQUENCE 312 AA; 35102 MW; 8DB478F8BD401461 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 312;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
Db 13 DYLN 17  
|||:  
RESULT 12  
Q9LSS4 PRELIMINARY; PRT; 327 AA.  
ID Q9LSS4  
AC Q9LSS4;  
DT 01-OCT-2000 (TREMREL. 15, Created)  
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE SIMILARITY TO SENESCENCE-ASSOCIATED PROTEIN.  
OS *Arabidopsis thaliana* (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
RA Tabata S.;  
RT "Structural analysis of *Arabidopsis thaliana* chromosome 5. XI.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB026632; BAA97503.1; -;  
DR InterPro; IPR000301; -;  
DR Pfam; PF00335; transmembrane4; 1.  
DR PRINTS; PR00259; TMFOUR.  
SQ SEQUENCE 327 AA; 37178 MW; 505A06D6A2D39F8D CRC64;

Query Match 90.3%; Score 28; DB 10; Length 327;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
|||:  
RESULT 13  
Q9LSS4 PRELIMINARY; PRT; 327 AA.  
ID Q9LSS4  
AC Q9LSS4;  
DT 01-OCT-2000 (TREMREL. 15, Created)  
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE SIMILARITY TO SENESCENCE-ASSOCIATED PROTEIN.  
OS *Arabidopsis thaliana* (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
RA Tabata S.;  
RT "Structural analysis of *Arabidopsis thaliana* chromosome 5. XI.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB026632; BAA97503.1; -;  
DR InterPro; IPR000301; -;  
DR Pfam; PF00335; transmembrane4; 1.  
DR PRINTS; PR00259; TMFOUR.  
SQ SEQUENCE 327 AA; 37178 MW; 505A06D6A2D39F8D CRC64;

Query Match 90.3%; Score 28; DB 10; Length 327;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5  
|||:  
RESULT 13  
Q9LSS4 PRELIMINARY; PRT; 327 AA.  
ID Q9LSS4  
AC Q9LSS4;  
DT 01-OCT-2000 (TREMREL. 15, Created)  
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE SIMILARITY TO SENESCENCE-ASSOCIATED PROTEIN.  
OS *Arabidopsis thaliana* (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
RA Tabata S.;  
RT "Structural analysis of *Arabidopsis thaliana* chromosome 5. XI.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB026632; BAA97503.1; -;  
DR InterPro; IPR000301; -;  
DR Pfam; PF00335; transmembrane4; 1.  
DR PRINTS; PR00259; TMFOUR.  
SQ SEQUENCE 327 AA; 37178 MW; 505A06D6A2D39F8D CRC64;



Db 112 DYVLN 116

## RESULT 13

ID O18100 PRELIMINARY; PRT; 341 AA.  
 AC O18100;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE T21B4.6 PROTEIN.  
 GN T21B4.6.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Smye R.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Korshaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL; Z81124; CAB03372.1; -.  
 DR InterPro; IPR000168; -.  
 DR InterPro; IPR003003; -.  
 DR Pfam; PF01604; 7tm\_5; 1.  
 SQ SEQUENCE 341 AA; 38576 MW; A03E40826370CD5 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 341;  
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 5 DYVLN 9

## RESULT 14

ID Q9ZMH6 PRELIMINARY; PRT; 390 AA.  
 AC Q9ZMH6;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE TYPE II DNA MODIFICATION ENZYME (METHYLTRANSFERASE).  
 GN JHP0244.  
 OS Helicobacter pylori J99 (Campylobacter pylori J99).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 OC Helicobacter.  
 OX NCBI\_TaxID=85963;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99120557; PubMed=9923682;  
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.;

RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen Helicobacter pylori.";  
 RL Nature 397:176-180(1999).  
 DR EMBL; AE001462; RAD05820.1; -.  
 DR InterPro; IPR001091; -.  
 DR InterPro; IPR002052; -.  
 DR InterPro; IPR002295; -.  
 DR InterPro; IPR002941; -.  
 DR Pfam; PF01555; N6\_N4\_Mtase; 1.  
 DR PRINTS; PR00506; D21N6MTFRASE.  
 DR PRINTS; PR00508; S21N4MTFRASE.  
 DR PROSITE; PS00092; N6\_MTASE; UNKNOWN\_1.  
 SQ SEQUENCE 390 AA; 45410 MW; 2274550598A1256C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 390;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 328 DYVLN 332

## RESULT 15

ID O17131 PRELIMINARY; PRT; 399 AA.  
 AC O17131;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE F31F4.12 PROTEIN.  
 GN F31F4.12.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Blanchard M., Kramer J., Elliott G., Twyman B.;  
 RT "The sequence of C. elegans cosmid F31F4.";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF024503; AAG24095.1; -.  
 DR InterPro; IPR000536; -.  
 DR InterPro; IPR001628; -.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR SMART; SM00430; HOLI; 1.  
 SQ SEQUENCE 399 AA; 46884 MW; D3763348D9CEC734 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 399;  
 Best Local Similarity 80.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 338 DYVLN 342

Search completed: June 28, 2001, 16:08:24  
Job time: 952 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:37 ; Search time 362.28 Seconds  
(without alignments)  
3.179 Million cell updates/sec

Title: US-09-724-406-22  
Perfect score: 97  
Sequence: 1 FIRNKANGYTFESASVMG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	85.6	124	17 AAR90831	2B5 heavy chain va
2	82	84.5	124	18 AAW01594	Lead binding MAb 2
3	82	84.5	359	20 AAY29913	Human MCP-3 and mu
4	82	84.5	361	20 AAY29911	Human IP-10 and mu
5	82	84.5	374	20 AAY29916	Artificial synthe
6	81	83.5	140	13 AAR20790	Unprocessed variab
7	81	83.5	141	13 AAR30431	A5B7 antibody heav
8	81	83.5	146	13 AAR20793	CDR-grafted, human
9	81	83.5	146	13 AAR22373	CDR-grafted, human
10	81	83.5	146	13 AAR26150	A5B7 gH-2 antibody
11	81	83.5	146	13 AAR26151	A5B7 gH-2 antibody

12	81	83.5	250	17 AAW06179	Humanised A5B57 Fd
13	81	83.5	250	17 AAW06177	Murine A5B57 Fd fr
14	81	83.5	473	18 AAW41415	Human B7.1-murine
15	81	83.5	643	20 AAW82739	Clone PNG4/A5B7VH-
16	81	83.5	647	20 AAW82747	Plasmid pUC19/muA5
17	80	82.5	115	16 AAR82825	Variable heavy reg
18	80	82.5	129	21 AAY43866	Heavy chain (VH) g
19	80	82.5	142	16 AAR92828	Cl79Fv-pp variable
20	80	82.5	392	16 AAR82835	scFv-PP. Syntheti
21	79	81.4	19	16 AAR74934	H-CDR-2 of anti-id
22	79	81.4	122	16 AAR74942	Immunoglobulin hea
23	79	81.4	138	16 AAR74963	Anti-idiotypic anti
24	77	79.4	249	13 AAR21262	pSCFVNQ11 encoding
25	76	78.4	141	17 AAR92761	Human/murine chima
26	76	78.4	141	17 AAR92762	Human/murine chima
27	76	78.4	141	17 AAR92763	Human/murine chima
28	76	78.4	141	17 AAR92764	Human/murine chima
29	76	78.4	141	17 AAR92765	Human/murine chima
30	76	78.4	141	17 AAR92766	Human/murine chima
31	76	78.4	141	17 AAR92767	Human/murine chima
32	76	78.4	141	17 AAR92768	Human/murine chima
33	76	78.4	141	17 AAR92769	Human/murine chima
34	75	77.3	19	16 AAR74933	Murine anti-human
35	75	77.3	122	16 AAR74941	H-CDR-2 of anti-id
36	75	77.3	146	16 AAR74962	Immunoglobulin hea
37	73	75.3	19	18 AAW23392	Anti-idiotypic anti
38	73	75.3	100	21 AAB40059	Mutant 3 of the CD
39	73	75.3	100	21 AAB40070	Anti-hiL12 antibod
40	73	75.3	100	21 AAB40071	Anti-hiL12 antibod
41	72	74.2	19	18 AAW37006	Complementarity de
42	72	74.2	19	21 AAY51371	Mouse monoclonal a
43	72	74.2	119	11 AAR07316	VH domain of antib
44	72	74.2	119	15 AAR47221	Antibody heavy cha
45	72	74.2	119	17 AAW14484	Monoclonal antibod

ALIGNMENTS

RESULT 1  
AAR90831  
ID AAR90831 standard; Protein; 124 AA.  
XX  
AC AAR90831;  
XX  
DT 25-JUN-1996 (first entry)  
XX  
DE 2B5 heavy chain variable region from pCIB4615.  
XX  
delta endotoxin; Bacillus thuringiensis; western corn rootworm;  
KW WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;  
KW antibody.  
XX  
OS Insecta sp.  
XX  
PN WO9600783-A1.  
XX  
PD 11-JAN-1996.  
XX  
PF 20-JUN-1995; 95WO-IB00497.  
XX  
PR 28-JUN-1994; 94US-0267641.  
XX  
PA (CIBA ) CIBA GEIGY AG.  
XX  
PI Carozzi NB, Kozziel MG;  
XX  
DR WPI; 1996-077494/08.  
XX  
N-PSDB; AAT15727.  
XX  
PT New monoclonal antibodies which bind insect gut proteins - used  
PT partic. with toxin moieties for the control of insect pests, partic.  
PT in plants

CC e.g. aqueous liquid systems, in biological or environmental systems or  
CC in such compositions as perfumes, cosmetics, pharmaceuticals, health  
CC care products, skin treatment products, pesticides, herbicides,  
CC solvents used in the production of semi-conductor and integrated  
CC circuit components and production materials for electronic components.  
CC The products can provide for applications involving minute amounts of  
CC specific heavy metals.  
XX  
SQ Sequence 124 AA;  
  
Query Match 84.5%; Score 82; DB 18; Length 124;  
Best Local Similarity 88.9%; Pred. No. 7.1e-06;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 IRNKANGYTFESASVWG 19  
|||||:|||||  
DB 51 irnkangytfesavskg 68  
  
RESULT 3  
AAI29913  
ID AAY29913 standard; Protein; 359 AA.  
XX  
XX AC AAY29913;  
XX 17-NOV-1999 (first entry)  
XX Human MCP-3 and murine scFv38 fusion protein.  
XX  
XX Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
KW Immune response; HIV; infection.  
XX Homo sapiens.  
OS Mus sp.  
OS Synthetic.  
XX WO9946392-A1.  
XX  
XX 16-SEP-1999.  
XX  
XX 12-MAR-1999; 99WO-US05345.  
XX  
XX 12-MAR-1998; 98US-0077745.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Kwak LW, Biragyn A;  
PI WPI; 1999-551418/46.  
XX  
XX New fusion polypeptides comprising a chemokine and a tumour antigen or  
PT HIV antigen, used for treating cancers or treating or preventing HIV  
PT infection  
XX  
XX Disclosure; Page 118-119; 142pp; English.  
XX  
XX The present invention describes fusion proteins comprising a chemokine  
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins  
CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human  
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;  
CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human  
CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and  
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV  
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can  
CC be used for producing an immune response, e.g. an effector T cell immune  
CC response. They can also be used for treating cancer or treating or  
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences  
CC can be used in vitro diagnostic assays, as well as in screening assays  
CC for identifying unknown tumour antigen epitopes and fine mapping of  
CC tumour antigen epitopes. The present sequence represents a fusion protein  
CC from the present invention.  
XX

XX  
PS Claim 8; Page 54-55; 106pp; English.  
XX  
CC AAR90829-39 are monoclonal antibodies or a binding fragments produced by  
CC using insect guts, partic. insect brush border membranes (BBMs), esp.  
CC corn rootworm, as antigen; immunising a donor animal with the antigen;  
CC isolating immunocompetent B cells from the immunised animal; fusing B  
CC cells with a tumour cell line; isolating the fused cells, culturing them  
CC and cloning positive hybrid cells; and screening the hybrid cells for  
CC prodn. of the required MABs. The MABs bind to the gut of a target insect  
CC but do not bind to mammalian BBMs. The DNA sequence can be operably  
CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,  
CC Pseudomonas exotoxin and phytolectin, etc... The Abs are useful for  
CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and  
CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.  
CC maize.  
XX  
SQ Sequence 124 AA;  
  
Query Match 85.6%; Score 83; DB 17; Length 124;  
Best Local Similarity 84.2%; Pred. No. 4.9e-06;  
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 FIRNKANGYTFESASVWG 19  
|||||:|||||  
DB 50 firnkangytfesavskg 68  
  
RESULT 2  
AAW01594  
ID AAW01594 standard; Protein; 124 AA.  
XX  
XX AAW01594;  
XX 22-AUG-1997 (first entry)  
XX Lead binding MAB 2E7 heavy chain variable region.  
XX  
XX Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;  
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;  
KW heavy metal.  
XX Mus musculus.  
XX WO9639518-A1.  
XX  
XX 12-DEC-1996.  
XX  
XX 05-JUN-1996; 96WO-US09258.  
XX  
XX 10-OCT-1995; 95US-0541373.  
XX 05-JUN-1995; 95US-0462798.  
XX (BION-) BIONEERASKA INC.  
XX  
XX Lopez O, Murray PJ, Wylie DE;  
PI WPI; 1997-043140/04.  
XX N-PSDB; AAT58268.  
XX  
XX DNA encoding heavy metal binding polypeptide sequences - used for  
PT detecting, removing, adding or neutralising heavy metals, such as  
PT lead cations  
XX  
XX Claim 12; Page 91; 125pp; English.  
XX  
XX The present sequence represents the heavy chain variable region for  
CC monoclonal antibody (MAB) 2E7, which immunoreacts with a lead cation.  
CC The sequence was derived from RNA isolated from mouse hybridoma cells.  
CC The protein can be used for binding heavy metals, such as lead cations.  
CC It can be used for detecting, removing, adding or neutralising the  
CC heavy metals in biological and inanimate systems. It can be used in

SQ Sequence 359 AA;

Query Match 84.5%; Score 82; DB 20; Length 359;  
 Best Local Similarity 88.9%; Pred. No. 2.4e-05;  
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTFESASVMG 19  
 |||||:|||||  
 Db 140 lrnkangytteysasvkg 157

## RESULT 4

AAAY29911  
 ID AAY29911 standard; Protein; 361 AA.

AC AAY29911;

DT 17-NOV-1999 (first entry)

DE Human IP-10 and murine scFv38 fusion protein.

KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
 KW immune response; HIV; infection.

OS Homo sapiens.

OS Mus sp.

OS Synthetic.

PN WO9946392-A1.

PD 16-SEP-1999.

XX 12-MAR-1999; 99WO-US05345.

XX 12-MAR-1998; 98US-0077745.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Kwak LW, Biragyn A;

XX WPI; 1999-551418/46.

XX New fusion polypeptides comprising a chemokine and a tumour antigen or  
 PT HIV antigen, used for treating cancers or treating or preventing HIV  
 PT infection -

XX Disclosure; Page 115-116; 142pp; English.

XX The present invention describes fusion proteins comprising a chemokine  
 CC and a tumour antigen or HIV antigen. Specifically claimed fusion  
 CC proteins comprise: (1) human monocyte chemoattractant protein-3 (MCP-3) and human  
 CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human  
 CC (3) human macrophage-derived chemokine (MDC) and human Muc-1;  
 CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and  
 CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV  
 CC gp120. The fusion proteins, and nucleotide sequences encoding them, can  
 CC be used for producing an immune response, e.g. an effector T cell immune  
 CC response. They can also be used for treating cancer or treating or  
 CC preventing HIV infection. The fusion proteins and/or nucleotide sequences  
 CC can be used in in vitro diagnostic assays, as well as in screening assays  
 CC for identifying unknown tumour antigen epitopes and fine mapping of  
 CC tumour antigen epitopes. The present sequence represents a fusion protein  
 CC from the present invention.

XX Sequence 361 AA;

Query Match 84.5%; Score 82; DB 20; Length 361;  
 Best Local Similarity 88.9%; Pred. No. 2.5e-05;  
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTFESASVMG 19

Db 142 lrnkangytteysasvkg 159  
 |||||:|||||

## RESULT 5

ID AAY29916 standard; Protein; 374 AA.

AC AAY29916;

DT 17-NOV-1999 (first entry)

DE Artificial synthetic construct protein SEQ ID NO:15.

XX Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
 KW immune response; HIV; infection.

OS Synthetic.

PN WO9946392-A1.

PD 16-SEP-1999.

XX 12-MAR-1999; 99WO-US05345.

XX 12-MAR-1998; 98US-0077745.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Kwak LW, Biragyn A;

XX WPI; 1999-551413/46.

XX New fusion polypeptides comprising a chemokine and a tumour antigen or  
 PT HIV antigen, used for treating cancers or treating or preventing HIV  
 PT infection -

XX Disclosure; Page 117-118; 142pp; English.

XX The present invention describes fusion proteins comprising a chemokine  
 CC and a tumour antigen or HIV antigen. Specifically claimed fusion  
 CC proteins comprise: (1) human monocyte chemoattractant protein-3 (MCP-3) and  
 CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human  
 CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)  
 CC human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human  
 CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and  
 CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,  
 CC can be used for producing an immune response, e.g. an effector T cell  
 CC immune response. They can also be used for treating cancer or treating  
 CC or preventing HIV infection. The fusion proteins and/or nucleotide  
 CC sequences can be used in in vitro diagnostic assays, as well as in  
 CC screening assays for identifying unknown tumour antigen epitopes and fine  
 CC mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are  
 CC sequences given in the SEQ ID LISTING in the present invention but which  
 CC are not mentioned further within the specification.

XX Sequence 374 AA;

Query Match 84.5%; Score 82; DB 20; Length 374;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-05;  
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTFESASVMG 19

Db 265 lrnkangytteysasvkg 282  
 |||||:|||||

## RESULT 6

AAAR20790  
 ID AAR20790 standard; Protein; 140 AA.

XX AAR20790;

XX 19-MAY-1992 (first entry)  
DT  
XX Unprocessed variable region of heavy chain of A5B7 antibody.  
DE  
XX murine monoclonal antibody; MAB; VH domain; humanised antibody; CEA;  
KW complementarity determining region.  
XX Mus musculus.  
OS  
XX  
FH Key Location/Qualifiers  
FT Cleavage-site 19..20 /note= "putative signal peptide cleavage site"  
FT  
XX  
PN WO9201059-A.  
XX  
PD 23-JAN-1992.  
XX  
PF 05-JUL-1991; 91WO-GB01108.  
XX  
PR 05-JUL-1991; 91WO-GB01108.  
PR 05-JUL-1990; 90GB-0014932.  
PR 21-DEC-1990; 90WO-GB02017.  
XX  
PA (CELL-) CELLTECH LTD.  
XX  
PI Adair JR, Bodmer MW, Mountain A, Owens RJ;  
XX  
DR WPI; 1992-056874/07.  
DR N-PSDB; AAQ20984.  
XX  
PT New CDR-grafted anti carcinoembryonic antigen antibodies - useful  
PT in therapy and diagnosis of carcinoma  
XX  
PS Example 1; Fig 1; 70pp; English.  
XX  
CC The A5B7 MAB is a mouse MAB of the type IgG1-kappa raised against  
CC CEA which had been denatured by heating to 85 degrees C for 35  
CC minutes. The MAB has been extensively studied by Harwood et al.  
CC (Br. J. Cancer, 54, 75-82, 1986). A cDNA library was prepared from  
CC polyA RNA isolated from the A5B7 hybridoma cell line. A probe  
CC complementary to mouse heavy chain constant region was used to  
CC identify clone pBGI containing the complete leader, variable and  
CC constant regions of the heavy chain. The amino acid sequence  
CC predicted from the sequence encoding the unprocessed variable  
CC region is given here.  
XX  
XX Sequence 140 AA;  
SQ  
Query Match 83.5%; Score 81; DB 13; Length 140;  
Best Local Similarity 84.2%; Pred. No. 1.2e-05;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FIRNKANGYTTFFSASVMG 19  
Db 69 fignkangytteysasvkg 87  
RESULT 7  
AAR30431  
ID AAR30431 standard; Protein; 141 AA.  
XX  
AC AAR30431;  
XX  
DT 03-FEB-1993 (first entry)  
DE  
XX A5B7 antibody heavy chain sequence.  
XX  
KW humanised antibody; chimaeric; carcino-embryonic antigen; therapy;  
KW diagnosis; carcinomas; CDR; IgG; human; murine; ss.  
XX  
OS Chimaeric.

XX WO9201059-A.  
PN  
XX 23-JAN-1992.  
PD  
XX 05-JUL-1991; 91WO-GB01108.  
PF  
XX 05-JUL-1991; 91WO-GB01108.  
PR 05-JUL-1990; 90GB-0014932.  
PR 21-DEC-1990; 90WO-GB02017.  
XX  
PA (CELL-) CELLTECH LTD.  
XX  
PI Adair JR, Bodmer MW, Mountain A, Owens RJ;  
XX  
DR WPI; 1992-284316/34.  
DR N-PSDB; AAQ27351.  
XX  
PT Humanised antibody molecules - comprising murine and human regions,  
PT specific for carcino-embryonic antigen, useful for diagnosis and  
PT therapy  
XX  
XX Example 1; Figure 1; 71pp; English.  
PS  
CC This sequence represents the A5B7 monoclonal antibody heavy chain.  
CC It was decoded from the cDNA (AAQ27351). Sequence analysis confirmed  
CC A5B7 to be an IgG1 K antibody.  
XX  
XX Sequence 141 AA;  
SQ  
Query Match 83.5%; Score 81; DB 13; Length 141;  
Best Local Similarity 84.2%; Pred. No. 1.2e-05;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FIRNKANGYTTFFSASVMG 19  
Db 69 fignkangytteysasvkg 87  
RESULT 8  
AAR20793  
ID AAR20793 standard; Protein; 146 AA.  
XX  
AC AAR20793;  
XX  
DT 19-MAY-1992 (first entry)  
DE  
XX CDR-grafted, humanised heavy chain gH1.  
XX  
KW murine monoclonal antibody; MAB; A5B7; humanised antibody; CEA;  
KW complementarity determining region.  
XX  
OS Homo sapiens.  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19 /label= signal  
FT Protein 20..146 /label= VH  
FT /note= "human LAY framework with A5B7 CDRs"  
FT Region 45..54 /label= CDR1  
FT /note= "murine residues"  
FT Region 69..87 /label= CDR2  
FT /note= "murine residues"  
FT Region 120..129 /label= CDR3  
FT /note= "murine residues"  
FT Misc-difference 20 /note= "murine residue"  
FT

FT Misc-difference 67..68 /note= "murine residues"  
 FT FT Misc-difference 94..95 /note= "murine residues"  
 FT FT Misc-difference 98 /note= "murine residue"  
 FT FT Misc-difference 118 /note= "murine residue"  
 XX XX  
 PN WO9201059-A.  
 XX XX  
 XX PD 23-JAN-1992.  
 XX XX  
 XX PF 05-JUL-1991; 91WO-GB01108.  
 XX XX  
 PR 05-JUL-1991; 91WO-GB01108.  
 PR 05-JUL-1990; 90GB-0014932.  
 PR 21-DEC-1990; 90WO-GB02017.  
 XX XX  
 PA (CELL-) CELLTech LTD.  
 XX XX  
 XX PI Adair JR, Bodmer MW, Mountain A, Owens RJ;  
 XX XX  
 DR WPI; 1992-056874/07.  
 DR N-PSDB; AAQ20987.  
 XX XX  
 XX PT New CDR-grafted anti carcinoembryonic antigen antibodies - useful  
 XX PT in therapy and diagnosis of carcinoma  
 XX PS Claim 14; Fig 10; 70pp; English.  
 XX CC This heavy chain sequence comprises a human framework (i.e. the LAY  
 CC region) which contains murine sequences (from the murine anti-CEA  
 CC A5B7 Mab) in the CDRs and at other positions predicted to be  
 CC important for antigen-binding and at which human and A5B7 sequences  
 CC differ. (See AAQ20984 for A5B7 heavy chain coding sequence).  
 XX XX  
 SQ Sequence 146 AA;

Query Match 83.5%; Score 81; DB 13; Length 146;  
 Best Local Similarity 84.2%; Pred. No. 1.2e-05;  
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVMG 19  
 || |||||:|||||  
 Db 69 fignkangytfesavskg 87

RESULT 9  
 AAR22373  
 ID AAR22373 standard; Protein; 146 AA.  
 XX AC AAR22373;  
 XX XX  
 DT 19-MAY-1992 (first entry)  
 XX XX  
 DE CDR-grafted, humanised heavy chain gH2.  
 XX XX  
 KW murine monoclonal antibody; Mab; A5B7; humanised antibody; CEA;  
 KW complementarity determining region.  
 XX XX  
 OS Homo sapiens.  
 OS Mus musculus.

Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /label= signal  
 FT 20..146  
 FT /label= VH  
 FT /note= "human LAY framework with A5B7 CDRs"  
 FT 45..54  
 FT /label= CDR1

FT Region /note= "murine residues"  
 FT 59..87  
 FT /label= CDR2  
 FT /note= "murine residues"  
 FT 120..129  
 FT /label= CDR3  
 FT /note= "murine residues"  
 FT Misc-difference 20 /note= "murine residue"  
 FT Misc-difference 67..68 /note= "murine residues"  
 FT Misc-difference 94..95 /note= "murine residues"  
 FT Misc-difference 98 /note= "murine residues"  
 FT Misc-difference 106 /note= "murine residue"  
 FT Misc-difference 111 /note= "murine residue"  
 FT Misc-difference 118 /note= "murine residue"  
 FT XX  
 PN WO9201059-A.  
 XX XX  
 XX PD 23-JAN-1992.  
 XX XX  
 XX PF 05-JUL-1991; 91WO-GB01108.  
 XX XX  
 PR 05-JUL-1991; 91WO-GB01108.  
 PR 05-JUL-1990; 90GB-0014932.  
 PR 21-DEC-1990; 90WO-GB02017.  
 XX XX  
 PA (CELL-) CELLTech LTD.  
 XX XX  
 XX PI Adair JR, Bodmer MW, Mountain A, Owens RJ;  
 XX XX  
 DR WPI; 1992-056874/07.  
 DR N-PSDB; AAQ20988.  
 XX XX  
 XX PT New CDR-grafted anti carcinoembryonic antigen antibodies - useful  
 XX PT in therapy and diagnosis of carcinoma  
 XX PS Claim 14; Fig 11; 70pp; English.  
 XX CC This heavy chain sequence comprises a human framework (i.e. the LAY  
 CC region) which contains murine sequences (from the murine anti-CEA  
 CC A5B7 Mab) in the CDRs and at other positions predicted to be  
 CC important for antigen-binding and at which human and A5B7 sequences  
 CC differ. (See AAQ20984 for A5B7 heavy chain coding sequence).  
 XX XX  
 SQ Sequence 146 AA;

Query Match 83.5%; Score 81; DB 13; Length 146;  
 Best Local Similarity 84.2%; Pred. No. 1.2e-05;  
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVMG 19  
 || |||||:|||||  
 Db 69 fignkangytfesavskg 87

RESULT 10  
 AAR26150  
 ID AAR26150 standard; Protein; 146 AA.  
 XX AC AAR26150;  
 XX XX

DT 03-FEB-1993 (first entry)  
 XX XX  
 DE A5B7 gH-2 antibody grafted heavy chain.  
 XX XX  
 KW humanised antibody; chimaeric; carcino-embryonic antigen; therapy;

•

Region 26..35

[illegible]



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XX PR 16-AUG-1995; 95GB-0016810.
XX PR 23-DEC-1994; 94GB-0026192.
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Blakey DC, Boyle FT, Davies DH, Eggelte HJ, Heaton DW;
XX PI Hennem JF, Hennequin LFA, Marsham PR, Rabin BR, Slater AM;
XX PI Tarragona-Fiola A, Taylorson CJ;
XX
XX DR WPI; 1996-321650/32.
XX DR N-PSDB; AAT42509.
XX
XX PT Two component system for anti-tumour therapy - comprising targeting
XX PT moiety linked to mutated enzyme which can transform an
XX PT anti-neoplastic prodrug
XX
XX PS Example 6; Page 121-122; 182pp; English.
XX
XX CC A two-component system for anti-tumour therapy comprises a targeting
XX CC moiety linked to a mutated enzyme which can transform an anti-neoplastic
XX CC prodrug. The system is based on antibody directed enzyme prodrug therapy
XX CC (ADEPT) using a non-naturally occurring mutant form of a host enzyme,
XX CC pref. human pancreatic ribonuclease (HP-RNase), (see AAT42478-83). The
XX CC targeting moiety can be an antibody, in partic. murine monoclonal
XX CC antibody A5B7 (which binds to human carcinoembryonic antigen). A5B7 is
XX CC suitable for targeting colorectal carcinoma. Fragments, esp. F(ab')2,
XX CC of the antibody can be conjugated to HP-RNase. A5B7 Fd and L chain
XX CC fragments were isolated by PCR using cDNA isolated from A5B7 hybridoma
XX CC cells. The present sequence is that of a humanised A5B7 Fd fragment.
XX
XX SQ Sequence 250 AA;
XX
XX Query Match 83.5%; Score 81; DB 17; Length 250;
XX Best Local Similarity 84.2%; Pred. No. 2.3e-05;
XX Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTTTFSASVMG 19
Db 69 fignkangytteysavskg 87
|| |||||:|||||
|| |||||:|||||

RESULT 13
AAW06177
ID AAW06177 standard; Protein; 250 AA.
XX
XX AC AAW06177;
XX
XX DT 17-FEB-1997 (first entry)
XX
XX DE Murine A5B57 Fd fragment.
XX
XX KW ribonuclease; human; bovine; pancreatic; anti-tumour therapy; ADEPT;
XX KW mustard-ribonucleotide; antibody directed enzyme prodrug therapy;
XX KW anti-neoplastic; prodrug; reverse polarity; ion pair interaction;
XX KW reduced immunogenicity; non-selective triggering; primer;
XX KW polymerase chain reaction; PCR; HP-RNase; Fd; F(ab')2.
XX
XX OS Synthetic.
XX
XX PN W09620011-A1.
XX
XX PD 04-JUL-1996.
XX
XX PF 21-DEC-1995; 95WO-G802991.
XX
XX PR 16-AUG-1995; 95GB-0016810.
XX PR 23-DEC-1994; 94GB-0026192.
XX
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Blakey DC, Boyle FT, Davies DH, Eggelte HJ, Heaton DW;
XX
XX Hennem JF, Hennequin LFA, Marsham PR, Rabin BR, Slater AM;
XX Tarragona-Fiola A, Taylorson CJ;
XX
XX WPI; 1996-321650/32.
XX N-PSDB; AAT42509.
XX
XX Two component system for anti-tumour therapy - comprising targeting
XX moiety linked to mutated enzyme which can transform an
XX anti-neoplastic prodrug
XX
XX Example 6; Page 118-119; 182pp; English.
XX
XX A two-component system for anti-tumour therapy comprises a targeting
XX moiety linked to a mutated enzyme which can transform an anti-neoplastic
XX prodrug. The system is based on antibody directed enzyme prodrug therapy
XX (ADEPT) using a non-naturally occurring mutant form of a host enzyme,
XX pref. human pancreatic ribonuclease (HP-RNase), (see AAT42478-83). The
XX targeting moiety can be an antibody, in partic. murine monoclonal
XX antibody A5B7 (which binds to human carcinoembryonic antigen). A5B7 is
XX suitable for targeting colorectal carcinoma. Fragments, esp. F(ab')2,
XX of the antibody can be conjugated to HP-RNase. A5B7 Fd and L chain
XX fragments were isolated by PCR using cDNA isolated from A5B7 hybridoma
XX cells. The present sequence is that of the murine A5B7 Fd fragment.
XX
XX Sequence 250 AA;
XX
XX Query Match 83.5%; Score 81; DB 17; Length 250;
XX Best Local Similarity 84.2%; Pred. No. 2.3e-05;
XX Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTTTFSASVMG 19
Db 69 fignkangytteysavskg 87
|| |||||:|||||
|| |||||:|||||

RESULT 14
AAW41415
ID AAW41415 standard; Protein; 473 AA.
XX
XX AC AAW41415;
XX
XX DT 02-JUN-1998 (first entry)
XX
XX DE Human B7.1-murine A5B7 F(ab')2 fusion protein.
XX
XX KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
XX KW cancer diagnosis; complementarity determining region.
XX
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Mus sp.
XX
XX PN W09742329-A1.
XX
XX PD 13-NOV-1997.
XX
XX PF 29-APR-1997; 97WO-G801165.
XX
XX PR 14-FEB-1997; 97GB-0003103.
XX PR 04-MAY-1996; 96GB-0009405.
XX
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Copley CG, Edge MD, Emery SC;
XX
XX DR WPI; 1997-558987/51.
XX DR N-PSDB; AAV17340.
XX
XX PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
XX PT diagnosis and therapy of cancer
XX
XX PS Reference Example 3; Page 190-193; 208pp; English.
XX

```

XX SQ





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds  
(without alignments)  
2.767 Million cell updates/sec

Title: US-09-724-406-22

Perfect score: 97

Sequence: 1 FIRNKANGYTEFSASVMG 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	85.6	124	1	US-08-442-542-6
2	83	85.6	124	3	US-08-765-469-6
3	82	84.5	124	4	US-08-767-128-38
4	81	83.5	140	2	US-08-449-287-4
5	81	83.5	146	2	US-08-449-287-10
6	81	83.5	146	2	US-08-449-287-12
7	80	82.5	116	1	US-08-401-908-1
8	79	81.4	19	1	US-08-318-9708-6
9	76	78.4	19	2	US-08-765-783A-85
10	76	78.4	141	2	US-08-765-783A-29
11	76	78.4	141	2	US-08-765-783A-41
12	76	78.4	141	2	US-08-765-783A-45
13	76	78.4	141	2	US-08-765-783A-49
14	76	78.4	141	2	US-08-765-783A-51
15	76	78.4	141	2	US-08-765-783A-55
16	76	78.4	141	2	US-08-765-783A-59
17	76	78.4	141	2	US-08-765-783A-63
18	76	78.4	141	2	US-08-765-783A-65
19	76	78.4	141	3	US-08-921-100-29
20	76	78.4	141	3	US-08-921-100-41
21	76	78.4	141	3	US-08-921-100-45
22	76	78.4	141	3	US-08-921-100-49
23	76	78.4	141	3	US-08-921-100-51
24	76	78.4	141	3	US-08-921-100-55
25	76	78.4	141	3	US-08-921-100-59
26	76	78.4	141	3	US-08-921-100-63
27	76	78.4	141	3	US-08-921-100-65

28	76	78.4	141	3	US-08-880-142-29	Sequence 29, Appl
29	76	78.4	141	3	US-08-880-142-41	Sequence 41, Appl
30	76	78.4	141	3	US-08-880-142-45	Sequence 45, Appl
31	76	78.4	141	3	US-08-880-142-49	Sequence 49, Appl
32	76	78.4	141	3	US-08-880-142-51	Sequence 51, Appl
33	76	78.4	141	3	US-08-880-142-55	Sequence 55, Appl
34	76	78.4	141	3	US-08-880-142-59	Sequence 59, Appl
35	76	78.4	141	3	US-08-880-142-63	Sequence 63, Appl
36	76	78.4	141	3	US-08-880-142-65	Sequence 65, Appl
37	76	78.4	141	3	US-08-902-201-29	Sequence 29, Appl
38	76	78.4	141	3	US-08-902-201-41	Sequence 41, Appl
39	76	78.4	141	3	US-08-902-201-45	Sequence 45, Appl
40	76	78.4	141	3	US-08-902-201-49	Sequence 49, Appl
41	76	78.4	141	3	US-08-902-201-51	Sequence 51, Appl
42	76	78.4	141	3	US-08-902-201-55	Sequence 55, Appl
43	76	78.4	141	3	US-08-902-201-59	Sequence 59, Appl
44	76	78.4	141	3	US-08-902-201-63	Sequence 63, Appl
45	76	78.4	141	3	US-08-902-201-65	Sequence 65, Appl

#### ALIGNMENTS

RESULT 1  
US-08-442-542-6  
; Sequence 6, Application US/08442542  
; Patent No. 5686600  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine B.  
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut  
; TITLE OF INVENTION: Proteins and their Use  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,542  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/267,641  
; FILING DATE: 28-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCID NUMBER: CGC 1750  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8615  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-442-542-6

Query Match 85.6%; Score 83; DB 1; Length 124;  
Best Local Similarity 84.2%; Pred. No. 9.3e-07;  
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTEFSASVMG 19

Db 50 FIRKANGYTTTEVSASVKG 68  
|||:|||||:|||||

## RESULT 2

US-08-765-469-6  
; Sequence 6, Application US/08765469  
; Patent No. 6069301  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine B.  
; APPLICANT: Koziel, Michael G.  
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut  
; TITLE OF INVENTION: Proteins and their Use  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,469  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/267,641  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: CGC 1750  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8615  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-765-469-6

Query Match 85.6%; Score 83; DB 3; Length 124;  
Best Local Similarity 84.2%; Pred. No. 9.3e-07;  
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRKANGYTTTEFSASVMG 19  
|||:|||||:|||||

Db 50 FIRKANGYTTTEVSASVKG 68

## RESULT 3

US-08-767-128-38  
; Sequence 38, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GOEBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079 West Center, 90 South Seventh St

CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/767,128  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 04-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 05-JUN-1996  
PCT/US96/09258  
APPLICATION NUMBER:  
FILING DATE: 05-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/541,373  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/462,798  
FILING DATE: 05-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.4905F1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/371-5278  
TELEFAX: 612/332-9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-767-128-38

Query Match 84.5%; Score 82; DB 4; Length 124;  
Best Local Similarity 88.9%; Pred. No. 1.4e-06;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRKANGYTTTEFSASVMG 19

Db 51 IRKANGYTTTEVSASVKG 68

## RESULT 4

US-08-449-287-4  
; Sequence 4, Application US/08449287  
; Patent No. 5877293  
; GENERAL INFORMATION:  
; APPLICANT: ADAIR, John Robert  
; APPLICANT: BODMER, Mark William  
; APPLICANT: MOUNTAIN, Andrew  
; APPLICANT: OWENS, Raymond John  
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and  
; TITLE OF INVENTION: Their Production  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.

```

; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; APPLICATION DATA:
; PCT GB91/01108
; FILING DATE: 05-JUL-1991
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 21-DEC-1990
; APPLICATION DATA:
; PCT GB90/02017
; FILING DATE: 05-JUL-1990
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-4

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Query Match 83.5%; Score 81; DB 2; Length 140;
Best Local Similarity 84.2%; Pred. No. 2.3e-06;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 FIRKANGYTTEFSASVGM 19
Db 69 FIGNKANGYTTEYSASVKG 87

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RESULT 5
US-08-449-287-10
; Sequence 10, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; APPLICATION DATA:
; PCT GB91/01108
; FILING DATE: 05-JUL-1991
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; APPLICATION DATA:
; PCT GB90/02017
; FILING DATE: 21-DEC-1990
; APPLICATION INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-10

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Query Match 83.5%; Score 81; DB 2; Length 146;
Best Local Similarity 84.2%; Pred. No. 2.4e-06;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 FIRKANGYTTEFSASVGM 19
Db 69 FIGNKANGYTTEYSASVKG 87

```

```

RESULT 6
US-08-449-287-12
; Sequence 12, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-401-908-1

Query Match      82.5%; Score 80; DB 1; Length 116;
Best Local Similarity 78.9%; Pred. No. 2.7e-06;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FIRNKANGYTTTEFSASVMG 19
      III::IIIIII::IIII I
Db      50 FIRDRANGYTTTEYSASVKG 68

RESULT      8
US-08-318-970B-6
; Sequence 6, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR2-3
; OTHER INFORMATION: hypervariable region
US-08-318-970B-6

Query Match      81.4%; Score 79; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.8e-07;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FIRNKANGYTTTEFSASVMG 19
      IIIIIII IIIII::IIII I
Db      1 FIRNKANGYTTTEYSASVKG 19

RESULT      9
US-08-765-783A-85
; Sequence 85, Application US/08765783A
; Patent No. 5994524

```



```

; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-765-783A-85

Query Match 78.4%; Score 76; DB 2; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 IRNKANGYTTTFSASVMG 19
Db 2 IRNKANGYTTREYSASVMG 19

RESULT 10
US-08-765-783A-29
; Sequence 29, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington

```

```

; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; US-08-765-783A-29

Query Match 78.4%; Score 76; DB 2; Length 141;
Best Local Similarity 83.3%; Pred. No. 1.6e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 IRNKANGYTTTFSASVMG 19
Db 70 IRNKANGYTTREYSASVMG 87

RESULT 11
US-08-765-783A-41
; Sequence 41, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/765,783A  
;; FILING DATE: 07-MAR-1997  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Murashige, Kate H  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 35029-20001.20  
;; TELEPHONE: 202-887-1500  
;; TELEFAX: 202-822-0168  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 41:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 141 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: internal  
;; FEATURE:  
;; NAME/KEY: Signal Sequence  
;; LOCATION: 1...19  
;; OTHER INFORMATION:  
US-08-765-783A-41

Query Match 78.4%; Score 76; DB 2; Length 141;  
Best Local Similarity 83.3%; Pred. No. 1.6e-05;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRNKANGYTTFSASVMG 19  
|||||||1:|||||  
DB 70 IRNKANGYTREYSASVKG 87

RESULT 12  
US-08-765-783A-45  
; Sequence 45, Application US/08765783A  
; Patent No. 5994524  
; GENERAL INFORMATION:  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Matsumoto, Yoshihiro  
; APPLICANT: Yamada, Yoshiki  
; APPLICANT: Sato, Koh  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yamazaki, Tatsumi  
; TITLE OF INVENTION: Reshaped Human Antibody to  
; TITLE OF INVENTION: Interleukin-8  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,783A  
; FILING DATE: 07-MAR-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

;; NAME: Murashige, Kate H  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 35029-20001.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-887-1500  
;; TELEFAX: 202-822-0168  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 45:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 141 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: internal  
;; FEATURE:  
;; NAME/KEY: Signal Sequence  
;; LOCATION: 1...19  
;; OTHER INFORMATION:  
US-08-765-783A-45

Query Match 78.4%; Score 76; DB 2; Length 141;  
Best Local Similarity 83.3%; Pred. No. 1.6e-05;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRNKANGYTTFSASVMG 19  
|||||||1:|||||  
DB 70 IRNKANGYTREYSASVKG 87

RESULT 13  
US-08-765-783A-49  
; Sequence 49, Application US/08765783A  
; Patent No. 5994524  
; GENERAL INFORMATION:  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Matsumoto, Yoshihiro  
; APPLICANT: Yamada, Yoshiki  
; APPLICANT: Sato, Koh  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yamazaki, Tatsumi  
; TITLE OF INVENTION: Reshaped Human Antibody to  
; TITLE OF INVENTION: Interleukin-8  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,783A  
; FILING DATE: 07-MAR-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 35029-20001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-822-0168  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:  
LENGTH: 141 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Signal Sequence  
LOCATION: 1...19  
OTHER INFORMATION:  
US-08-765-783A-49

Query Match 78.4%; Score 76; DB 2; Length 141;  
Best Local Similarity 83.3%; Pred. No. 1.6e-05;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRNKANGYTTEFSASVMG 19  
|||||I:|||||  
Db 70 IRNKANGYTREYSASVKG 87

RESULT 14  
US-08-765-783A-51  
Sequence 51, Application US/08765783A  
Patent No. 5994524  
GENERAL INFORMATION:  
APPLICANT: Matsushima, Kouji  
APPLICANT: Matsumoto, Yoshihiro  
APPLICANT: Yamada, Yoshiki  
APPLICANT: Sato, Koh  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yamazaki, Tatsumi  
TITLE OF INVENTION: Reshaped Human Antibody to  
TITLE OF INVENTION: Interleukin-8  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,783A  
FILING DATE: 07-MAR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 141 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:

NAME/KEY: Signal Sequence  
LOCATION: 1...19  
OTHER INFORMATION:  
US-08-765-783A-51

Query Match 78.4%; Score 76; DB 2; Length 141;  
Best Local Similarity 83.3%; Pred. No. 1.6e-05;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRNKANGYTTEFSASVMG 19  
|||||I:|||||  
Db 70 IRNKANGYTREYSASVKG 87

RESULT 15  
US-08-765-783A-55  
Sequence 55, Application US/08765783A  
Patent No. 5994524  
GENERAL INFORMATION:  
APPLICANT: Matsushima, Kouji  
APPLICANT: Matsumoto, Yoshihiro  
APPLICANT: Yamada, Yoshiki  
APPLICANT: Sato, Koh  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yamazaki, Tatsumi  
TITLE OF INVENTION: Reshaped Human Antibody to  
TITLE OF INVENTION: Interleukin-8  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,783A  
FILING DATE: 07-MAR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 141 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Signal Sequence  
LOCATION: 1...19  
OTHER INFORMATION:  
US-08-765-783A-55

Query Match 78.4%; Score 76; DB 2; Length 141;  
Best Local Similarity 83.3%; Pred. No. 1.6e-05;

Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRNKANGYTTTFSASVNG 19

||||| | | | | | | | | |

Db 70 IRNKANGITREISASVKG 87

Search completed: June 28, 2001, 16:01:14  
Job time: 522 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:45 ; Search time 234.85 Seconds  
(without alignments)  
6.163 Million cell updates/sec

Title: US-09-724-406-22  
Perfect score: 97  
Sequence: 1 FIRNKANGYTEFSASVMG 19  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	90.7	81	2 D33936	Ig heavy chain V r
2	88	90.7	119	2 S24492	Ig heavy chain V r
3	88	90.7	119	2 S24493	Ig heavy chain V r
4	88	90.7	119	2 S24491	Ig heavy chain V r
5	88	90.7	119	2 S24525	Ig heavy chain V r
6	88	90.7	119	2 S24520	Ig heavy chain V r
7	88	90.7	119	2 S24518	Ig heavy chain V r
8	88	90.7	119	2 S24511	Ig heavy chain V r
9	88	90.7	119	2 S24494	Ig heavy chain V r
10	88	90.7	119	2 S24490	Ig heavy chain V r
11	88	90.7	119	2 S24517	Ig heavy chain V r
12	88	90.7	119	2 D30540	Ig heavy chain V r
13	88	90.7	123	2 S32186	Ig heavy chain V r
14	83	85.6	118	2 E30540	Ig heavy chain V r
15	82	84.5	91	2 S24523	Ig heavy chain V r
16	82	84.5	101	2 PU0002	Ig heavy chain V r
17	82	84.5	105	2 PL0255	Ig heavy chain V r
18	82	84.5	113	2 PH1029	Ig heavy chain V r
19	82	84.5	114	2 PH1027	Ig heavy chain V r
20	82	84.5	119	2 S24522	Ig heavy chain V r
21	82	84.5	119	2 S24513	Ig heavy chain V r
22	82	84.5	119	2 S24515	Ig heavy chain V r
23	82	84.5	119	2 S24497	Ig heavy chain V r
24	82	84.5	122	1 AVMSX2	Ig heavy chain V r
25	82	84.5	124	2 PT0388	Ig heavy chain V r
26	82	84.5	126	2 S16280	Ig heavy chain V r
27	82	84.5	145	2 S03844	Ig heavy chain pre
28	79	81.4	101	2 PU0003	Ig heavy chain V r
29	79	81.4	119	2 S24519	Ig heavy chain V r

## ALIGNMENTS

### RESULT 1

D33936  
Ig heavy chain V region (VM201) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 09-May-1997  
C:Accession: D33936  
R:Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989  
A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin  
A:Reference number: A33936; MUID:89282831  
A:Accession: D33936  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-81 <MEE>  
A:Cross-references: GB:J04579  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

30	79	81.4	119	2	S24514	Ig heavy chain V r
31	79	81.4	119	2	S24496	Ig heavy chain V r
32	78	80.4	119	2	S24524	Ig heavy chain V r
33	78	80.4	121	2	PT0391	Ig heavy chain V r
34	78	80.4	123	2	PT0385	Ig heavy chain V r
35	78	80.4	124	2	PT0389	Ig heavy chain V r
36	77	79.4	119	2	PT0377	Ig heavy chain V r
37	76	78.4	120	2	PT0393	Ig heavy chain V r
38	76	78.4	123	2	PT0386	Ig heavy chain V r
39	75	77.3	122	2	PT0379	Ig heavy chain V r
40	75	77.3	123	2	PT0383	Ig heavy chain V r
41	74	76.3	121	2	E30502	Ig heavy chain V r
42	74	76.3	123	2	PT0387	Ig heavy chain V r
43	74	76.3	123	2	PT0380	Ig heavy chain V r
44	73	75.3	100	2	S26926	Ig heavy chain V r
45	73	75.3	119	2	S00981	Ig heavy chain pre

Query Match 90.7%; Score 88; DB 2; Length 81;  
Best Local Similarity 89.5%; Pred. No. 1.4e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTEFSASVMG 19  
|||||  
DB 13 FIRNKANGYTEFSASVKG 31

### RESULT 2

S24492  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S24492  
R:Kaartinen, M.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24490  
A:Accession: S24492  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-119 <KAA>  
A:Cross-references: EMBL:X66649; NID:951217; PIDN:CAA47211.1; PID:951218  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;  
Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTEFSASVMG 19

Fri Jun 29 08:04:48 2001

Db 69 FIRNKANGYTTTEFSASVKG 87  
|||||  
RESULT 3  
S24493  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S24493  
R:Kaartinen, M.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24490  
A:Accession: S24493  
A:Molecule type: mRNA  
A:Residues: 1-119 <KAA>  
A:Cross-references: EMBL:X66650; NID:g51219; PIDN:CAA47212.1; PID:g51220  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>  
Query Match 90.7%; Score 88; DB 2; Length 119;  
Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FIRNKANGYTTTEFSASVGM 19  
|||||  
Db 69 FIRNKANGYTTTEFSASVKG 87  
|||||  
RESULT 4  
S24491  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S24491  
R:Kaartinen, M.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24490  
A:Accession: S24491  
A:Molecule type: mRNA  
A:Residues: 1-119 <KAA>  
A:Cross-references: EMBL:X66648; NID:g51215; PIDN:CAA47210.1; PID:g51216  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>  
Query Match 90.7%; Score 88; DB 2; Length 119;  
Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FIRNKANGYTTTEFSASVGM 19  
|||||  
Db 69 FIRNKANGYTTTEFSASVKG 87  
|||||  
RESULT 5  
S24525  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S24525  
R:Kaartinen, M.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24490  
A:Accession: S24525  
A:Molecule type: mRNA  
A:Residues: 1-119 <KAA>  
A:Cross-references: EMBL:X66663; NID:g51245; PIDN:CAA47225.1; PID:g51246  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>  
Query Match 90.7%; Score 88; DB 2; Length 119;  
Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FIRNKANGYTTTEFSASVGM 19  
|||||  
Db 69 FIRNKANGYTTTEFSASVKG 87  
|||||  
RESULT 6  
S24520  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S24520  
R:Kaartinen, M.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24490  
A:Accession: S24520  
A:Molecule type: mRNA  
A:Residues: 1-119 <KAA>  
A:Cross-references: EMBL:X66663; NID:g51245; PIDN:CAA47225.1; PID:g51246  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>  
Query Match 90.7%; Score 88; DB 2; Length 119;  
Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FIRNKANGYTTTEFSASVGM 19  
|||||  
Db 69 FIRNKANGYTTTEFSASVKG 87  
|||||  
RESULT 7  
S24518  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S24518  
R:Kaartinen, M.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24490  
A:Accession: S24518  
A:Molecule type: mRNA  
A:Residues: 1-119 <KAA>  
A:Cross-references: EMBL:X66661; NID:g51241; PIDN:CAA47223.1; PID:g51242  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>  
Query Match 90.7%; Score 88; DB 2; Length 119;  
Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FIRNKANGYTTTEFSASVGM 19  
|||||  
Db 69 FIRNKANGYTTTEFSASVKG 87  
|||||  
RESULT 8  
S24511

Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S24511  
 R:Kaartinen, M.  
 submitted to the EMBL Data Library, October 1991  
 A:Reference number: S24490  
 A:Accession: S24511  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <KAA>  
 A:Cross-references: EMBL:X66659; NID:g51237; PIDN:CAA47221.1; PID:g51238  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;  
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSASVVG 19  
 Db 69 FIRNKANGYTTTFSASVVG 87  
 |||||

RESULT 9  
 S24490  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S24494  
 R:Kaartinen, M.  
 submitted to the EMBL Data Library, October 1991  
 A:Reference number: S24490  
 A:Accession: S24494  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <KAA>  
 A:Cross-references: EMBL:X66651; NID:g51221; PIDN:CAA47213.1; PID:g51222  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;  
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSASVVG 19  
 Db 69 FIRNKANGYTTTFSASVVG 87  
 |||||

RESULT 10  
 S24490  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S24490  
 R:Kaartinen, M.  
 submitted to the EMBL Data Library, October 1991  
 A:Reference number: S24490  
 A:Accession: S24490  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <KAA>  
 A:Cross-references: EMBL:X66647; NID:g51213; PIDN:CAA47209.1; PID:g51214  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;  
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSASVVG 19  
 Db 69 FIRNKANGYTTTFSASVVG 87  
 |||||

RESULT 11  
 S24517  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S24517; S24541  
 R:Kaartinen, M.  
 submitted to the EMBL Data Library, October 1991  
 A:Reference number: S24490  
 A:Accession: S24517  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <KAA>  
 A:Cross-references: EMBL:X66660; NID:g51239; PIDN:CAA47222.1; PID:g51240; EMBL:X66669  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;  
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSASVVG 19  
 Db 69 FIRNKANGYTTTFSASVVG 87  
 |||||

RESULT 12  
 D30540  
 Ig heavy chain V region (174.3F4) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996  
 C:Accession: D30540  
 R:Clafin, J.L.; Berry, J.  
 J. Immunol. 141, 4012-4019, 1988  
 A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus p  
 A:Reference number: A30534; MUID:89035545  
 A:Accession: D30540  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <CLA>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;  
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;  
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSASVVG 19  
 Db 50 FIRNKANGYTTTFSASVVG 68  
 |||||

RESULT 13  
 S32186  
 Ig heavy chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S32186  
 R:izul, S.  
 submitted to the EMBL Data Library, February 1993

Fri Jun 29 08:04:48 2001

us-09-724-406-22.rpr

Db 42 IRNKANGYTFEYSASVKG 59  
Search completed: June 28, 2001, 15:58:45  
Job time: 373 sec

A:Reference number: S32185  
A:Accession: S32186  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <I20>  
A:Cross-references: EMBL:X70093; NID:g288249; PIDN:CAA49698.1; PID:g288250  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 123;  
Best Local Similarity 89.5%; Pred. No. 2.2e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVMG 19  
|||||  
Db 50 FIRNKANGYTFEYSASVKG 68

RESULT 14  
E30540  
Ig heavy chain V region (252.8G3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996  
C:Accession: E30540  
R:Clafin, J.L.; Berry, J.  
J: Immunol. 141, 4012-4019, 1988  
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae  
A:Reference number: A30534; MUID:89035545  
A:Accession: E30540  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-118 <CLA>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 83; DB 2; Length 118;  
Best Local Similarity 84.2%; Pred. No. 1.4e-06;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVMG 19  
|||||  
Db 50 FIRNKANGYTFEYSASVKG 68

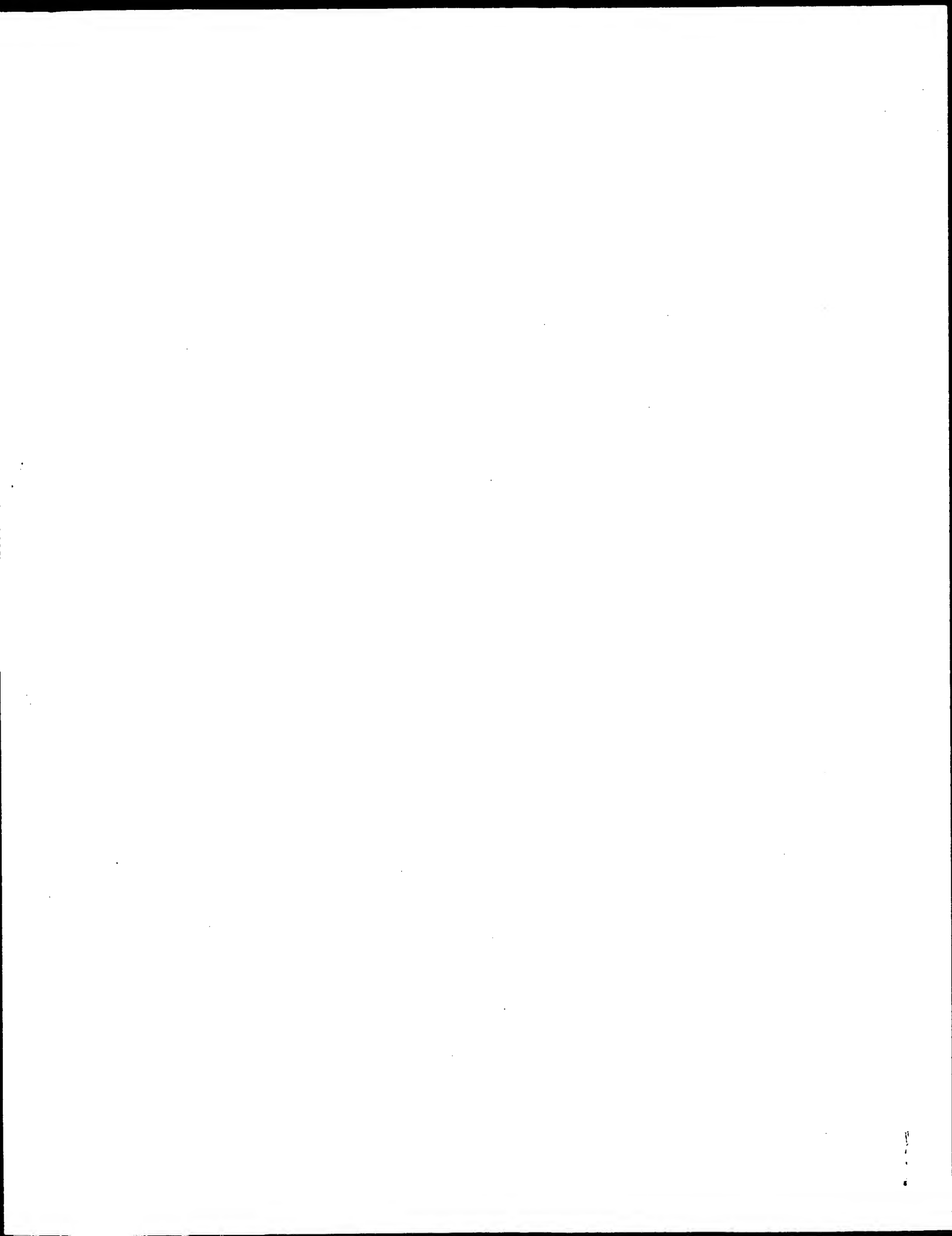
RESULT 15  
S24523  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S24523  
R:Kaartinen, M.  
Submitted to the EMBL Data Library, October 1991  
A:Reference number: S24490  
A:Accession: S24523  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-91 <KAA>  
A:Cross-references: EMBL:X66666; NID:g51251; PIDN:CAA47228.1; PID:g388532  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:6-91/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 82; DB 2; Length 91;  
Best Local Similarity 88.9%; Pred. No. 1.6e-06;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTFEFSASVMG 19  
|||||







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:37 ; Search time 105.36 Seconds  
(without alignments)  
6.177 Million cell updates/sec

Title: US-09-724-406-22  
Perfect score: 97  
Sequence: 1 FIRNKANGYTFESASVMG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	74.2	117	1	HV17_MOUSE
2	71	73.2	122	1	HV21_MOUSE
3	71	73.2	123	1	HV18_MOUSE
4	71	73.2	123	1	HV19_MOUSE
5	71	73.2	123	1	HV22_MOUSE
6	71	73.2	123	1	HV25_MOUSE
7	66	68.0	122	1	HV20_MOUSE
8	62	63.9	123	1	HV23_MOUSE
9	59	60.8	123	1	HV24_MOUSE
10	55	56.7	144	1	HV26_MOUSE
11	47	48.5	142	1	HV01_RAT
12	46	47.4	115	1	HV32_MOUSE
13	41	42.3	113	1	HV27_MOUSE
14	41	42.3	113	1	HV28_MOUSE
15	41	42.3	113	1	HV29_MOUSE
16	41	42.3	113	1	HV30_MOUSE
17	41	42.3	115	1	HV33_MOUSE
18	41	42.3	381	1	GVPC_HALME
19	41	42.3	639	1	TETM_STRLI
20	41	42.3	690	1	VATI_DEIRA
21	40	41.2	113	1	HV31_MOUSE
22	40	41.2	824	1	HELI_HSV60
23	40	41.2	824	1	HELI_HSV62
24	40	41.2	1183	1	CNA_STRAU
25	39	40.2	252	1	YAGI_ECOLI
26	39	40.2	352	1	STSV_CATRO
27	39	40.2	358	1	TRMU_CHLTR
28	39	40.2	401	1	HAT2_YEAST
29	39	40.2	666	1	COI4_BRAJA
30	39	40.2	993	1	FLT3_HUMAN
31	39	40.2	1267	1	VL3_REOVJ
32	39	40.2	2244	1	PYRL_SCHPO
33	38.5	39.7	450	1	HEMN_BRAJA

34 38.5 39.7 658 1 LYTB\_STRPN  
35 38 39.2 131 1 RS17\_SCHPO  
36 38 39.2 136 1 R17A\_YEAST  
37 38 39.2 136 1 R17B\_YEAST  
38 38 39.2 146 1 RS17\_NEUCR  
39 38 39.2 237 1 OPAC\_NEIGO  
40 38 39.2 331 1 Y119\_SYNY3  
41 38 39.2 527 1 SECY\_PEA  
42 38 39.2 889 1 GLK2\_MOUSE  
43 38 39.2 907 1 AVRA\_PSESG  
44 38 39.2 908 1 GLK2\_HUMAN  
45 38 33.2 908 1 GLK2\_RAT

O9z4p7 streptococc  
O42984 schizosacch  
P02407 saccharomyc  
P14127 saccharomyc  
P27770 neurospora  
Q04880 neisseria g  
P73709 synchocyst  
Q9xqu4 pium sativ  
P39087 mus musculu  
P11437 pseudomonas  
Q13002 homo sapien  
P42260 rattus norv

## ALIGNMENTS

RESULT 1  
HV17\_MOUSE  
ID HV17\_MOUSE STANDARD; PRT; 117 AA.  
AC P01786;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION MOPC 47A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80049769; PubMed=115869;  
RA Robinson E.A., Appella E.;  
RT "Amino acid sequence of a mouse myeloma immunoglobulin heavy chain  
(MOPC 47 A) with a 100-residue deletion.";  
RL J. Biol. Chem. 254:11418-11430(1979).  
CC - MISCELANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA  
LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA  
MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A  
LIGHT-HEAVY CHAIN DISULFIDE BOND.  
CC PIR: A02069; ALMS47.  
DR HSP: P01789; 2MCP.  
DR InterPro; IPR003006; -.  
DR Pfam; PF00047; Ig; 1.  
KW Immunoglobulin V region.  
FT NON\_TER 117  
SQ SEQUENCE 117 AA; 12975 MW; 0C74BE8BB154BDF4 CRC64;

Query Match 74.2% Score 72; DB 1; Length 117;  
Best Local Similarity 86.7%; Pred. No. 1.4e-05;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTFESA 15  
|||||:|||||:|  
Db 50 FIRNKABGYTFESA 64

RESULT 2  
HV21\_MOUSE  
ID HV21\_MOUSE STANDARD; PRT; 122 AA.  
AC P01790;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION M511.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.

Fri Jun 29 08:04:48 2001

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RX MEDLINE-81054880; PubMed-6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
RL (MOPC 511).";
CC Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR: A02070; AVMT5.
CC HSP: P01789; 2MCP.
CC InterPro: IPR003006; -.
CC Pfam: PF00047; Ig; 1.
CC Immunoglobulin V region.
KW NON_TER 122 122
FT SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 73.2%; Score 71; DB 1; Length 122;
Best Local Similarity 82.4%; Pred. No. 2.2e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTFSASVMG 19
DB 52 RNKANDYTTFSASVKG 68
||||| ||||| |||||

RESULT 4
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA Barstad P.; California Institute of Technology / Pasadena, U.S.A.
RL Thesis (1975). THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR: A02070; AVMT5.
CC HSP: P01789; 2MCP.
CC InterPro: IPR003006; -.
CC Pfam: PF00047; Ig; 1.
CC Immunoglobulin V region.
KW NON_TER 123 123
FT SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;

Query Match 73.2%; Score 71; DB 1; Length 123;
Best Local Similarity 82.4%; Pred. No. 2.3e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTFSASVMG 19
DB 52 RNKANDYTTFSASVKG 68
||||| ||||| |||||

RESULT 5
ID HV22_MOUSE STANDARD; PRT; 123 AA.
AC P01791;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCM6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RL "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
CC Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR: A02070; AVMT5.
CC HSP: P01789; 2MCP.
CC InterPro: IPR003006; -.
KW Immunoglobulin V region; Hybridoma.

RX MEDLINE-81054880; PubMed-6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
RL (MOPC 511).";
CC Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR: A02070; AVMT5.
CC HSP: P01789; 2MCP.
CC InterPro: IPR003006; -.
CC Pfam: PF00047; Ig; 1.
CC Immunoglobulin V region.
KW NON_TER 122 122
FT SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 73.2%; Score 71; DB 1; Length 122;
Best Local Similarity 82.4%; Pred. No. 2.2e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTFSASVMG 19
DB 52 RNKANDYTTFSASVKG 68
||||| ||||| |||||

RESULT 3
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 15).
RA Rudikoff S., Potter M.;
RL "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins.";
CC Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RP SEQUENCE FROM N.A. (H107).
RX MEDLINE-80199926; PubMed-6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RL three segments of DNA: VH, D and JH.";
RN [3]
RP SEQUENCE (S107).
RX MEDLINE-76110488; PubMed-813561;
RA Rudikoff S., Barstad P., Potter M., Hood L.;
RL Unpublished results, cited by:
RL Hood L., Campbell J.H., Elgin S.C.R.;
RL Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX MEDLINE-81197602; PubMed-7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RL their IgM counterparts.";
CC Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
CC PIR: A02070; AVMT5.
CC HSP: P01789; 2MCP.
CC InterPro: IPR003006; -.
CC Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma.
```

```

DR Pfam: PF00047; ig: 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;

Query Match 73.2%; Score 71; DB 1; Length 123;
Best Local Similarity 82.4%; Pred. No. 2.3e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTTFSASVVG 19
Db 52 RNKANDYTTTFSASVKG 68

RESULT 6
HV25_MOUSE
ID HV25_MOUSE STANDARD; PRT; 123 AA.
AC P01794;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCG14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RL their IgM counterparts."
RL Nature 291:29-34(1981).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMS75.
DR HSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig: 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13807 MW; A7584FE098B7785D CRC64;

Query Match 73.2%; Score 71; DB 1; Length 123;
Best Local Similarity 82.4%; Pred. No. 2.3e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTTFSASVVG 19
Db 52 RNKANDYTTTFSASVKG 68

RESULT 7
HV20_MOUSE
ID HV20_MOUSE STANDARD; PRT; 122 AA.
AC P01789;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION M603.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RL three segments of DNA: VH, D and JH."
RL Cell 19:981-992(1980).

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RN RP SEQUENCE OF 1-120.
RX MEDLINE=75017346; PubMed=4213527;
RA Rudikoff S., Potter M.;
RT "Variable region sequence of the heavy chain from a phosphorylcholine
RL binding myeloma protein."
RL Biochemistry 13:4033-4038(1974).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.
RX MEDLINE=75065510; PubMed=4530984;
RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,
RA Davies D.R.;
RT "The three-dimensional structure of a phosphorylcholine-binding mouse
RL immunoglobulin Fab and the nature of the antigen binding site."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMS75.
DR PDB: 1MCP; 15-JUL-92.
DR PDB: 2MCP; 15-JUL-92.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig: 1.
KW Immunoglobulin V region; 3D-structure.
FT SITE 33 33
FT SITE 52 52
FT SITE 52 52
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 17 25
FT HELIX 29 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 50
FT TURN 54 55
FT STRAND 61 61
FT TURN 64 66
FT STRAND 67 67
FT TURN 68 69
FT STRAND 70 75
FT TURN 76 79
FT STRAND 80 86
FT HELIX 90 92
FT STRAND 94 103
FT STRAND 107 112
FT STRAND 116 120
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13626 MW; BA2C864438B64F0F CRC64;

Query Match 68.0%; Score 66; DB 1; Length 122;
Best Local Similarity 76.5%; Pred. No. 0.00016;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RNKANGYTTTFSASVVG 19
Db 52 RNKNGYTTTFSASVKG 68

RESULT 8
HV23_MOUSE
ID HV23_MOUSE STANDARD; PRT; 123 AA.
AC P01792;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCG8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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Fri Jun 29 08:04:48 2001

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93358330; PubMed=6101208;
RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
RT "Antibody diversity; somatic hypermutation of rearranged VH genes.";
RL Cell 27:573-581(1981).
CC [2]
CC SEQUENCE OF 20-142.
CC MEDLINE=76222762; PubMed=819932;
CC Rudikoff S., Potter M.;
CC "Size differences among immunoglobulin heavy chains from
CC phosphorylcholine-binding proteins.";
CC Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS PHOSPHORYLCHOLINE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00516; AAC18867.1; -.
DR PIR; A02071; AVMS67.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION M167.
FT CONFLICT 125 125 N -> D (IN REF. 2).
FT NON_TER 144 144
FT SEQUENCE 144 AA; 16219 MW; BECBA42C956CF769 CRC64;
SQ SEQUENCE 144 AA; 16219 MW; BECBA42C956CF769 CRC64;

Query Match 56.7%; Score 55; DB 1; Length 144;
Best Local Similarity 64.7%; Pred. No. 0.016;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RNKANGYTFESASVMG 19
Db 71 RSKAHDYTFESASVKG 87
|:::|:::|:::|

RESULT 11
ID HV01_RAT STANDARD; PRT; 142 AA.
AC P01805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION IR2 PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
RT E.";
RL Nucleic Acids Res. 10:6041-6049(1982).
CC -|- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
CC IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
CC PIR; A02075; EVTR2.
DR HSSP; P01789; 2MCP.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR; A02070; AVMS5.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Hybridoma.
KW NON_TER 123 123
FT SEQUENCE 123 AA; 13879 MW; 4559D3106CAF7D8D CRC64;
SQ SEQUENCE 123 AA; 13879 MW; 4559D3106CAF7D8D CRC64;

Query Match 63.9%; Score 62; DB 1; Length 123;
Best Local Similarity 76.5%; Pred. No. 0.00082;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RNKANGYTFESASVMG 19
Db 52 RNKAFDYTFESASVKG 68
|:::|:::|:::|

RESULT 9
ID HV24_MOUSE STANDARD; PRT; 123 AA.
AC P01793;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCG13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR; A02070; AVMS5.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Hybridoma.
KW NON_TER 123 123
FT SEQUENCE 123 AA; 13808 MW; 6599F256ECCEDE50 CRC64;
SQ SEQUENCE 123 AA; 13808 MW; 6599F256ECCEDE50 CRC64;

Query Match 60.8%; Score 59; DB 1; Length 123;
Best Local Similarity 70.8%; Pred. No. 0.0027;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 RNKANGYTFESASVMG 19
Db 52 RNKYDYTFESASVKG 68
|:::|:::|:::|

RESULT 10
ID HV26_MOUSE STANDARD; PRT; 144 AA.
AC P01795;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION M167 PRECURSOR.

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DR InterPro: IPR003006; -  
 KW Pfam: PF00047; ig; 1.  
 FT SIGNAL 19  
 FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.  
 FT NON\_TER 142 142  
 SQ SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;

Query Match 48.5%; Score 47; DB 1; Length 142;  
 Best Local Similarity 50.0%; Pred. No. 0.38;  
 Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 IRNKANGYTFEFSASVVG 19  
 ||||| | : | : |  
 DB 70 IRNKANNVAYGKSLAG 87

RESULT 12  
 HV32\_MOUSE  
 ID HV32\_MOUSE STANDARD; PRT; 115 AA.  
 AC P01801;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 13-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V-III REGION J606.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82099361; PubMed=6798111;  
 RA Johnson N., Stankard J., Paul L., Hood L.;  
 RT "The complete V domain amino acid sequences of two myeloma inulin-  
 binding proteins.";  
 RL J. Immunol. 128:302-307(1982).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS INULIN.  
 CC PIR: C92811; AVMS06.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; ig; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 22 98  
 FT NON\_TER 115 115 BY SIMILARITY.  
 SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Query Match 47.4%; Score 46; DB 1; Length 115;  
 Best Local Similarity 50.0%; Pred. No. 0.45;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRNKANGYTFEFSASVVG 19  
 ||||| | : | : |  
 DB 51 IRLKSNYATHVAESVKG 68

RESULT 13  
 HV27\_MOUSE  
 ID HV27\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01796;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V-III REGION A4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;

RT "Sequence variation among heavy chains from inulin-binding myeloma  
 proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS INULIN.  
 CC PIR: A93818; AVMSAB.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; ig; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 22 98 BY SIMILARITY.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 42.3%; Score 41; DB 1; Length 113;  
 Best Local Similarity 44.4%; Pred. No. 3.2;  
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRNKANGYTFEFSASVVG 19  
 ||||| | : | : |  
 DB 51 IRLKSHNYATHVAESVKG 68

RESULT 14  
 HV28\_MOUSE  
 ID HV28\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01797;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V-III REGION U61.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS INULIN.  
 CC PIR: B93818; AVMS61.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; ig; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 22 98 BY SIMILARITY.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Query Match 42.3%; Score 41; DB 1; Length 113;  
 Best Local Similarity 44.4%; Pred. No. 3.2;  
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRNKANGYTFEFSASVVG 19  
 ||||| | : | : |  
 DB 51 IRLKSHNYATHVAESVKG 68

RESULT 15  
 HV29\_MOUSE  
 ID HV29\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01798;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V-III REGION E109.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 RL proteins."; Acad. Sci. U.S.A. 75:1957-1961(1978).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS INULIN.  
 DR PIR; C93818; AVMS09.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; ig: 1.  
 KW Immunoglobulin V region. BY SIMILARITY.  
 FT DISULFID 22 98  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;

Query Match 42.3%; Score 41; DB 1; Length 113;  
 Best Local Similarity 44.4%; Pred. No. 3.2;  
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy 2 IRNKANGYTFEFSASVMG 19  
 |||::||::|||  
 Db 51 IRLKSHNYATHYAESVKG 68

Search completed: June 28, 2001, 15:54:38  
 Job time: 126 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:24 ; Search time 411.58 Seconds  
(without alignments)  
6.108 Million cell updates/sec

Title: US-09-724-406-22  
Perfect score: 97  
Sequence: 1 FIRKANGYTTFSASVWG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-unclassified:\*  
13: sp-vertebrate:\*  
14: sp-virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	69.1	80	4	075727
2	47	48.5	76	4	075733
3	46	47.4	295	1	026691
4	46	47.4	877	10	042497
5	46	47.4	2516	2	09RN43
6	45	46.4	808	5	09V995
7	44	45.4	86	4	075740
8	44	45.4	131	4	09UL88
9	42	43.3	117	5	P91362
10	42	43.3	346	2	007414
11	42	43.3	1792	5	097417
12	42	43.3	1792	5	09V4M6
13	41	42.3	635	2	09EWR9
14	41	42.3	702	5	09VSH4
15	41	42.3	745	3	09HE61
16	41	42.3	1320	2	09X2Y4
17	40.5	41.8	463	3	09P4E8
18	40	41.2	199	14	09QCY8
19	40	41.2	418	2	09HWP4

20	40	41.2	453	2	09KQS1
21	40	41.2	487	2	050901
22	40	41.2	493	5	017454
23	40	41.2	516	5	017455
24	40	41.2	530	10	082811
25	40	41.2	547	2	007475
26	40	41.2	584	2	09KEB2
27	40	41.2	655	2	09RXY9
28	40	41.2	824	14	057139
29	40	41.2	1146	5	09N8Q9
30	40	41.2	1282	2	046348
31	39.5	40.7	196	10	09FGT3
32	39.5	40.7	995	5	09W2L7
33	39	40.2	81	4	075736
34	39	40.2	224	10	09SNW5
35	39	40.2	245	1	09YAP5
36	39	40.2	261	2	09RGL9
37	39	40.2	283	10	09LYX4
38	39	40.2	301	2	053796
39	39	40.2	311	14	09DVR8
40	39	40.2	427	10	09SZ39
41	39	40.2	471	5	09U6D6
42	39	40.2	474	2	09PAX0
43	39	40.2	590	10	09LYK7
44	39	40.2	607	5	09GZF2
45	39	40.2	868	14	09QEY5

## ALIGNMENTS

RESULT 1

075727 PRELIMINARY; PRT; 80 AA.

AC 075727; 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 GN VH.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]

RC SEQUENCE FROM H.A.

RA Fischer M., Kueppers R.;

RT "Human IgA and IgM secreting intestinal plasma cells carry heavily

RL mutated VH region genes.";

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL; AJ009524; CAA08731.1; -.

DR InterPro; IPR003006; -.

DR InterPro; IPR003596; -.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON\_TER 1

FT NON\_TER 80

SQ SEQUENCE 80 AA; 9351 MW; B5A34A4210437A4E CRC64;

Query Match 69.1%; Score 67; DB 4; Length 80;  
 Best Local Similarity 72.2%; Pred. No. 0.00044;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IRKANGYTTFSASVWG 19

Db 19 IRKANGYTTFSASVWG 36

RESULT 2

```

075733 ID O75733 PRELIMINARY; PRT; 76 AA.
AC O75733;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
DE VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=INTESTINE.
RC Fischer M., Kueppers R.;
RC "Human IgA and IgM secreting intestinal plasma cells carry heavily
RT mutated VH region genes.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AJ009530; CAA08737.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 76
DR NON_TER 76
DR SEQUENCE 76 AA; 8543 MW; F4C0FAEFC63A4EC CRC64;
SQ
Query Match 48.5%; Score 47; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 IRNKANGYTTEFSASVMG 19
|||:|:|:|:|:|
DB 20 IRSKTHSYATAYAAASVEG 37
|||:|:|:|:|:|
RESULT 3
ID O26691 PRELIMINARY; PRT; 295 AA.
AC O26691;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CONSERVED PROTEIN.
DE MTH591.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
NCBI_TaxID=145262;
[1]
SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RC MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang F., Wierzbowski J., Gibson R.,
RA Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RA "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155 (1997).
DR EMBL: AE000841; AAB85097.1; -.
DR InterPro: IPR001440; -.
DR Pfam: PF00515; TPR; 3.
DR SMART: SM00028; TPR; 1.
DR SEQUENCE 295 AA; 33717 MW; AA9FA49B5C28C85A CRC64;
075733 ID O75733 PRELIMINARY; PRT; 76 AA.
AC O75733;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
DE VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=INTESTINE.
RC Fischer M., Kueppers R.;
RC "Human IgA and IgM secreting intestinal plasma cells carry heavily
RT mutated VH region genes.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AJ009530; CAA08737.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 76
DR NON_TER 76
DR SEQUENCE 76 AA; 8543 MW; F4C0FAEFC63A4EC CRC64;
SQ
Query Match 48.5%; Score 47; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 IRNKANGYTTEFSASVMG 19
|||:|:|:|:|:|
DB 20 IRSKTHSYATAYAAASVEG 37
|||:|:~|:|:|:|:|
075733 ID O75733 PRELIMINARY; PRT; 76 AA.
AC O75733;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
DE VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=INTESTINE.
RC Fischer M., Kueppers R.;
RC "Human IgA and IgM secreting intestinal plasma cells carry heavily
RT mutated VH region genes.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AJ009530; CAA08737.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 76
DR NON_TER 76
DR SEQUENCE 76 AA; 8543 MW; F4C0FAEFC63A4EC CRC64;
SQ
Query Match 48.5%; Score 47; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 IRNKANGYTTEFSASVMG 19
|||:|:~|:|:|:|:|
DB 20 IRSKTHSYATAYAAASVEG 37
|||:|:~|:|:|:|:|
075733 ID O75733 PRELIMINARY; PRT; 76 AA.
AC O75733;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
DE VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=INTESTINE.
RC Fischer M., Kueppers R.;
RC "Human IgA and IgM secreting intestinal plasma cells carry heavily
RT mutated VH region genes.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AJ009530; CAA08737.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 76
DR NON_TER 76
DR SEQUENCE 76 AA; 8543 MW; F4C0FAEFC63A4EC CRC64;
SQ
Query Match 48.5%; Score 47; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 IRNKANGYTTEFSASVMG 19
|||:|:~|:|:|:|:|
DB 20 IRSKTHSYATAYAAASVEG 37
|||:|:~|:|:|:|:|
075733 ID O75733 PRELIMINARY; PRT; 76 AA.
AC O75733;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
DE VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=INTESTINE.
RC Fischer M., Kueppers R.;
RC "Human IgA and IgM secreting intestinal plasma cells carry heavily
RT mutated VH region genes.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AJ009530; CAA08737.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 76
DR NON_TER 76
DR SEQUENCE 76 AA; 8543 MW; F4C0FAEFC63A4EC CRC64;
SQ
Query Match 48.5%; Score 47; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 IRNKANGYTTEFSASVMG 19
|||:|:~|:|:|:~|:|
DB 20 IRSKTHSYATAYAAASVEG 37
|||:|:~|:|:|:~|:|
075733 ID O75733 PRELIMINARY; PRT; 76 AA.
AC O75733;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
DE VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=INTESTINE.
RC Fischer M., Kueppers R.;
RC "Human IgA and IgM secreting intestinal plasma cells carry heavily
RT mutated VH region genes.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AJ009530; CAA08737.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig, 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 76
DR NON_TER 76
DR SEQUENCE 76 AA; 8543 MW; F4C0FAEFC63A4EC CRC64;
SQ
Query Match 48.5%; Score 47; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 IRNKANGYTTEFSASVMG 19
|||:|:~|
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OC Photorhabdus.  
 OX NCBI\_TaxID=29488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-W-14;  
 RA Merlo D.J., Wegrich L.M., Roberts J.L., Petell J.K.;  
 RT "Expression of Photorhabdus luminescens tcdA gene in maize confers  
 corn rootworm tolerance."  
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF188483; AAF05542.1;  
 DR InterPro: IPR001589;  
 DR PROSITE: PS00019; ACTININ.1; UNKNOWN.1.  
 SQ SEQUENCE 2516 AA; 282953 MW; 8250A0650B614B99 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 2516;  
 Best Local Similarity 64.3%; Pred. No. 78;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 KANGYTTTFFSASVM 18  
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 Db 2159 EATGYVMEFSANVM 2172

RESULT 6  
 ID Q9V995 PRELIMINARY; PRT; 808 AA.  
 AC Q9V995;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)  
 DE CG15236 PROTEIN.  
 GN CG15236.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Abril J.F., Aghavani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein D., Bolshakov S.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Deyanov L., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacht J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003790; AAF57401.1;  
 DR FlyBase: FBgn0033108; CG15236.  
 DR InterPro: IPR001781;  
 DR PRODOM: PD000094; -, 1.  
 SQ SEQUENCE 808 AA; 87716 MW; 04AC2B699DA5F9AD CRC64;

Query Match 46.4%; Score 45; DB 5; Length 808;  
 Best Local Similarity 44.4%; Pred. No. 32;  
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 FIRKANGYTTTFFSASVM 18  
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 Db 640 FFRSSYNDYSSEFNGSVV 657

RESULT 7  
 ID 075740 PRELIMINARY; PRT; 86 AA.  
 AC 075740;  
 DT 01-NOV-1998 (T-EMBLrel. 08, Created)  
 DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)  
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 GN VH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=INTESTINE;  
 RA Fischer M., Kueppers R.;  
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily  
 mutated VH region genes."  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN  
 DR EMBL: AJ009539; CAA08744.1;  
 DR InterPro: IPR003006;  
 DR InterPro: IPR003596;  
 DR Pfam: PF00047; ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR NON\_TER 1  
 FT NON\_TER 86  
 SQ SEQUENCE 86 AA; 9625 MW; F529E1FBCF8CBEB3 CRC64;

Query Match 45.4%; Score 44; DB 4; Length 86;  
 Best Local Similarity 44.4%; Pred. No. 3.9;  
 Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRNKANGYTTTFFSASVM 19  
 :||| :|||:  
 Db 21 IKSKTDGTTDYAAPVK 38

RESULT 8  
 ID Q9UL88 PRELIMINARY; PRT; 131 AA.  
 AC Q9UL88;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).

Fri Jun 29 08:04:49 2001

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 DOMAIN.

DR EMBL: AF035026; AAD56262.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 FT NON\_TER 1 131  
 FT NON\_TER 131 131  
 SQ SEQUENCE 131 AA; 14142 MW; 967D668E375DEA0 CRC64;

Query Match 45.4%; Score 44; DB 4; Length 131;  
 Best Local Similarity 44.4%; Pred. No. 6.3;  
 Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 2 IRNKANGYTTFSASVMG 19  
 ID P91362 PRELIMINARY; PRT; 117 AA.

AC P91362;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE COSMID F59A3.  
 GN F59A3.10.

OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Cooley T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,  
 RA Snaledon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,  
 RA Thierrey-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans";  
 RL Nature 368:32-38(1994).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX Waterston R.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U80448; AAB37824.1; -.

SQ SEQUENCE 117 AA; 13808 MW; 8113F031205E2C3A CRC64;

Query Match 43.3%; Score 42; DB 5; Length 117;  
 Best Local Similarity 60.0%; Pred. No. 12;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 FIRKANGYTTESA 15  
 ID 50 FLRQTAGGATTYFSA 64

RESULT 10  
 O07414 PRELIMINARY; PRT; 346 AA.

AC O07414;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE HYPOTHETICAL 37.7 KDA PROTEIN.  
 GN RV0170 OR MFC128.10.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,  
 RA Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence";  
 RL Nature 393:537-544(1998).  
 DR EMBL: Z97050; CAB09753.1; -.  
 DR Tuberculist; RV0170; -.  
 DR InterPro: IPR003399; -.  
 DR Pfam: PF02470; mce; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 346 AA; 37727 MW; 0B6F5BC6E612805F CRC64;

Query Match 43.3%; Score 42; DB 2; Length 346;  
 Best Local Similarity 63.6%; Pred. No. 41;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 NKANGYTTES 14  
 ID 34 DRTNGYTTAES 44

RESULT 11  
 O97417 PRELIMINARY; PRT; 1792 AA.

AC O97417;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE MYOSIN V.  
 GN DIDUM OR CG2146.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]

RP SEQUENCE FROM N.A.

RA Bonafe N., Odenwald W.F., Sellers J.R.:  
 RT "Molecular cloning of myosin V in Drosophila : association with  
 RL hindgut epithelium in late embryos.";  
 RL Mol. Biol. Cell 7:372-372(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98197503; PubMed=9536440;  
 RA Bonafe N., Sellers J.R.:  
 RT "Molecular characterization of myosin V from Drosophila  
 RL melanogaster.";  
 RL J. Muscle Res. Cell. Motil. 19:129-141(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Bonafe N., Sellers J.R.:  
 RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RL [4]  
 RP SEQUENCE FROM N.A.  
 RA Bonafe N., Sellers J.R.:  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF003826; AAC99496.1; -;  
 DR HSSP; P08799; IMMN.  
 DR FlyBase; FBgn0015933; didum.  
 DR InterPro; IPR000048; -;  
 DR InterPro; IPR001609; -;  
 DR InterPro; IPR002710; -;  
 DR Pfam; PF00063; myosin\_head; 1.  
 DR Pfam; PF00612; IQ; 6.  
 DR Pfam; PF01843; DIL; 1.  
 DR ProDom; PD000355; -; 1.  
 DR ProDom; PD003376; -; 1.  
 DR SMART; SM00015; IQ; 1.  
 SQ SEQUENCE 1792 AA; 207246 MW; 08B2EF25767678DD CRC64;

Query Match 43.3%; Score 42; DB 5; Length 1792;  
 Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRNKANGYTFESASV 17  
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 Db 1383 IRNKNGTSADVGVANV 1398

RESULT 12  
 QYV4M6  
 ID QYV4M6 PRELIMINARY; PRT; 1792 AA.  
 AC QYV4M6;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE DIDUM PROTEIN.  
 GN DIDUM OR CG2146.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERLEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacliet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou X., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003841; AAF5241.2; -;  
 DR HSSP; P08799; IMMN  
 DR FlyBase; FBgn0015933; didum.  
 DR InterPro; IPR000048; -;  
 DR InterPro; IPR001609; -;  
 DR InterPro; IPR002710; -;  
 DR Pfam; PF00063; myosin\_head; 1.  
 DR Pfam; PF00612; IQ; 6.  
 DR Pfam; PF01843; DIL; 2.  
 DR PRINTS; PR00193; MYOSINHEAVY.  
 DR PROSITE; PS00193; MYOSINHEAVY.  
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Query Match 43.3%; Score 42; DB 5; Length 1792;  
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QY 2 IRNKANGYTFESASV 17  
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 QYEW9  
 ID QYEW9 PRELIMINARY; PRT; 635 AA.  
 AC QYEW9;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE TETRACYCLINE RESISTANCE PROTEIN.  
 GN TETM.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Seeger K.J., Harris D.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RA Yeh J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AF003556; AAF50445.1; -;  
 DR FlyBase; FBgn0035872; CG7185.  
 DR InterPro; IPR000504; -;  
 DR InterPro; IPR002965; -;  
 DR Pfam; PF00076; rim; 1;  
 DR PRINTS; PRO1217; PRICEXTENS.  
 DR SMART; SM00360; RRM; 1;  
 SQ SEQUENCE 702 AA; 75780 MW; 085A7E3D40F37604 CRC64;

Query Match 42.3%; Score 41; DB 5; Length 702;  
 Best Local Similarity 42.1%; Pred. No. 1.3e+02;  
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 FIRNKANGYTTTFSASVM 19  
 | : | | | : | | : |  
 Db 126 FFENRANGQSGFVSLG 144

RESULT 15  
 Q9HE61 PRELIMINARY; PRT; 745 AA.  
 AC Q9HE61;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE RELATED TO MKT1 PROTEIN.  
 GN B2F7.10.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RA Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AL451013; CAC18153.1; -;  
 SQ SEQUENCE 745 AA; 84185 MW; 45F372292C354970 CRC64;

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QY 2 IRNKANGYTTTFSASVM 18  
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Search completed: June 28, 2001, 16:08:25  
 Job time: 953 sec

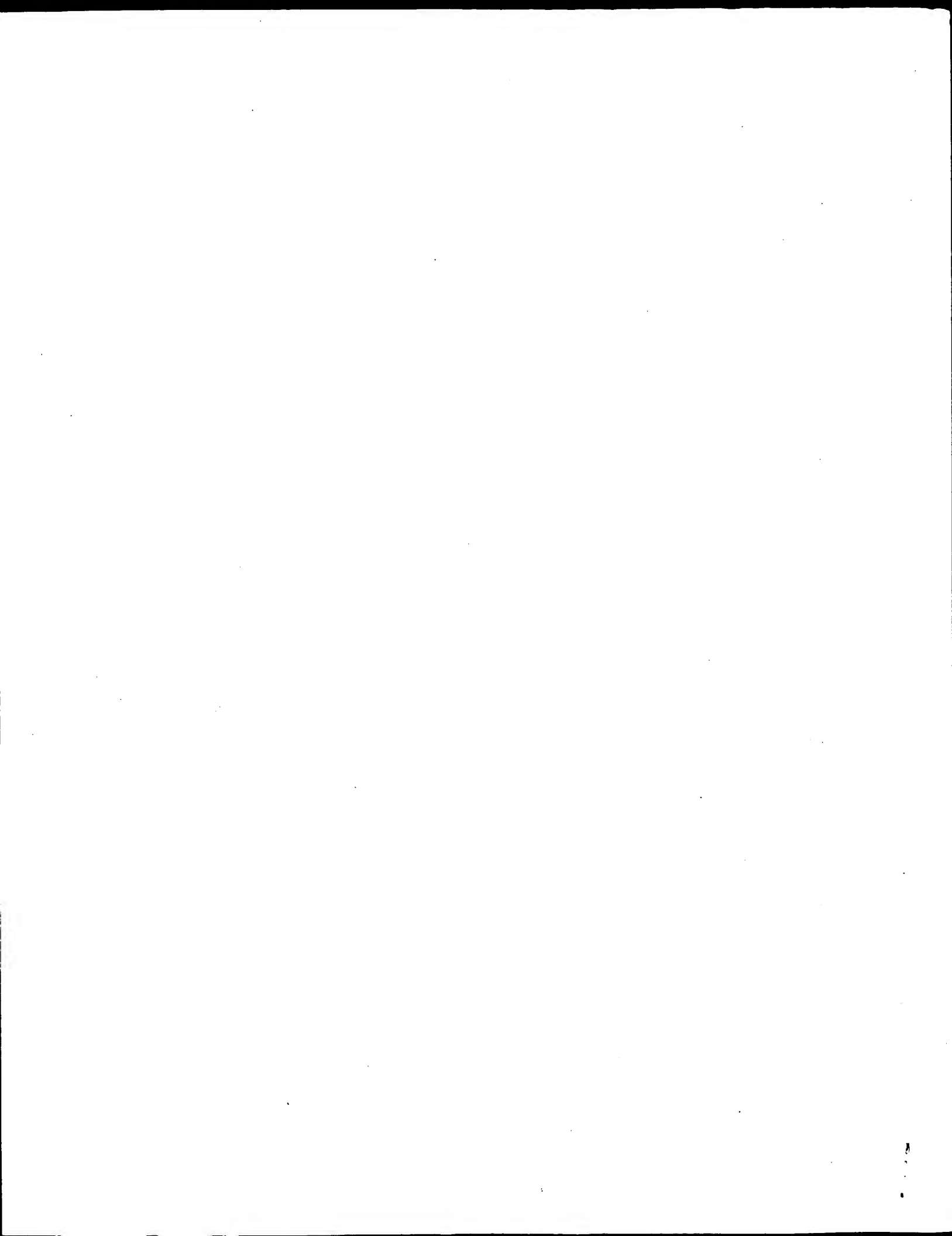
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 RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb streptomycetes coelicolor A3(2) chromosome.";  
 RL Mol. Microbiol. 21:77-96(1996).  
 DR EMBL; AL445945; CAC14348.1; -;  
 KW Cyclin.  
 SQ SEQUENCE 635 AA; 66884 MW; FD8DBCB2BF2310FF CRC64;

Query Match 42.3%; Score 41; DB 2; Length 635;  
 Best Local Similarity 47.1%; Pred. No. 1.2e+02;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 FIRNKANGYTTTFSASV 17  
 | : | : | | | | | : |  
 Db 288 FLRRESGRTTEVSGRV 304

RESULT 14  
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 ID Q9VSH4;  
 AC Q9VSH4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE CG7185 PROTEIN.  
 GN CG7185  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Adayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
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 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
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 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
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 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:37 ; Search time 362.28 Seconds

(without alignments)

2.343 Million cell updates/sec

Title: US-09-724-406-24

Perfect score: 90

Sequence: 1 DPPYGNPHYAMYD 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	63.3	115	AAW04595	Anti-DNA antibody
2	57	63.3	123	AAW07438	Anti-DNA antibody
3	49	54.4	14	AAW70907	CDR3 of the heavy
4	49	54.4	14	AAW70931	CDR3 of the heavy
5	49	54.4	23	AAW70913	Peptide pEP3H, hom
6	49	54.4	114	AAW70947	Heavy chain of mon
7	45.5	50.6	225	AAW63118	Heavy chain of 58.
8	45.5	50.6	289	AAW61541	3DX sfv protein se
9	45.5	50.6	304	AAW27978	Arabidopsis thalia
10	45.5	50.6	349	AAW27977	Arabidopsis thalia
11	45.5	50.6	422	AAW27976	Arabidopsis thalia

12	45	50.0	281	19	AAW82314	Human ScFvCD19 pro
13	45	50.0	483	19	AAW82315	Chimeric CD19/cfCR
14	44	48.9	125	22	AAW48937	Anti-TrkA murine m
15	44	48.9	295	22	AAW48934	Anti-TrkA single c
16	43.5	48.3	2573	21	AAW18234	Plasmodium falci
17	43	47.8	327	21	AAW45474	Human secreted pro
18	43	47.3	415	21	AAW1576	Streptococcus pneu
19	43	47.3	541	21	AAW42845	Human OREX ORF2609
20	43	47.3	574	21	AAW97032	Caspase 8-interact
21	43	47.3	1066	20	AAW37493	Amino acid sequenc
22	43	47.3	1428	21	AAW97033	Caspase 8-interact
23	42.5	47.2	120	18	AAW19915	Heavy chain of MAB
24	42	46.7	123	16	AAW81323	Humanized VLA-4 an
25	42	46.7	123	16	AAW81330	Mouse anti-VLA-4 a
26	42	46.7	140	16	AAW81327	Mouse VLA-4 antibo
27	42	46.7	140	18	AAW22410	Alpha-4 integrin m
28	42	46.7	142	16	AAW81333	Human VLA-4 reshap
29	42	46.7	142	18	AAW22428	Humanized alpha-4
30	42	46.7	169	21	AAW84852	Protein encoded by
31	41	45.5	337	21	AAW12715	Arabidopsis thalia
32	41	45.5	349	21	AAW12714	Arabidopsis thalia
33	41	45.5	417	21	AAW12713	Arabidopsis thalia
34	41	45.5	1592	14	AAW32925	Glucosyltransferase
35	41	45.5	2197	21	AAW18352	Plasmodium falci
36	41	45.5	2476	20	AAW67738	Pig p105 zona pell
37	40.5	45.0	116	21	AAW32655	Eucalyptus grandis
38	40.5	45.0	253	21	AAW57023	Human prostate can
39	40.5	45.0	316	14	AAW45759	Thermolysin like p
40	40	44.4	166	21	AAW45081	Human secreted pro
41	40	44.4	209	19	AAW57839	Wild type penicill
42	40	44.4	209	19	AAW57841	F146A mutant penic
43	40	44.4	209	19	AAW57842	M142A mutant penic
44	40	44.4	268	21	AAW44972	Recombinant mouse
45	40	44.4	268	21	AAW44973	Recombinant mouse

#### ALIGNMENTS

#### RESULT 1

AAW04595

ID AAW04595 standard; Protein; 115 AA.

AC AAW04595;

XX 12-AUG-1997 (first entry)

DT Anti-DNA antibody 11f8 heavy chain variable region.

DE Heavy chain; variable region; anti-DNA; monoclonal; antibody;  
KW MAB 11f8; hairpin; diagnosis; inflammatory glomerulonephritis;  
KW systemic lupus erythematosus; screening; treatment; prevention;  
KW SLE; disease.

OS Mus spp.

FH Key Location/Qualifiers

FT Region 1..22 /label= framework\_I

FT Region 23..27 /label= CDR\_I

FT Region 28..41 /label= framework\_II

FT Region 42..58 /label= CDR\_II

FT Region 59..90 /label= framework\_III

FT Region 91..102 /label= CDR\_III

FT Region 103..115 /label= J\_region

XX W09636361-A1.

```

XX PD 21-NOV-1996.
XX XX
XX PF 16-MAY-1996; 96WO-US07113.
XX PR 18-MAY-1995; 95US-0443540.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Glick GD, Swanson PC;
XX DR WPI; 1997-011854/01.
XX XX
XX XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
XX develop prods. for diagnosis and treatment of disorders, e.g.
XX glomerulonephritis or systemic lupus erythematosus
XX Example; Fig 7; 102pp; English.
XX
XX The present sequence is the heavy chain variable region of the
XX anti-DNA monoclonal antibody (MAB) 11f8, which has a high affinity
XX for single stranded DNA, low or no affinity for double stranded DNA
XX and specifically binds a DNA hairpin. The MAB can be used to diagnose
XX disorders associated with the pathological complexation of DNA,
XX e.g. inflammatory glomerulonephritis and systemic lupus
XX erythematosus. It can also be used to generate reagents to screen
XX for pharmaceutical agents, and treat and/or prevent an above
XX disorder.
XX
XX Cal thymus DNA was used to immunise a MRL-lpr mouse, spleen cells
XX from which were then fused with Sp2/0 myeloma cells to give
XX hybridomas producing the anti-DNA MAB. 1f8 was found to react
XX strongly with single stranded DNA and poly(dT).
XX
XX Sequence 115 AA;
SQ
Query Match 63.3%; Score 57; DB 18; Length 115;
Best Local Similarity 83.3%; Pred. NO. 0.13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 PYGNPHYYAMDY 14
Db 93 pygnygyyamy 104

RESULT 2
AAW07438
XX ID AAW07438 standard; Protein; 123 AA.
XX AC AAW07438;
XX XX
XX DT 12-AUG-1997 (first entry)
XX DE Anti-DNA antibody 11f8 group heavy chain variable region.
XX
XX Heavy chain; variable region; anti-DNA; monoclonal; antibody;
KW 11f8 group; hairpin; diagnosis; inflammatory glomerulonephritis;
KW systemic lupus erythematosus; screening; treatment; prevention;
KW SLE; disease; consensus; putative.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1..30
XX FT /label= framework_I
XX FT 31..35
XX FT /label= CDR_I
XX FT 36..49
XX FT /label= framework_II
XX FT 50..66
XX FT /label= CDR_II
XX FT 67..98

/label= framework_III
99..112
/label= CDR_III
113..123
/label= J_region

WO9636361-A1.
21-NOV-1996.
16-MAY-1996; 96WO-US07113.
18-MAY-1995; 95US-0443540.
(UNMI ) UNIV MICHIGAN.
Glick GD, Swanson PC;
WPI; 1997-011854/01.

Anti-DNA antibody which specifically binds DNA hairpin - useful to
develop prods. for diagnosis and treatment of disorders, e.g.
glomerulonephritis or systemic lupus erythematosus
Example; Fig 9; 102pp; English.

The present sequence is the heavy chain variable region of the
group 11f8 putative consensus anti-DNA monoclonal antibody (MAB),
which has a high affinity for single stranded DNA, low or no
affinity for double stranded DNA and specifically binds a DNA
hairpin. The MAB can be used to diagnose disorders associated with the
pathological complexation of DNA, e.g. inflammatory
glomerulonephritis and systemic lupus erythematosus. It can also be
used to generate reagents to screen for pharmaceutical agents, and
treat and/or prevent an above disorder.
The sequence was derived by aligning homologous anti-DNA MAB, of
whose sequences have been published, as well as several MAB of
other specificities obtained from a database search.

SQ Sequence 123 AA;

Query Match 63.3%; Score 57; DB 18; Length 123;
Best Local Similarity 83.3%; Pred. NO. 0.14;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 PYGNPHYYAMDY 14
Db 101 pygnygyyamy 112

RESULT 3
AAW70907
XX ID AAW70907 standard; peptide; 14 AA.
XX AC AAW70907;
XX XX
XX DT 14-OCT-1998 (first entry)
XX DE CDR3 of the heavy chain of monoclonal antibody RS-348.
XX
XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
KW viral infection; inhibit; fusion; protection; transcription;
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX
XX Synthetic.
XX OS Mus sp.
XX PN FR2758331-A1.
XX PD 17-JUL-1998.
XX XX

```

PF 14-JAN-1997; 97FR-0000300.  
 XX  
 PR 14-JAN-1997; 97FR-0000300.  
 XX  
 FA (UYBO-) UNIV BOURGOGNE.  
 XX  
 PI Bourgeois C, Kohli E, Pothier P;  
 XX  
 DR WPI; 1998-390320/34.  
 XX  
 XX New peptide(s) recognising viral epitope with tropism to mucosa -  
 PT useful for, e.g. diagnosing, preventing and treating viral  
 PT infection(s)  
 XX  
 PS Claim 8; Fig 3; 5lpp; French.  
 XX  
 CC AAW70905-46 represent peptide sequences that can recognise, by  
 CC antigen-antibody type reactions, at least 1 epitope of a pathogenic  
 CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are  
 CC analogous to CDR regions of monoclonal antibodies specific for  
 CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR  
 CC regions of monoclonal antibodies specific for site III or IV of the  
 CC VP6 protein of rota virus (RV). The peptides can neutralise viral  
 CC infections and may also inhibit fusion between infected and uninfected  
 CC cells or cells and viruses. They provide passive or active protection  
 CC and/or inhibit transcription of the virus, so are useful as antiviral  
 CC agents or for prophylaxis, in human or veterinary medicine. The peptides  
 CC can be labelled and used to diagnose infection or contamination by the  
 CC virus. The peptides are particularly directed against RSV or RS but may  
 CC also be used against papilloma, adeno, entero, polio, influenza or  
 CC immune deficiency viruses.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 54.4%; Score 49; DB 19; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 0.25;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DPPYGNPHYAMDY 14  
 ||| : : : ||||  
 Db 1 dpdyndnyfyamdy 14  
 RESULT 4  
 AAW70931  
 ID AAW70931 standard; peptide; 14 AA.  
 XX  
 AC AAW70931;  
 XX  
 DT 14-OCT-1998 (first entry)  
 XX  
 DE CDR3 of the heavy chain of monoclonal antibody RS-18B2.  
 XX  
 KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
 KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;  
 KW viral infection; inhibit; fusion; protection; transcription;  
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 PN FR2758331-A1.  
 XX  
 PD 17-JUL-1998.  
 XX  
 PF 14-JAN-1997; 97FR-0000300.  
 XX  
 PR 14-JAN-1997; 97FR-0000300.  
 XX  
 PA (UYBO-) UNIV BOURGOGNE.  
 XX  
 PI Bourgeois C, Kohli E, Pothier P;

XX  
 DR WPI; 1998-390320/34.  
 XX  
 PT New peptide(s) recognising viral epitope with tropism to mucosa -  
 PT useful for, e.g. diagnosing, preventing and treating viral  
 PT infection(s)  
 XX  
 PS Claim 12; Page 33; 5lpp; French.  
 XX  
 CC AAW70905-46 represent peptide sequences that can recognise, by  
 CC antigen-antibody type reactions, at least 1 epitope of a pathogenic  
 CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are  
 CC analogous to CDR regions of monoclonal antibodies specific for  
 CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR  
 CC regions of monoclonal antibodies specific for site III or IV of the  
 CC VP6 protein of rota virus (RV). The peptides can neutralise viral  
 CC infections and may also inhibit fusion between infected and uninfected  
 CC cells or cells and viruses. They provide passive or active protection  
 CC and/or inhibit transcription of the virus, so are useful as antiviral  
 CC agents or for prophylaxis, in human or veterinary medicine. The peptides  
 CC can be labelled and used to diagnose infection or contamination by the  
 CC virus. The peptides are particularly directed against RSV or RS but may  
 CC also be used against papilloma, adeno, entero, polio, influenza or  
 CC immune deficiency viruses.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 54.4%; Score 49; DB 19; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 0.25;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DPPYGNPHYAMDY 14  
 ||| : : : ||||  
 Db 1 dpdyndnyfyamdy 14  
 RESULT 5  
 AAW70913  
 ID AAW70913 standard; peptide; 23 AA.  
 XX  
 AC AAW70913;  
 XX  
 DT 14-OCT-1998 (first entry)  
 XX  
 DE Peptide PEP3H, homologous to heavy chain CDR3 of antibody RS-348.  
 XX  
 KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
 KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;  
 KW viral infection; inhibit; fusion; protection; transcription;  
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 PN FR2758331-A1.  
 XX  
 PD 17-JUL-1998.  
 XX  
 PF 14-JAN-1997; 97FR-0000300.  
 XX  
 PR 14-JAN-1997; 97FR-0000300.  
 XX  
 PA (UYBO-) UNIV BOURGOGNE.  
 XX  
 PI Bourgeois C, Kohli E, Pothier P;  
 XX  
 DR WPI; 1998-390320/34.  
 XX  
 PT New peptide(s) recognising viral epitope with tropism to mucosa -  
 PT useful for, e.g. diagnosing, preventing and treating viral  
 PT infection(s)  
 XX

PS Claim 8; Fig 5; 51pp; French.

XX AAW70905-46 represent peptide sequences that can recognise, by  
CC antigen-antibody type reactions, at least 1 epitope of a pathogenic  
CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are  
CC analogous to CDR regions of monoclonal antibodies specific for  
CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR  
CC regions of monoclonal antibodies specific for site III or IV of the  
CC VP6 protein of rota virus (RV). The peptides can neutralise viral  
CC infections and may also inhibit fusion between infected and uninfected  
CC cells or cells and viruses. They provide passive or active protection  
CC and/or inhibit transcription of the virus, so are useful as antiviral  
CC agents or for prophylaxis, in human or veterinary medicine. The peptides  
CC can be labelled and used to diagnose infection or contamination by the  
CC virus. The peptides are particularly directed against RSV or RS but may  
CC also be used against papilloma, adeno, entero, polio, influenza or  
CC immune deficiency viruses.

XX Sequence 23 AA;

Query Match 54.4%; Score 49; DB 19; Length 23;  
Best Local Similarity 57.1%; Pred. No. 0.41;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPYGNPHYAMDY 14  
||| : :|||  
Db 4 dpdydnyfyamdy 17

RESULT 6

AAW70947  
ID AAW70947 standard; protein; 114 AA.

XX AAW70947;

XX 14-OCT-1998 (first entry)

XX Heavy chain of monoclonal antibody RS-348.

XX Pathogenic virus; tropism: mucosa; CDR region; monoclonal antibody;  
KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;  
KW viral infection; inhibit; fusion; protection; transcription;  
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.

XX Mus sp.

XX FR2758331-A1.

XX 17-JUL-1998.

XX 14-JAN-1997; 97FR-0000300.

XX 14-JAN-1997; 97FR-0000300.

XX (UYBO-) UNIV BOURGOGNE.

XX Bourgeois C, Kohli E, Pothier P;

XX WPI; 1998-390320/34.

XX New peptide(s) recognising viral epitope with tropism to mucosa -  
PT useful for, e.g. diagnosing, preventing and treating viral  
PT infection(s)

XX Disclosure; Fig 2; 51pp; French.

XX The present sequence represents the heavy chain of monoclonal antibody  
CC RS-348, which is directed against the respiratory syncytial virus (RSV).  
CC The specification describes peptides which recognise, by  
CC antigen-antibody type reactions, at least 1 epitope of a pathogenic virus  
CC having tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous  
CC to CDR regions of monoclonal antibodies specific for RSV. AAW70917-28 are

CC analogous to CDR regions of monoclonal antibodies specific for site III  
CC or IV of the VP6 protein of rota virus (RV). The peptides can neutralise  
CC viral infections and may also inhibit fusion between infected and  
CC uninfected cells or cells and viruses. They provide passive or active  
CC protection and/or inhibit transcription of the virus, so are useful as  
CC antiviral agents or for prophylaxis, in human or veterinary medicine. The  
CC peptides can be labelled and used to diagnose infection or contamination  
CC by the virus. The peptides are particularly directed against RSV or RS  
CC but may also be used against papilloma, adeno, entero, polio, influenza  
CC or immune deficiency viruses.

XX Sequence 114 AA;

Query Match 54.4%; Score 49; DB 19; Length 114;  
Best Local Similarity 57.1%; Pred. No. 2.1;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPYGNPHYAMDY 14  
||| : :|||  
Db 98 dpdydnyfyamdy 111

RESULT 7

AAW63118  
ID AAW63118 standard; peptide; 225 AA.

XX AAW63118;

XX 26-JUN-1995 (first entry)

XX Heavy chain of 58.2 an anti-HIV antibody.

XX Identifying compounds; anti-HIV antibodies; HIV treatment;  
KW peptide AS; antibody 58.2.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 160

FT /label= OTHER

FT /note= "CPR no further definition"

FT Modified-site 162

FT /label= OTHER

FT /note= "CPR no further definition "

FT Modified-site 201

FT /label= OTHER

FT /note= "CPR no further definition"

XX WO9418232-A.

XX 18-AUG-1994.

XX 09-FEB-1994; 94WO-US01458.

XX 12-FEB-1993; 93US-0017485.

XX (REPK ) REPLIGEN CORP.

XX (SCRI ) SCRIPPS RES INST.

XX Profy AT, Wilson IA;

XX WPI; 1994-332662/41.

XX Identifying cpds. which elicit, or bind to, anti-HIV antibodies -  
PT and new antibodies which neutralise a broad range of HIV strains

XX Disclosure; Page 50; 137pp; English.

XX AAW63118 describes the amino acid sequence of the heavy chain of  
CC 58.2 an anti-HIV antibody (Ab), it was used in the development of  
CC the peptide AS (AAW63119). This peptide can bind to anti-HIV Abs or  
CC elicit new Abs effective against a broad range of HIV strains,

CC that can be used in the treatment of HIV infection.

XX Sequence 225 AA;

Query Match 50.6%; Score 45.5; DB 15; Length 225;  
Best Local Similarity 75.0%; Pred. No. 14;  
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 3 PYGN-PHYAMD 13  
||||:|||||  
Db 103 pygndqyyamd 114

# RESULT 8

AAB61541  
ID AAB61541 standard; Protein; 269 AA.

XX AC AAB61541;

DT 03-APR-2001 (first entry)

XX DE 3DX sfv protein sequence.

XX KW 3DX; single chain antibody; ScFv; modular protein binding domain; MPBD;  
KW protein-protein interaction.

XX OS Unidentified.

XX FN WO200101137-A1.

XX PD 04-JAN-2001.

XX PF 29-JUN-2000; 2000WO-US17929.

XX PR 30-JUN-1999; 99US-0141896.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.  
PA (BLOO-) CENT BLOOD RES.

XX PI Mayer BJ, Saksele K, Kirchausen T;

XX WPI; 2001-123027/13.

DR N-PSDB; AAF28599.

XX FT New fusion proteins, useful for validating protein-protein interaction  
FT causing a specific biological activity, comprises a single chain  
FT antibody instead of a modular protein binding domain

XX PS Example 1; Fig 1; 34pp; English.

XX CC The present invention relates to fusion proteins containing a single  
CC chain antibody (sfv) in place of a modular protein binding domain (MPBD),  
CC or an antibody epitope in place of the linear binding epitope for a MPBD.  
CC The fusion proteins can be used in assays to identify protein-protein  
CC interactions. The present sequence is the protein sequence for 3DX  
CC antibody. 3DX is derived from 9E10. 3DX was used in the method of the  
CC present invention.

XX Sequence 269 AA;

Query Match 50.6%; Score 45.5; DB 22; Length 269;  
Best Local Similarity 75.0%; Pred. No. 17;  
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 4 YGNPHY-AMDY 14  
||||:|||||  
Db 110 ygntyysamyd 121

# RESULT 9

AAG27978

ID AAG27978 standard; Protein; 304 AA.

XX AC AAG27978;

DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 33024.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 23-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 23-APR-1999; 99US-0130891.

XX PR 28-APR-1999; 99US-0131449.

XX PR 30-APR-1999; 99US-0132048.

XX PR 30-APR-1999; 99US-0132407.

XX PR 04-MAY-1999; 99US-0132484.

XX PR 05-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 06-MAY-1999; 99US-0132487.

XX PR 07-MAY-1999; 99US-0132863.

XX PR 11-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.

XX PR 14-MAY-1999; 99US-0134219.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 14-MAY-1999; 99US-0134370.

XX PR 18-MAY-1999; 99US-0134768.

XX PR 19-MAY-1999; 99US-0134941.

XX PR 20-MAY-1999; 99US-0135124.

XX PR 21-MAY-1999; 99US-0135353.

XX PR 24-MAY-1999; 99US-0135629.

XX PR 25-MAY-1999; 99US-0136021.

XX PR 27-MAY-1999; 99US-0136392.

XX PR 28-MAY-1999; 99US-0136782.

XX PR 01-JUN-1999; 99US-0137222.

XX PR 03-JUN-1999; 99US-0137528.

XX PR 04-JUN-1999; 99US-0137502.

XX PR 07-JUN-1999; 99US-0137724.

XX PR 08-JUN-1999; 99US-0138094.

XX PR 10-JUN-1999; 99US-0138540.

XX PR 14-JUN-1999; 99US-0138847.

XX PR 14-JUN-1999; 99US-0139119.

XX PR 16-JUN-1999; 99US-0139452.

XX PR 16-JUN-1999; 99US-0139453.

XX PR 17-JUN-1999; 99US-0139492.

XX PR 18-JUN-1999; 99US-0139454.

XX PR 18-JUN-1999; 99US-0139455.

XX PR 18-JUN-1999; 99US-0139456.

XX PR 18-JUN-1999; 99US-0139457.

XX PR 18-JUN-1999; 99US-0139458.

XX PR 18-JUN-1999; 99US-0139459.

XX PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.  
 PR 18-JUN-1999; 99US-0139462.  
 PR 18-JUN-1999; 99US-0139463.  
 PR 18-JUN-1999; 99US-0139750.  
 PR 18-JUN-1999; 99US-0139763.  
 PR 21-JUN-1999; 99US-0139817.  
 PR 22-JUN-1999; 99US-0139899.  
 PR 23-JUN-1999; 99US-0140353.  
 PR 23-JUN-1999; 99US-0140354.  
 PR 24-JUN-1999; 99US-0140695.  
 PR 24-JUN-1999; 99US-0140823.  
 PR 28-JUN-1999; 99US-0140991.  
 PR 29-JUN-1999; 99US-0141287.  
 PR 30-JUN-1999; 99US-0141842.  
 PR 01-JUL-1999; 99US-0142154.  
 PR 02-JUL-1999; 99US-0142055.  
 PR 06-JUL-1999; 99US-0142390.  
 PR 08-JUL-1999; 99US-0142803.  
 PR 09-JUL-1999; 99US-0142920.  
 PR 12-JUL-1999; 99US-0142977.  
 PR 13-JUL-1999; 99US-0143542.  
 PR 14-JUL-1999; 99US-0143624.  
 PR 15-JUL-1999; 99US-0144005.  
 PR 16-JUL-1999; 99US-0144085.  
 PR 16-JUL-1999; 99US-0144086.  
 PR 19-JUL-1999; 99US-0144325.  
 PR 19-JUL-1999; 99US-0144331.  
 PR 19-JUL-1999; 99US-0144332.  
 PR 19-JUL-1999; 99US-0144333.  
 PR 19-JUL-1999; 99US-0144334.  
 PR 19-JUL-1999; 99US-0144335.  
 PR 20-JUL-1999; 99US-0144352.  
 PR 20-JUL-1999; 99US-0144632.  
 PR 20-JUL-1999; 99US-0144884.  
 PR 21-JUL-1999; 99US-0144814.  
 PR 21-JUL-1999; 99US-0145086.  
 PR 21-JUL-1999; 99US-0145088.  
 PR 22-JUL-1999; 99US-0145085.  
 PR 22-JUL-1999; 99US-0145087.  
 PR 22-JUL-1999; 99US-0145089.  
 PR 22-JUL-1999; 99US-0145192.  
 PR 23-JUL-1999; 99US-0145145.  
 PR 23-JUL-1999; 99US-0145218.  
 PR 23-JUL-1999; 99US-0145224.  
 PR 26-JUL-1999; 99US-0145276.  
 PR 27-JUL-1999; 99US-0145913.  
 PR 27-JUL-1999; 99US-0145918.  
 PR 27-JUL-1999; 99US-0145919.  
 PR 28-JUL-1999; 99US-0145951.  
 PR 02-AUG-1999; 99US-0146386.  
 PR 02-AUG-1999; 99US-0146388.  
 PR 02-AUG-1999; 99US-0146389.  
 PR 03-AUG-1999; 99US-0147038.  
 PR 04-AUG-1999; 99US-0147204.  
 PR 04-AUG-1999; 99US-0147302.  
 PR 05-AUG-1999; 99US-0147192.  
 PR 05-AUG-1999; 99US-0147260.  
 PR 06-AUG-1999; 99US-0147303.  
 PR 06-AUG-1999; 99US-0147416.  
 PR 09-AUG-1999; 99US-0147493.  
 PR 09-AUG-1999; 99US-0147935.  
 PR 10-AUG-1999; 99US-0148171.  
 PR 11-AUG-1999; 99US-0148319.  
 PR 12-AUG-1999; 99US-0148341.  
 PR 13-AUG-1999; 99US-0148565.  
 PR 13-AUG-1999; 99US-0148684.  
 PR 16-AUG-1999; 99US-0149368.  
 PR 17-AUG-1999; 99US-0149175.  
 PR 18-AUG-1999; 99US-0149426.  
 PR 20-AUG-1999; 99US-0149722.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 20-AUG-1999; 99US-0149929.  
 PR 23-AUG-1999; 99US-0149902.

PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150566.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151086.  
 PR 27-AUG-1999; 99US-0151080.  
 PR 30-AUG-1999; 99US-0151303.  
 PR 31-AUG-1999; 99US-0151438.  
 PR 01-SEP-1999; 99US-0151930.  
 PR 07-SEP-1999; 99US-0152363.  
 PR 10-SEP-1999; 99US-0153070.  
 PR 13-SEP-1999; 99US-0153758.  
 PR 15-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 22-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159331.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
 PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 50.6%; Score 45.5; DB 21; Length 304;  
 Best Local Similarity 53.3%; Pred. No. 19;  
 Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 3 PYG---NPHYAMDY 14  
 ||| :||| :||  
 Db 96 pygfpvdpdphgwdy 110

RESULT 10  
 AAG27977  
 ID AAG27977 standard; Protein; 349 AA.  
 XX  
 AC AAG27977;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 33023.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
XX EPI033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0123180.  
XX 09-MAR-1999; 99US-0123548.  
XX 23-MAR-1999; 99US-0125788.  
XX 25-MAR-1999; 99US-0126264.  
XX 29-MAR-1999; 99US-0126785.  
XX 01-APR-1999; 99US-0127462.  
XX 06-APR-1999; 99US-0128234.  
XX 08-APR-1999; 99US-0128714.  
XX 16-APR-1999; 99US-0129845.  
XX 19-APR-1999; 99US-0130077.  
XX 21-APR-1999; 99US-0130449.  
XX 23-APR-1999; 99US-0130510.  
XX 28-APR-1999; 99US-0130891.  
XX 30-APR-1999; 99US-0131449.  
XX 30-APR-1999; 99US-0132048.  
XX 04-MAY-1999; 99US-0132407.  
XX 05-MAY-1999; 99US-0132484.  
XX 06-MAY-1999; 99US-0132485.  
XX 06-MAY-1999; 99US-0132486.  
XX 07-MAY-1999; 99US-0132487.  
XX 11-MAY-1999; 99US-0132863.  
XX 14-MAY-1999; 99US-0134256.  
XX 14-MAY-1999; 99US-0134218.  
XX 14-MAY-1999; 99US-0134219.  
XX 14-MAY-1999; 99US-0134321.  
XX 14-MAY-1999; 99US-0134370.  
XX 18-MAY-1999; 99US-0134768.  
XX 19-MAY-1999; 99US-0134941.  
XX 20-MAY-1999; 99US-0135124.  
XX 21-MAY-1999; 99US-0135353.  
XX 24-MAY-1999; 99US-0135629.  
XX 25-MAY-1999; 99US-0136021.  
XX 27-MAY-1999; 99US-0136392.  
XX 28-MAY-1999; 99US-0136782.  
XX 01-JUN-1999; 99US-0137222.  
XX 03-JUN-1999; 99US-0137528.  
XX 04-JUN-1999; 99US-0137502.  
XX 07-JUN-1999; 99US-0137724.  
XX 08-JUN-1999; 99US-0138094.  
XX 10-JUN-1999; 99US-0138540.  
XX 10-JUN-1999; 99US-0138847.  
XX 14-JUN-1999; 99US-0139119.  
XX 16-JUN-1999; 99US-0139452.  
XX 16-JUN-1999; 99US-0139453.  
XX 17-JUN-1999; 99US-0139492.  
XX 18-JUN-1999; 99US-0139454.  
XX 18-JUN-1999; 99US-0139455.  
XX 18-JUN-1999; 99US-0139456.  
XX 18-JUN-1999; 99US-0139457.  
XX 18-JUN-1999; 99US-0139458.  
XX 18-JUN-1999; 99US-0139459.  
XX 18-JUN-1999; 99US-0139460.  
XX 18-JUN-1999; 99US-0139461.  
XX 18-JUN-1999; 99US-0139462.  
XX 18-JUN-1999; 99US-0139463.  
XX 18-JUN-1999; 99US-0139750.  
XX 18-JUN-1999; 99US-0139763.  
XX 21-JUN-1999; 99US-0139817.  
XX 22-JUN-1999; 99US-0139899.  
XX 23-JUN-1999; 99US-0140353.  
XX 23-JUN-1999; 99US-0140354.  
XX 24-JUN-1999; 99US-0140695.  
XX 28-JUN-1999; 99US-0140823.  
XX 29-JUN-1999; 99US-0140991.  
XX 30-JUN-1999; 99US-0141287.  
XX 01-JUL-1999; 99US-0141842.  
XX 01-JUL-1999; 99US-0142154.  
XX 02-JUL-1999; 99US-0142055.  
XX 06-JUL-1999; 99US-0142390.  
XX 08-JUL-1999; 99US-0142803.  
XX 09-JUL-1999; 99US-0142920.  
XX 12-JUL-1999; 99US-0142977.  
XX 13-JUL-1999; 99US-0143542.  
XX 14-JUL-1999; 99US-0143624.  
XX 15-JUL-1999; 99US-0144005.  
XX 16-JUL-1999; 99US-0144085.  
XX 16-JUL-1999; 99US-0144086.  
XX 19-JUL-1999; 99US-0144325.  
XX 19-JUL-1999; 99US-0144331.  
XX 19-JUL-1999; 99US-0144332.  
XX 19-JUL-1999; 99US-0144333.  
XX 19-JUL-1999; 99US-0144334.  
XX 19-JUL-1999; 99US-0144335.  
XX 20-JUL-1999; 99US-0144352.  
XX 20-JUL-1999; 99US-0144632.  
XX 20-JUL-1999; 99US-0144884.  
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XX 21-JUL-1999; 99US-0145086.  
XX 21-JUL-1999; 99US-0145088.  
XX 22-JUL-1999; 99US-0145085.  
XX 22-JUL-1999; 99US-0145087.  
XX 22-JUL-1999; 99US-0145089.  
XX 22-JUL-1999; 99US-0145192.  
XX 23-JUL-1999; 99US-0145145.  
XX 23-JUL-1999; 99US-0145218.  
XX 23-JUL-1999; 99US-0145224.  
XX 26-JUL-1999; 99US-0145276.  
XX 27-JUL-1999; 99US-0145913.  
XX 27-JUL-1999; 99US-0145918.  
XX 27-JUL-1999; 99US-0145919.  
XX 28-JUL-1999; 99US-0145951.  
XX 02-AUG-1999; 99US-0146386.  
XX 02-AUG-1999; 99US-0146388.  
XX 02-AUG-1999; 99US-0146389.  
XX 03-AUG-1999; 99US-0147038.  
XX 04-AUG-1999; 99US-0147204.  
XX 04-AUG-1999; 99US-0147302.  
XX 05-AUG-1999; 99US-0147192.  
XX 05-AUG-1999; 99US-0147260.  
XX 06-AUG-1999; 99US-0147303.  
XX 06-AUG-1999; 99US-0147416.  
XX 09-AUG-1999; 99US-0147493.  
XX 09-AUG-1999; 99US-0147935.  
XX 10-AUG-1999; 99US-0148171.  
XX 11-AUG-1999; 99US-0148319.  
XX 12-AUG-1999; 99US-0148341.  
XX 13-AUG-1999; 99US-0148565.  
XX 13-AUG-1999; 99US-0148684.  
XX 16-AUG-1999; 99US-0149368.  
XX 17-AUG-1999; 99US-0149175.  
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XX 23-AUG-1999; 99US-0149902.  
XX 23-AUG-1999; 99US-0149930.  
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XX 27-AUG-1999; 99US-0151065.  
XX 27-AUG-1999; 99US-0151066.  
XX 27-AUG-1999; 99US-0151080.  
XX 30-AUG-1999; 99US-0151303.

PR	31-AUG-1999;	99US-0151438.	PN	EPI033405-A2.
PR	01-SEP-1999;	99US-0151930.	XX	
PR	07-SEP-1999;	99US-0152363.	PD	
PR	10-SEP-1999;	99US-0153070.	XX	06-SEP-2000.
PR	13-SEP-1999;	99US-0153758.	XX	
PR	15-SEP-1999;	99US-0154018.	PF	*25-FEB-2000; 2000EP-0301439.
PR	16-SEP-1999;	99US-0154039.	XX	
PR	20-SEP-1999;	99US-0154779.	PR	25-FEB-1999;
PR	22-SEP-1999;	99US-0155139.	PR	99US-0121825.
PR	23-SEP-1999;	99US-0155486.	PR	99US-0123180.
PR	24-SEP-1999;	99US-0155659.	PR	99US-0123548.
PR	28-SEP-1999;	99US-0156458.	PR	99US-0125788.
PR	29-SEP-1999;	99US-0156596.	PR	99US-0126284.
PR	04-OCT-1999;	99US-0157117.	PR	99US-0126785.
PR	05-OCT-1999;	99US-0157753.	PR	99US-0127462.
PR	06-OCT-1999;	99US-0157865.	PR	99US-0128234.
PR	07-OCT-1999;	99US-0158029.	PR	99US-0128714.
PR	08-OCT-1999;	99US-0158232.	PR	99US-0128845.
PR	12-OCT-1999;	99US-0158369.	PR	99US-0130077.
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PR	14-OCT-1999;	99US-0159330.	PR	99US-0132048.
PR	14-OCT-1999;	99US-0159331.	PR	99US-0132407.
PR	14-OCT-1999;	99US-0159637.	PR	99US-0132484.
PR	14-OCT-1999;	99US-0159638.	PR	99US-0132486.
PR	18-OCT-1999;	99US-0159584.	PR	99US-0132487.
PR	21-OCT-1999;	99US-0160741.	PR	99US-0132863.
PR	21-OCT-1999;	99US-0160767.	PR	99US-0134256.
PR	21-OCT-1999;	99US-0160768.	PR	99US-0134218.
PR	21-OCT-1999;	99US-0160770.	PR	99US-0134219.
PR	21-OCT-1999;	99US-0160814.	PR	99US-0134221.
PR	21-OCT-1999;	99US-0160815.	PR	99US-0134370.
PR	22-OCT-1999;	99US-0160880.	PR	99US-0134768.
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PR	26-OCT-1999;	99US-0161360.	PR	99US-0136782.
PR	26-OCT-1999;	99US-0161361.	PR	99US-0137222.
PR	28-OCT-1999;	99US-0161920.	PR	99US-0137528.
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PR	28-OCT-1999;	99US-0161993.	PR	99US-0137724.
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PR			PR	99US-0139119.
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PR			PR	99US-0139461.
PR			PR	99US-0139462.
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PR			PR	99US-0139750.
PR			PR	99US-0139763.
PR			PR	99US-0139817.
PR			PR	99US-0139899.
PR			PR	99US-0140353.
PR			PR	99US-0140354.
PR			PR	99US-0140695.
PR			PR	99US-0140823.
PR			PR	99US-0140991.
PR			PR	99US-0141287.
PR			PR	99US-0141842.

Query Match 50.8%; Score 45.5; DB 21; Length 349;

Best Local Similarity 53.3%; Pred. No. 22;

Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 3 PYG---NPHYXAMDY 14

Db 141 pygfpvphgwdy 155

RESULT 11

AAG27976

ID AAG27976 standard; Protein; 422 AA.

AC AAG27976;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 33022.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX

OS Arabidopsis thaliana.

XX



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PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
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PR 21-JUL-1999; 99US-0145086.
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PR 22-JUL-1999; 99US-0145085.
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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145313.
PR 27-JUL-1999; 99US-0145318.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
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PR 08-AUG-1999; 99US-0147493.
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PR 12-AUG-1999; 99US-0148341.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.

PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 50.6%; Score 45.5; DB 21; Length 422;
Best Local Similarity 53.3%; Pred No. 27;
Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 3 PYG---NPHYAMDY 14
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Db 214 pygfpvdpvphgwdy 228

RESULT 12
AAW82314
ID AAW82314 standard; Protein; 281 AA.
XX
AC AAW82314;
XX
DT 26-FEB-1999 (first entry)
XX
DE Human ScFvCD19 protein.
XX
KW ScFvCD19; anti-CD19; single chain; antibody; B-cell marker; CD19; T cell;
KW retroviral vector; gene therapy; tumour-associated antigen; cancer.
XX
OS Homo sapiens.
XX
PN DE19720152-A1.
XX
PD 05-NOV-1998.
XX
PF 02-MAY-1997; 97DE-1020152.
XX
PR 02-MAY-1997; 97DE-1020152.
XX
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PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX Bargou R, Schroeder A, Schwenkenbecher J;  
 XX WPI; 1998-584686/50.  
 DR N-PSDB; AAV73323.  
 XX Retroviral vector system for gene therapy - by expression of  
 PT therapeutic gene in T cells  
 XX Claim 8; Page 5; 10pp; German.  
 XX This sequence represents a novel human recombinant anti-CD19 single chain  
 CC antibody, ScFvCD19 which recognizes the extracellular domain of the  
 CC B-cell marker CD19. This sequence is used in a retroviral vector system  
 CC for gene transfer and expression in primary human T cells which involves  
 CC a retroviral vector containing cDNA corresponding to a therapeutic gene,  
 CC a promoter selected from the SV40 immediate early promoter or the human  
 CC IL-2 or MHC I promoter and a selectable marker, and a packaging cell  
 CC line (i.e. a modified retroviral packaging line for enhanced transfer  
 CC into primary human T lymphocytes). This vector system in which the cDNA  
 CC encodes a single-chain antibody (scFv) specific for a tumour-associated  
 CC antigen can be used for gene therapy of cancer, especially by isolating  
 CC T cells from the patient's blood, stimulating the T cells in vitro,  
 CC introducing the retroviral vector into the T cells and returning the T  
 CC cells to the patient, preferably by intravenous injection.  
 XX SQ Sequence 281 AA;

Query Match 50.0%; Score 45; DB 19; Length 281;  
 Best Local Similarity 87.5%; Pred. No. 21;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 PHYVAMYD 14  
 Db 125 pyyyamyd 132

RESULT 13

AAW82315  
 ID AAW82315 standard; Protein; 483 AA.

AC AAW82315;

DT 26-FEB-1999 (first entry)

DE Chimeric CD19/CTCR protein.

XX Single chain; antibody; B-cell marker; CD19; ScFvCD19; gene therapy;  
 KW retroviral vector; tumour-associated antigen; cancer; immunoglobulin;  
 KW CD8 alpha chain; hinge region; theta chain; transmembrane domain;  
 KW intracellular domain; T-cell receptor-CD3 complex.

OS Homo sapiens.  
 OS Synthetic.

PN DE19720152-AL.

PD 05-NOV-1998.

PF 02-MAY-1997; 97DE-1020152.

PR 02-MAY-1997; 97DE-1020152.

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX Bargou R, Schroeder A, Schwenkenbecher J;

XX WPI; 1998-584686/50.

DR N-PSDB; AAV73324.

XX Retroviral vector system for gene therapy - by expression of

PT therapeutic gene in T cells

XX Claim 9; Page 6; 10pp; German.

XX This sequence represents a novel chimeric CD19/CTCR protein which is  
 CC composed of an immunoglobulin leader sequence, an anti-CD19 single chain  
 CC antibody fragment (ScFvCD19), a hinge region from the CD8 alpha-chain  
 CC and the transmembrane and intracellular domain of the T-cell  
 CC receptor-CD3 complex theta chain. This sequence is used in a retroviral  
 CC vector system for gene transfer and expression in primary human T cells  
 CC which involves a retroviral vector containing cDNA corresponding to a  
 CC therapeutic gene, a promoter selected from the SV40 immediate early  
 CC promoter or the human IL-2 or MHC I promoter and a selectable marker, and  
 CC a packaging cell line (i.e. a modified retroviral packaging line for  
 CC enhanced transfer into primary human T lymphocytes). This vector system  
 CC in which the cDNA encodes a single-chain antibody (scFv) specific for a  
 CC tumour-associated antigen can be used for gene therapy of cancer,  
 CC especially by isolating T cells from the patient's blood, stimulating the  
 CC T cells in vitro, introducing the retroviral vector into the T cells and  
 CC returning the T cells to the patient, preferably by intravenous  
 CC injection.

XX SQ Sequence 483 AA;

Query Match 50.0%; Score 45; DB 19; Length 483;  
 Best Local Similarity 87.5%; Pred. No. 37;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 PHYVAMYD 14  
 Db 125 pyyyamyd 132

RESULT 14

AAW48937

ID AAW48937 standard; Protein; 125 AA.

AC AAW48937;

DT 16-MAR-2001 (first entry)

DE Anti-TrkA murine monoclonal antibody MNAC13 light chain variable region.

XX Murine monoclonal antibody MNAC13; heavy chain variable region; VH;

KW human TrkA antagonist; NGF receptor; nerve growth factor;

KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;

KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging;

KW diagnosis.

OS Mus sp.

PN WO200073344-A2.

PD 07-DEC-2000.

PF 26-MAY-2000; 2000WO-IT00218.

PR 26-MAY-1999; 99IT-RM00333.

PA (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.

PI Novak MM;

DR WPI; 2001-061515/07.

DR N-PSDB; AAC87642.

XX Monoclonal antibody and its derivatives specific to high affinity  
 PT tyrosine kinase receptor of nerve growth factor useful for treating and  
 PT diagnosing neuropathological disorders such as pain, neuromas, TrkA  
 PT expressing neoplastic tumors

XX Claim 3; Page -; 33pp; English.

XX The invention relates to a murine monoclonal antibody, MNAC13, which  
 CC recognises the human nerve growth factor (NGF) receptor tyrosine  
 CC kinase, TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13  
 CC has a light chain variable region (VL) as given in AAB48936, and a heavy  
 CC chain variable region (VH) as given in AAB48937. The invention also  
 CC encompasses synthetic derivatives of monoclonal antibody MNAC13, such as  
 CC the single chain antibody, scFvMNAC13 (AAB48934), which comprises the  
 CC VL and VH regions of MNAC13 in one polypeptide chain. The invention  
 CC additionally relates to pharmaceutical compositions comprising the  
 CC antibody or antibody derivatives of the invention, engineered eukaryotic  
 CC cells able to express the MNAC13 antibody or its derivatives, and a  
 CC diagnostic composition comprising the antibody or its derivatives for in  
 CC vivo imaging. NGF antagonist (inhibitor of binding of NGF to TrkA  
 CC receptor) The MNAC13 monoclonal antibody and its derivatives are useful  
 CC for treating neurological pathologies such as acute or chronic pain,  
 CC neuromas, and TrkA-expressing neoplastic tumours. A composition  
 CC comprising MNAC13 or its derivatives with a diagnostically acceptable  
 CC carrier is useful for in vivo imaging diagnostics. The present  
 CC sequence represents the heavy chain variable region of the anti-TrkA  
 CC murine monoclonal antibody MNAC13.  
 CC Note: The present sequence is derived from that of the single chain  
 CC antibody scFvMNAC13 shown on pages 32-33 and the information given in  
 CC claim 3.

XX Sequence 125 AA;

Query Match 48.9%; Score 44; DB 22; Length 125;  
 Best Local Similarity 63.6%; Pred. No. 13;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 YGNPHYVAMDY 14  
 DB 101 YGndffypmDY 111

# RESULT 15

AAB48934  
 ID AAB48934 standard; Protein: 295 AA.

XX AAB48934;

XX 16-MAR-2001 (first entry)

XX Anti-TrkA single chain antibody scFvMNAC13.

KW Single chain antibody; murine monoclonal antibody MNAC13; scFvMNAC13;  
 KW human TrkA antagonist; NGF receptor; nerve growth factor;  
 KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;  
 KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging;  
 KW diagnosis.

OS Mus sp.  
 OS Synthetic.

XX WO200073344-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-IT00218.

XX 26-MAY-1999; 99IT-RM00333.

XX (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.

XX Novak MM;

XX WPI: 2001-061515/07.

XX N-PSDB; AAC87642.

XX Monoclonal antibody and its derivatives specific to high affinity  
 PT tyrosine kinase receptor of nerve growth factor useful for treating and

PT diagnosing neuropathological disorders such as pain, neuromas, TrkA  
 PT expressing neoplastic tumors

XX Claim 8; Page 32-33; 33pp; English.

XX The invention relates to a murine monoclonal antibody, MNAC13, which  
 CC recognises the human nerve growth factor (NGF) receptor tyrosine  
 CC kinase, TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13  
 CC has a light chain variable region (VL) as given in AAB48936, and a heavy  
 CC chain variable region (VH) as given in AAB48937. The invention also  
 CC encompasses synthetic derivatives of monoclonal antibody MNAC13, such as  
 CC the single chain antibody, scFvMNAC13 (AAB48934), which comprises the  
 CC VL and VH regions of MNAC13 in one polypeptide chain. The invention  
 CC additionally relates to pharmaceutical compositions comprising the  
 CC antibody or antibody derivatives of the invention, engineered eukaryotic  
 CC cells able to express the MNAC13 antibody or its derivatives, and a  
 CC diagnostic composition comprising the antibody or its derivatives for in  
 CC vivo imaging. NGF antagonist (inhibitor of binding of NGF to TrkA  
 CC receptor) The MNAC13 monoclonal antibody and its derivatives are useful  
 CC for treating neurological pathologies such as acute or chronic pain,  
 CC neuromas, and TrkA-expressing neoplastic tumours. A composition  
 CC comprising MNAC13 or its derivatives with a diagnostically acceptable  
 CC carrier is useful for in vivo imaging diagnostics. The present  
 CC sequence represents the anti-TrkA single chain antibody scFvMNAC13.

XX Sequence 295 AA;

Query Match 48.9%; Score 44; DB 22; Length 295;  
 Best Local Similarity 63.6%; Pred. No. 32;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 YGNPHYVAMDY 14  
 DB 252 YGndffypmDY 262

Search completed: June 28, 2001, 16:14:37  
 Job time: 1325 sec



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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 seconds  
(without alignments)  
2.039 Million cell updates/sec

Title: US-09-724-406-24  
Perfect score: 90  
Sequence: 1 DPYGNPHYAMDY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	63.3	115	3	US-08-881-037-22
2	57	63.3	121	3	US-08-881-037-67
3	52	57.8	108	1	US-08-436-463-17
4	42	46.7	123	2	US-08-561-521-9
5	42	46.7	123	2	US-08-561-521-11
6	42	46.7	123	5	PCT-US95-01219-9
7	42	46.7	123	5	PCT-US95-01219-11
8	42	46.7	140	5	PCT-US95-01219-4
9	42	46.7	140	5	PCT-US95-01219-17
10	42	46.7	142	2	US-08-561-521-17
11	42	46.7	142	5	PCT-US95-01219-17
12	41	45.6	2476	2	US-08-276-967-2
13	40	44.4	209	3	US-08-793-229-28
14	40	44.4	209	3	US-08-793-229-28
15	40	44.4	846	1	US-07-731-157A-5
16	40	44.4	846	2	US-08-541-780-5
17	39	43.3	209	2	US-08-793-229-29
18	39	43.3	209	3	US-08-793-229-29
19	39	43.3	246	1	US-08-197-834-7
20	39	43.3	284	3	US-08-793-229-31
21	39	43.3	284	3	US-08-793-229-31
22	39	43.3	348	4	US-09-285-957-28
23	39	43.3	348	5	PCT-US95-05785-2
24	39	43.3	399	2	US-08-282-197C-54
25	39	43.3	609	2	US-08-716-301-4
26	39	43.3	844	1	US-07-731-157A-6
27	39	43.3	844	2	US-08-541-780-6

28	39	43.3	3898	2	US-08-876-991-2	Sequence 2, Appl1
29	39	43.3	3898	2	US-09-059-853-2	Sequence 2, Appl1
30	38.5	42.8	481	4	US-08-843-659-4	Sequence 4, Appl1
31	38	42.2	27	6	5196510-1	Patent No. 5196510
32	38	42.2	113	2	US-08-273-146-59	Sequence 1, Appl1
33	38	42.2	115	1	US-08-468-661-1	Sequence 1, Appl1
34	38	42.2	115	1	US-08-466-272A-1	Sequence 1, Appl1
35	38	42.2	115	1	US-08-478-857-1	Sequence 1, Appl1
36	38	42.2	115	2	US-08-471-771-1	Sequence 1, Appl1
37	38	42.2	115	3	US-09-130-783-1	Sequence 1, Appl1
38	38	42.2	138	3	US-08-603-024-2	Sequence 1, Appl1
39	38	42.2	139	1	US-08-253-877C-8	Sequence 2, Appl1
40	38	42.2	139	1	US-08-253-877C-19	Sequence 8, Appl1
41	38	42.2	139	2	US-08-452-164A-8	Sequence 19, Appl1
42	38	42.2	139	2	US-08-452-164A-19	Sequence 8, Appl1
43	38	42.2	139	3	US-08-603-024-18	Sequence 18, Appl1
44	38	42.2	239	6	5455030-13	Patent No. 5455030
45	38	42.2	720	1	US-07-731-157A-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-881-037-22  
; Sequence 22, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Click, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1318  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 115 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-22

Query Match 63.3%; Score 57; DB 3; Length 115;  
Best Local Similarity 83.3%; Pred. No. 0.16;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Fri Jun 29 08:04:51 2001

us-09-724-406-24.ra1

QY 3 PYGNPHYAMDY 14  
Db 93 PYGNPHYAMDY 104

RESULT 2  
US-08-881-037-67  
; Sequence 67, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 121 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-67

Query Match 63.3%; Score 57; DB 3; Length 121;  
Best Local Similarity 83.3%; Pred. No. 0.17;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYGNPHYAMDY 14  
Db 100 PYGNPHYAMDY 111

RESULT 3  
US-08-436-463-17  
; Sequence 17, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-PELINE HERPES VIRUS-1 RECOMBINANT  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ANTI-BODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,463  
FILING DATE: 26-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 341255/1992  
FILING DATE: 28-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: KIMACHI=1  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-463-17

Query Match 57.8%; Score 52; DB 1; Length 108;  
Best Local Similarity 81.8%; Pred. No. 0.76;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
Db 92 YGNPHYAMDY 102

RESULT 4  
US-08-561-521-9  
; Sequence 9, Application US/08561521  
; Patent No. 5840299  
; GENERAL INFORMATION:  
; APPLICANT: Bendig, Mary M.  
; APPLICANT: Leger, Olivier J.  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Jones, S. Tarran  
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
; TITLE OF INVENTION: Adhesion Molecule VLA-4  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-9

Query Match 46.7%; Score 42; DB 2; Length 123;  
Best Local Similarity 72.7%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
||| |||||

Db 102 YGNYGVYAMDY 112

## RESULT 5

US-08-561-521-11  
Sequence 11, Application US/08561521  
Patent No 5840299

## GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:

## CLASSIFICATION: 424

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994

## ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043

## INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-561-521-11

Query Match 46.7%; Score 42; DB 2; Length 123;  
Best Local Similarity 72.7%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
||| |||||

Db 102 YGNYGVYAMDY 112

## RESULT 6

PCT-US95-01219-9  
Sequence 9, Application PC/TUS9501219  
GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043

## INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-9

Query Match 46.7%; Score 42; DB 5; Length 123;  
Best Local Similarity 72.7%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
||| |||||

Db 102 YGNYGVYAMDY 112

## RESULT 7

PCT-US95-01219-11

Sequence 11, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.

us-09-724-406-24.ra1

Fri Jun 29 08:04:51 2001

APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
ADHESION MOLECULE VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-11

Query Match 46.7%; Score 42; DB 5; Length 123;  
Best Local Similarity 72.7%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
111 11111

Db 102 YGNYGYAMDY 112

RESULT 8  
US-08-561-521-4  
Sequence 4, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
ADHESION MOLECULE VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-4

Query Match 46.7%; Score 42; DB 2; Length 140;  
Best Local Similarity 72.7%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
111 11111

Db 121 YGNYGYAMDY 131

RESULT 9  
PCT-US95-01219-4  
Sequence 4, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
ADHESION MOLECULE VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:



LENGTH: 140 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-4

Query Match 46.7%; Score 42; DB 5; Length 140;  
Best Local Similarity 72.7%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
||| |||||  
Db 121 YGNYGVYAMDY 131

RESULT 10  
US-08-561-521-17  
Sequence 17, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 142 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-17

Query Match 46.7%; Score 42; DB 2; Length 142;  
Best Local Similarity 72.7%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
||| |||||  
Db 121 YGNYGVYAMDY 131

RESULT 11

PCT-US95-01219-17  
Sequence 17, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 142 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-17

Query Match 46.7%; Score 42; DB 5; Length 142;  
Best Local Similarity 72.7%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
||| |||||  
Db 121 YGNYGVYAMDY 131

RESULT 12  
US-08-276-967-2  
Sequence 2, Application US/08276967  
Patent No. 5851817  
GENERAL INFORMATION:  
APPLICANT: Hardy, Daniel M.  
APPLICANT: Garbers, David L.  
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of  
TITLE OF INVENTION: Sperm  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,967  
FILING DATE: Submitted Herewith  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSD:418\KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2476 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-967-2

Query Match 45.6%; Score 41; DB 2; Length 2476;  
Best Local Similarity 60.0%; Pred. No. 7.4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMD 13  
||:|||||  
DB 804 YGDPHYLTFFD 813

RESULT 13  
US-08-793-229-28  
Sequence 28, Application US/08793229  
Patent No. 5891703  
GENERAL INFORMATION:  
APPLICANT: VAN DER LAAN, Jan Metske  
APPLICANT: RIEMENS, Adriana Marina  
APPLICANT: QUAX, Wilhelmus Johannes  
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,229  
FILING DATE: 23-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03249  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 97075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)913-0001  
TELEFAX: (312)913-0002  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 209 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-229-28

Query Match 44.4%; Score 40; DB 2; Length 209;  
Best Local Similarity 70.0%; Pred. No. .75;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMD 13  
||:|||||  
DB 14 YGMPHYIYAND 23

RESULT 14  
US-09-285-957-28  
Sequence 28, Application US/09285957  
Patent No. 6033823  
GENERAL INFORMATION:  
APPLICANT: VAN DER LAAN, Jan Metske  
APPLICANT: RIEMENS, Adriana Marina  
APPLICANT: QUAX, Wilhelmus Johannes  
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/285,957  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/793,229  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 97075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)913-0001  
TELEFAX: (312)913-0002  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 209 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-285-957-28

Query Match 44.4%; Score 40; DB 3; Length 209;  
Best Local Similarity 70.0%; Pred. No. .75;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMD 13  
||:|||||  
DB 14 YGMPHYIYAND 23

RESULT 15  
US-07-731-157A-5  
Sequence 5, Application US/07731157A  
Patent No. 5457032  
GENERAL INFORMATION:  
APPLICANT: Quax, Wilhelmus J.

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; APPLICANT: Misset, Onno
; APPLICANT: Van der Laan, Jan M.
; APPLICANT: Lenting, Herman B.M.
; TITLE OF INVENTION: Mutated beta-lactam acylase genes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/731,157A
; FILING DATE: 19910509
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90200962
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER PH.D., BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-027/0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-494-7622
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 846 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; AUTHORS: Schumacher, G
; AUTHORS: Sizmann, D
; AUTHORS: Haug, H
; AUTHORS: Buckel, P
; AUTHORS: Bock, A
; TITLE: Penicillin acylase from E.coli: unique
; TITLE: gene-protein realtion.
; JOURNAL: Nucleic Acids Res.
; VOLUME: 14
; PAGES: 5713-5727
; DATE: 1986
; US-07-731-157A-5

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Query Match 44.4%; Score 40; DB 1; Length 846;
Best Local Similarity 70.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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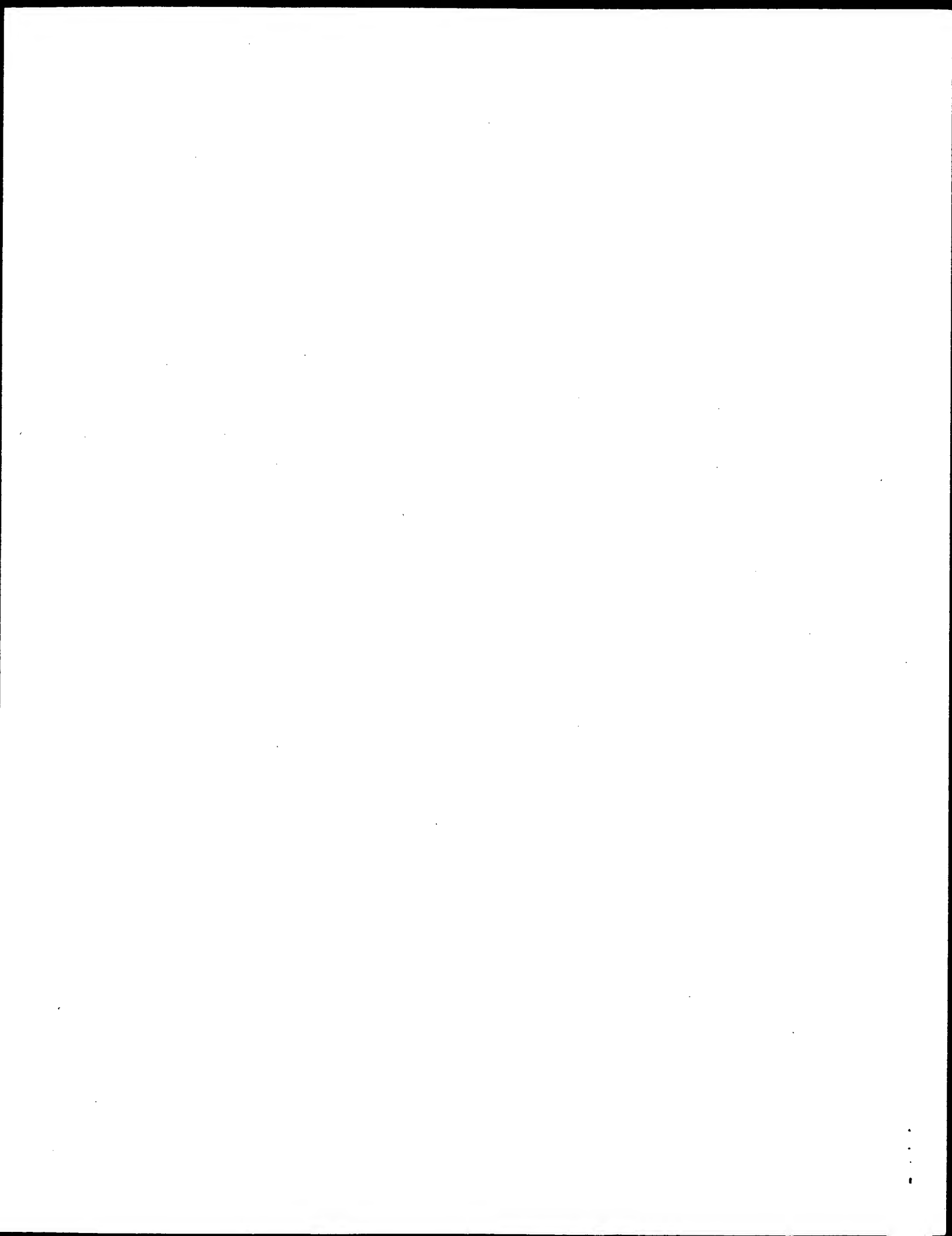
QY 4 YGNPHYAMD 13
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Db 40 YGNPHYAMD 49

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Search completed: June 28, 2001, 16:01:15
Job time: 523 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: June 28, 2001, 15:58:45 ; Search time 234.85 Seconds  
(without alignments)  
4.541 Million cell updates/sec

Title: US-09-724-406-24  
Perfect score: 90  
Sequence: 1 DPPYGNPHYAMDY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	57.8	15	2 PH1610	Ig H chain V-D-J r
2	52	57.8	94	2 PH0996	Ig heavy chain V r
3	51	56.7	113	2 S26468	Ig heavy chain V r
4	49	54.4	14	2 PH1608	Ig H chain V-D-J r
5	49	54.4	125	2 PH0100	Ig heavy chain V r
6	48	53.3	119	2 C53285	Ig heavy chain V a
7	48	53.3	139	2 A25912	Ig heavy chain pre
8	48	53.3	470	2 T49278	hypothetical prote
9	46	51.1	14	2 PH1615	Ig H chain V-D-J r
10	46	51.1	115	2 PC6026	acetylcholine recep
11	45	50.0	123	2 F48677	Ig heavy chain V-D
12	45	50.0	123	2 G48677	Ig heavy chain V-D
13	45	50.0	123	2 E48677	Ig heavy chain pre
14	45	50.0	136	1 GLMS21	ribulose-bisphosph
15	45	50.0	171	1 RKS25J	Ig H chain V-D-J r
16	44	48.9	13	2 PH1593	Ig H chain V-D-J r
17	44	48.9	16	2 PH1604	Ig heavy chain V r
18	44	48.9	118	2 A49026	Ig heavy chain V r
19	44	48.9	124	2 C27888	Ig heavy chain pre
20	44	48.9	140	2 S04575	Ig heavy chain pre
21	44	48.9	149	2 S30752	Ig heavy chain pre
22	44	48.9	1090	2 S59077	Ig heavy chain pre
23	43.5	48.3	2573	2 D71614	cellulose 1,4-beta
24	43	47.8	14	2 PH1597	hypothetical prote
25	43	47.8	119	2 E25114	Ig H chain V-D-J r
26	43	47.8	329	2 G71140	Ig heavy chain V r
27	43	47.8	381	2 A54415	hypothetical prote
28	43	47.8	647	2 S48471	transcription fact
29	43	47.8	878	2 T17245	probable membrane
					hypothetical prote

30	43	47.8	1080	2 A71485	probable pbp2-tran
31	43	47.8	2809	2 T30213	G-cadherin - sea u
32	42	46.7	45	2 PL0094	Ig heavy chain V r
33	42	46.7	77	2 D43331	sor 3'-region hypo
34	42	46.7	114	2 PH1027	Ig heavy chain V r
35	42	45.7	497	2 H83886	hypothetical prote
36	42	45.7	973	2 T35238	probable secreted
37	41.5	45.1	363	2 G81439	site-specific DNA-
38	41.5	45.1	856	2 G70483	pyruvate,water dik
39	41	43.6	14	2 PH1601	Ig H chain V-D-J r
40	41	43.6	17	2 PH1607	Ig H chain V-D-J r
41	41	43.6	110	2 S26323	Ig heavy chain V r
42	41	43.6	218	2 T36033	probable hydrolase
43	41	43.6	222	2 T36465	hypothetical prote
44	41	43.6	261	2 A84128	hypothetical prote
45	41	43.6	265	2 S32652	transcription fact

## ALIGNMENTS

### RESULT 1

PH1610  
Ig H chain V-D-J region (wild-type clone 337) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1610  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178; 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m  
A:Reference number: PH1580; MUID:93301609  
A:Accession: PH1610  
A:Molecule type: DNA  
A:Residues: 1-15 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 57.8%; Score 52; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.032;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GNPHYAMDY 14  
Db 6 GSPHYAMDY 15

### RESULT 2

PH0996  
Ig heavy chain V region (clone 165.3m) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PH0996  
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176; 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective  
A:Reference number: PH0971; MUID:92381444  
A:Accession: PH0996  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-94 <FIL>

C:Experimental source: B cell, strain [N2B x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 57.8%; Score 52; DB 2; Length 94;  
Best Local Similarity 64.3%; Pred. No. 0.23;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DPPYGNPHYAMDY 14  
Db 80 DPPLRRLYYAMDY 93

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;31-35/Region: complementarity-determining 1  
F;50-66/Region: complementarity-determining 2  
F;99-112/Region: complementarity-determining 3

Query Match 54.4%; Score 49; DB 2; Length 125;  
Best Local Similarity 72.7%; Pred. No. 0.95; Indels 0; Gaps 0;  
Matches 8; Conservative 2; Mismatches 1;

QY 4 YGNPHYVAMDY 14  
|||:|||||  
Db 102 YGSRNYAMDY 112

## RESULT 6

C53285  
Ig heavy chain V and J regions, monoclonal antibody OHP7D7.2.3 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C;Accession: C53285  
R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.  
Mol. Immunol. 28, 1063-1072, 1991  
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary st  
and their pH-reactivity profiles.  
A;Reference number: A53285; MUID:92017897  
A;Accession: C53285  
A;Status: preliminary  
A;Molecule type: mRNA; protein  
A;Residues: 1-119 <SAW>  
A;Cross-references: GB:D12734; NID:g220548; PIDN:BA02226.1; PID:g220549  
A;Note: sequence extracted from NCBI backbone (NCBI:63297, NCBI:63302)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 53.3%; Score 48; DB 2; Length 119;  
Best Local Similarity 80.0%; Pred. No. 1.3; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 1;

QY 5 GNPYYAMDY 14  
||:|||||  
Db 99 GNRYYAMDY 108

## RESULT 7

A25912  
Ig heavy chain precursor V region (W3129) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 23-Jul-1999  
C;Accession: A25912  
R;Borden, P.; Kabat, E.A.  
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987  
A;Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and ligh  
A;Reference number: A94147; MUID:87175689  
A;Accession: A25912  
A;Molecule type: mRNA  
A;Residues: 1-139 <BOR>  
A;Cross-references: GB:M15873; NID:g195268; PIDN:AAA38228.1; PID:g195269  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-139/Product: Ig heavy chain V region W3129 #status predicted <VAR>  
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 53.3%; Score 48; DB 2; Length 139;  
Best Local Similarity 80.0%; Pred. No. 1.5; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 1;

RESULT 3  
S26468  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S26468  
R;Kavaler, J.  
submitted to the EMBL Data Library, April 1991

A;Reference number: S26459  
A;Accession: S26468  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-113 <KAV>  
A;Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 56.7%; Score 51; DB 2; Length 113;  
Best Local Similarity 83.3%; Pred. No. 0.41; Indels 0; Gaps 1;  
Matches 10; Conservative 0; Mismatches 0;

QY 3 PYGNPHYVAMDY 14  
|||||:|||||  
Db 96 PYGN--YVAMDY 105

## RESULT 4

PH1608  
Ig H chain V-D-J region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1608  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609  
A;Accession: PH1608  
A;Molecule type: DNA  
A;Residues: 1-14 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte, wild-type clone 335  
A;Accession: PH1603  
A;Molecule type: DNA  
A;Residues: 1-14 <LEV2>  
A;Experimental source: bone marrow pre-B lymphocyte, wild-type clone 324  
C;Keywords: immunoglobulin

Query Match 54.4%; Score 49; DB 2; Length 14;  
Best Local Similarity 80.0%; Pred. No. 0.089; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 1;

QY 5 GNPYYAMDY 14  
||:|||||  
Db 5 GNSYYAMDY 14

## RESULT 5

PH0100  
Ig heavy chain V region (anti-cyclosporin E) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 21-Jan-2000  
C;Accession: PH0100  
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koehler, H.P.; Quesniaux, V.F.J.; V  
Mol. Immunol. 27, 1029-1038, 1990  
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.  
A;Reference number: PH0087; MUID:91042649  
A;Accession: PH0100  
A;Molecule type: mRNA  
A;Residues: 1-125 <SCH>

QY 5 GNPHYAMDY 14  
I: |||||  
Db 119 GDLHYAMDY 128

RESULT 8  
T49278  
hypothetical protein T21J18.90 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C:Accession: T49278  
R:Kieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: 225021  
A:Accession: T49278  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-470 <RIE>  
A:Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.90  
A:Experimental source: cultivar Columbia; BAC clone T21J18  
C:Genetics:  
A:Gene: ATSP:T21J18.90  
A:Map position: 3  
A:Introns: 35/2; 71/3; 123/3; 157/2; 174/2; 238/3; 269/1; 290/3; 342/2; 369/3; 406/2

Query Match 53.3%; Score 48; DB 2; Length 470;  
Best Local Similarity 63.8%; Pred. No. 5.7;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
I: |||||  
Db 83 YGLPYVVDY 93

RESULT 9  
PH1615  
Ig H chain V-D-J region (clone B-less 22) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1615  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609  
A:Accession: PH1615  
A:Molecule type: DNA  
A:Residues: 1-14 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 51.1%; Score 46; DB 2; Length 14;  
Best Local Similarity 88.9%; Pred. No. 0.26;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NPHYAMDY 14  
I: |||||  
Db 6 NPIYAMDY 14

RESULT 10  
PC6026  
acetylcholine receptor monoclonal antibody A7 heavy chain variable region - mouse (fragme  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jan-2000  
C:Accession: PC6026  
R:Meng, F.; Yang, K.; Graus, Y.; de Baets, M.  
Chinese J. Microbiol. Immunol. 16, 45-48, 1996  
A:Title: Pathogenicity and sequence analysis of a mouse anti-AChR monoclonal antibody A7  
A:Reference number: PC6026  
A:Accession: PC6026  
A:Molecule type: mRNA

A:Residues: 1-115 <HEN>  
A:Cross-references: EMBL:X80962  
C:Comment: This protein induces acetylcholine receptor loss and muscular weakness in m  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 51.1%; Score 46; DB 2; Length 115;  
Best Local Similarity 77.8%; Pred. No. 2.6;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 NPHYAMDY 14  
I: |||||  
Db 96 SPYIYAMDY 104

RESULT 11  
F48677  
Ig heavy chain V-D-J region (44.1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C:Accession: F48677  
R:Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann  
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993  
A:Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antio  
A:Reference number: A48677; MUID:94022404  
A:Accession: F48677  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-123 <TAS>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 45; DB 2; Length 123;  
Best Local Similarity 63.6%; Pred. No. 4;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
I: |||||  
Db 102 FGGYVYAMDY 112

RESULT 12  
G48677  
Ig heavy chain V-D-J region (419.1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C:Accession: G48677  
R:Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann  
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993  
A:Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antio  
A:Reference number: A48677; MUID:94022404  
A:Accession: G48677  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-123 <TAS>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 45; DB 2; Length 123;  
Best Local Similarity 63.6%; Pred. No. 4;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14  
I: |||||  
Db 102 FGGYVYAMDY 112

RESULT 13









GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:38 ; Search time 105.36 Seconds  
(without alignments)  
4.552 Million cell updates/sec

Title: US-09-724-406-24  
Perfect score: 90  
Sequence: 1 DPPYGNPHYANDY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues  
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	50.0	136	1	HV16_MOUSE
2	45	50.0	171	1	RBS_PINTH
3	44	48.9	1090	1	GUXB_CELFI
4	43	47.8	647	1	YIKI_YEAST
5	42	46.7	77	1	YSO4_ACIAM
6	41.5	46.1	856	1	PSA_AQUAE
7	41	45.6	265	1	OC3B_HUMAN
8	41	45.6	360	1	OC3A_HUMAN
9	41	45.6	407	1	MURG_MYCLE
10	41	45.6	1592	1	GTF2_STRDO
11	41	45.6	2476	1	ZAN_PIG
12	40.5	45.0	221	1	SFR9_HUMAN
13	40	44.4	482	1	YGFU_ECOLI
14	40	44.4	608	1	PKCK_NEOFR
15	40	44.4	834	1	TF1B_MOUSE
16	40	44.4	835	1	TF1B_HUMAN
17	40	44.4	846	1	PAC_ECOLI
18	39.5	43.9	3530	1	MY15_HUMAN
19	39	43.3	107	1	COTT_BACSU
20	39	43.3	180	1	RBS1_PETSP
21	39	43.3	180	1	RBS2_PETSP
22	39	43.3	230	1	PRP2_SOYBN
23	39	43.3	252	1	GSPN_AERHY
24	39	43.3	348	1	GALE_HUMAN
25	39	43.3	660	1	PRIA_BORBU
26	39	43.3	837	1	XYNZ_CLOTM
27	39	43.3	841	1	YAGX_ECOLI
28	39	43.3	844	1	PAC_KLUCI
29	39	43.3	3898	1	POIG_HCVA
30	38.5	42.8	481	1	KRL_HSV11
31	38	42.2	124	1	V124_ASFB7
32	38	42.2	124	1	V124_ASFL5
33	38	42.2	124	1	V125_ASFL5

34	38	42.2	162	1	CBP6_YEAST	P07253	saccharomyc
35	38	42.2	311	1	7B4C_PSESP	P07662	pseudomonas
36	38	42.2	366	1	1C03_HUMAN	P30501	homo sapien
37	38	42.2	366	1	1C04_HUMAN	P30502	homo sapien
38	38	42.2	381	1	ORIA_DROME	Q9W5G6	drosophila
39	38	42.2	772	1	CPTM_RAT	Q63704	rattus norv
40	38	42.2	877	1	INCE_CHICK	P53352	gallus gall
41	38	42.2	919	1	EXLS_HUMAN	O43909	homo sapien
42	38	42.2	960	1	VP41_LYCES	P93231	lycopersico
43	38	42.2	976	1	VP41_ARATH	P93043	arabidopsis
44	37.5	41.7	87	1	UV15_SCHPO	P40388	schizosacch
45	37.5	41.7	1569	1	GLI3_XENLA	Q91660	xenopus lae

## ALIGNMENTS

RESULT 1  
HV16\_MOUSE  
ID HV16\_MOUSE STANDARD; PRT; 136 AA.  
AC P01783;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.D.M., Paskin M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPb family of  
antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
RN [2]  
RP SEQUENCE OF 17-136.  
RX MEDLINE=77100368; PubMed=401950;  
RA Adetugbo K., Milstein C., Secher D.S.;  
RL "Molecular analysis of spontaneous somatic mutants.";  
RL Nature 265:299-304(1977).  
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CC EMBL; J00522; AAD15290.1; -  
CC PIR; A02066; GIMS21.  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; ig; 1.  
DR Immunoglobulin V region; Signal.  
FT NON\_TER 1  
FT SIGNAL <1 16  
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.  
FT DOMAIN 115 119 D SEGMENT.  
FT DOMAIN 120 136 JH4 SEGMENT.  
FT DISULFID 38 112  
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).  
FT CONFLICT 89 90 DN -> ND (IN REF. 2).  
FT CONFLICT 115 115 W -> H (IN REF. 2).  
FT CONFLICT 120 120 Y -> W (IN REF. 2).  
FT NON\_TER 136 136  
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 50.0%; Score 45; DB 1; Length 136;  
Best Local Similarity 72.7%; Pred. No. 2.2;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNPHYVAMY 14  
:||| |||||  
Db 115 WGNPHYVAMY 125

RESULT 2  
RBS\_PINTH  
ID RBS\_PINTH STANDARD; PRT; 171 AA.  
AC P10053;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (EC 4.1.1.39)  
DE (RUBISCO SMALL SUBUNIT).  
GN RCS.  
OS Pinus thunbergii (Green pine) (Japanese black pine).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=3350;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89098345; PubMed=3267239;  
RA Yamamoto N., Matsuo M., Kano Murakami Y., Tanaka Y., Ohashi Y.;  
RT "Mouse spleen derived cDNA clones containing per repeat sequence.";  
RL Nucleic Acids Res. 16:11831-11831(1988).  
CC -!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF  
D-RIBULOSE 1,5-BIPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC  
CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF  
THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH  
REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME  
ACTIVE SITE.  
CC -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BIPHOSPHATE + CO(2) =  
2 3-PHOSPHO-D-GLYCERATE.  
CC -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BIPHOSPHATE + O(2) =  
3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.  
CC -!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -!- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.  
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CC -----  
CC EMBL; X13408; CAA31774.1; -.  
CC PIR; S02046; RKSZSJ.  
CC HSSP; P00866; IRLC.  
CC Mendel; 447; PINTH; rbcS;1.  
CC InterPro; IPR000894; -.  
CC PRINTS; PR00101; RuBisCO\_small; 1.  
CC PRAM; PF00152; RUBISCO SMALL.  
CC Photosynthesis; Carbon dioxide fixation; Photorespiration;  
KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit peptide.  
FT TRANSIT 1 51  
FT CHAIN 52 171  
FT RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL  
FT CHAIN.  
SQ SEQUENCE 171 AA; 19312 MW; 8064DB3DDE87A448 CRC64;

Query Match 50.0%; Score 45; DB 1; Length 171;  
Best Local Similarity 46.2%; Pred. No. 2.8;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 PPGNPHYVAMY 14  
:||| :||  
Db 56 PPGNPHYVAMY 68

RESULT 3  
GUXB\_CELFI STANDARD; PRT; 1090 AA.  
AC P50899;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE EXOGLUCANASE B PRECURSOR (EC 3.2.1.91) (EXOCELLIOHYDROLASE B)  
DE (1,4-BETA-CELLIOHYDROLASE B) (CBP120).  
DE CBHB OR CENE.  
GN Cellulomonas fimi.  
OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Micrococcales; Cellulomonadaceae; Cellulomonas.  
OX NCBI\_TaxID=1708;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 456-461.  
RX STRAIN=ATCC 484;  
RX MEDLINE=96003898; PubMed=7575482;  
RA Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;  
RT "Cellulohydrolase B, a second exo-cellulohydrolase from the  
cellulolytic bacterium Cellulomonas fimi.";  
RL Biochem. J. 311:67-74(1995).  
RN [2]  
RP SEQUENCE OF 54-75.  
RX MEDLINE=93209933; PubMed=8458833;  
RA Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;  
RT "Cellulose-binding polypeptides from Cellulomonas fimi: endoglucanase  
D (CenD), a family A beta-1,4-glucanase.";  
RL J. Bacteriol. 175:1910-1918(1993).  
RN [3]  
RP SEQUENCE OF 54-78.  
RX MEDLINE=94197708; PubMed=8147863;  
RA Shen H., Tomme P., Meinke A., Gilkes N.R., Kilburn D.G.,  
Warren R.A.J., Miller R.C. Jr.;  
RT "Stereochemical course of hydrolysis catalysed by Cellulomonas fimi  
CenB, a member of a new family of beta-1,4-glucanases.";  
RL Biochem. Biophys. Res. Commun. 199:1223-1228(1994).  
CC -!- FUNCTION: HYDROLYSE CELLOHEXACSE TO A MIXTURE OF CELLOTETRAOSE,  
CELLOTRIOSE AND CELLOBIOSE, WITH ONLY A TRACE OF GLUCOSE. IT  
HYDROLYSED CELLOPENTAASE TO CELLOTRIOSE AND CELLOBIOSE, AND  
CELLOTETRAOSE TO CELLOBIOSE, BUT IT DID NOT HYDROLYSE CELLOTROSE.  
HAS ALSO WEAK ENDOGLUCANASE ACTIVITY. HYDROLYSES GLUCOSIDIC BONDS  
WITH INVERSION OF ANOMERIC CONFIGURATION.  
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC LINKAGES  
IN CELLULOSE AND CELLOTETRAOSE, RELEASING CELLOBIOSE FROM THE NON-  
REDUCING ENDS OF THE CHAINS.  
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN  
(CBD).  
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY L (FAMILY 48 OF GLYCOSYL  
HYDROLASES).  
CC -----  
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CC -----  
CC EMBL; L38827; AAB00822.1; -.  
CC HSSP; P07986; 1EXH.  
CC InterPro; IPR000556; -.  
CC InterPro; IPR001777; -.  
CC InterPro; IPR001919; -.  
CC Pfam; PF00553; CBD\_2; 1.  
CC Pfam; PF02011; Glyco\_hydro\_48; 1.  
CC Pfam; PF00041; fn3; 3.  
CC PRINTS; PR00014; FNTYPEIII.  
CC PRINTS; PR00844; GLHYDRLASE48.  
CC PROSITE; PS00561; CBD\_BACTERIAL; 1.  
KW Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.  
FT SIGNAL 1 33  
FT POTENTIAL.

FT PROPEP 34 53  
 FT CHAIN 54 1090  
 FT DOMAIN 54 699  
 FT DOMAIN 700 785  
 FT DOMAIN 794 884  
 FT DOMAIN 891 978  
 FT DOMAIN 989 1090  
 FT ACT\_SITE 513 513  
 FT DISULFID 990 1089  
 SQ SEQUENCE 1090 AA; 114829 MW; 046B9D956F2F399 CRC64;

Query Match 48.9%; Score 44; DB 1; Length 1090;  
 Best Local Similarity 53.8%; Pred. No. 29;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 PPGNPHYAMDY 14  
 |||||  
 Db 446 PPGTPTFGMGY 458

## RESULT 4

YIKI\_YEAST STANDARD; PRT; 647 AA.  
 AC P40489;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HYPOTHETICAL 72.7 KDA PROTEIN IN MOB1-SGAI INTERGENIC REGION.  
 GN YIL101C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,  
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,  
 RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,  
 RA Louis E., Lye G., Moule S., Moutie T., Odell C., Pearson D.,  
 RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,  
 RA Walsh S.V., Whitehead S.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL; Z38125; CAA86279.1; -  
 DR PIR; S48471; S48471.  
 DR SGD; S0001363; XBPI.  
 KW Hypothetical protein.  
 SQ SEQUENCE 647 AA; 72687 MW; 5087D00C1D1AC4A5 CRC64;

Query Match 47.8%; Score 43; DB 1; Length 647;  
 Best Local Similarity 50.0%; Pred. No. 24;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 PYGNPHYAMDY 14  
 |||||  
 Db 593 PYGDDHVFLLKY 604

## RESULT 5

Y504\_AC1AM STANDARD; PRT; 77 AA.  
 ID Y504\_AC1AM  
 AC P29088;

DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE HYPOTHETICAL PROTEIN IN SOR 3'REGION (ORF4) (FRAGMENT).  
 OS Acidianus ambivalens (Desulfurolobus ambivalens).  
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Acidianus.  
 OX NCBI\_TaxID=2283;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LEI 10 / DSM 3772;  
 RC MEDLINE=92394888; PubMed=1522063;  
 RA Kletzin A.;  
 RT "Molecular characterization of the sor gene, which encodes the sulfur  
 RT oxygenase/reductase of the thermoacidophilic Archaeum Desulfurolobus  
 RT ambivalens.";  
 RL J. Bacteriol. 174:5854-5859(1992).  
 CC -!- INDUCTION: ANAEROBICALLY INDUCED.  
 CC -----  
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 CC -----  
 CC EMBL; X56616; CAA39954.1; -  
 DR PIR; S24834; S24834.  
 DR PIR; D43331; D43331.  
 KW Hypothetical protein.  
 FT NON\_TER 77 77  
 SQ SEQUENCE 77 AA; 8665 MW; 1B954D055CDDAAE1 CRC64;

Query Match 46.7%; Score 42; DB 1; Length 77;  
 Best Local Similarity 85.7%; Pred. No. 3.5;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PYGNPHY 9  
 |||||  
 Db 4 PYGNPHY 10

## RESULT 6

PPSA\_AQUAE STANDARD; PRT; 856 AA.  
 ID PPSA\_AQUAE  
 AC O67899;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE PHOSPHONOLPYRUVATE SYNTHASE (EC 2.7.9.2) (PYRUVATE, WATER KINASE)  
 DE (PEP SYNTHASE).  
 GN PPSA OR AQ\_2142.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VF5;  
 RC MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus.";  
 RL Nature 392:353-358(1998).  
 CC -!- CATALYTIC ACTIVITY: ATP + PYRUVATE + H(2)O = AMP +  
 CC PHOSPHONOLPYRUVATE + PHOSPHATE.  
 CC -!- PATHWAY: ESSENTIAL STEP IN GLUCONEOGENESIS WHEN PYRUVATE AND  
 CC LACTATE ARE USED AS A CARBON SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE PEP-UTILIZING ENZYMES FAMILY.  
 CC -----  
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DR EMBL; AE000775; AAC07865.1; -  
 DR InterPro; IPR000121; -  
 DR InterPro; IPR002192; -  
 DR Pfam; PF00391; PEP-utilizers; 2.  
 DR Pfam; PF01326; PPK\_N-term; 1.  
 DR PROSITE; PS00370; PEP\_ENZYMES\_PHOS\_SITE; 1.  
 DR PROSITE; PS00742; PEP\_ENZYMES\_2; 1.  
 DR Transferase; Kinase; ATP-binding; Phosphorylation.  
 FT MOD\_RES 433 433 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 856 AA; 96406 MW; 0CB001DABE289912 CRC64;

Query Match 46.1%; Score 41.5; DB 1; Length 856;  
 Best Local Similarity 47.1%; Pred. No. 55;  
 Matches 8; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY 3 PYG-----NPHYVYMDY 14  
 ||| | : || : ||  
 Db 46 PYGVVVTANAYYYFLDY 62

RESULT 7  
 OC3B\_HUMAN STANDARD; PRT; 265 AA.  
 ID OC3B\_HUMAN STANDARD; PRT; 265 AA.  
 AC P31359;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OCTAMER-BINDING TRANSCRIPTION FACTOR 3B (OCT-3B).  
 GN POU5F1 OR OTF3 OR OCT3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=93027160; PubMed=1408763;  
 RA Takeda J., Seino S., Bell G.I.;  
 RT "Human Oct3 gene family: cDNA sequences, alternative splicing, gene  
 RT organization, chromosomal location, and expression at low levels in  
 RT adult tissues.";  
 RL Nucleic Acids Res. 20:4613-4620(1992).  
 CC -1- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE OCTAMER MOTIF  
 CC ('ATTTCAT'). PRIME CANDIDATE FOR AN EARLY DEVELOPMENTAL CONTROL  
 CC GENE.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; OCT-3A (AC Q01860) AND OCT-3B  
 CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS  
 CC TO CLASS-5 POU.

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DR EMBL; Z11899; CAA77952.1; -  
 DR HSPF; P20263; LOC.  
 DR TRANSFAC; T01872; -  
 DR MIM; 164177; -  
 DR InterPro; IPR000327; -  
 DR InterPro; IPR001356; -

DR Pfam; PF00046; homeobox; 1.  
 DR Pfam; PF00157; pou; 1.  
 DR PRINTS; PR00028; POU DOMAIN.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00035; POU\_1; 1.  
 DR PROSITE; PS00045; POU\_2; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW Homeobox; DNA-binding; Transcription regulation; Nuclear protein;  
 KW Alternative splicing; Polymorphism.  
 FT DOMAIN 47 117 POU  
 FT DNA\_BIND 135 194 HOMEBOX.  
 FT VARIANT 227 227 T->A.  
 FT VARIANT 262 262 /FTID=VAR\_003774.  
 FT VARIANT M->L.  
 FT FTID=VAR\_003775.  
 SQ SEQUENCE 265 AA; 30084 MW; 41C21E136EFCBB2 CRC64;

Query Match 45.6%; Score 41; DB 1; Length 265;  
 Best Local Similarity 54.5%; Pred. No. 19;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPYGNPHYVAM 12  
 |||:|:|:  
 Db 228 PYGSPHFTAL 238

RESULT 8  
 OC3A\_HUMAN STANDARD; PRT; 360 AA.  
 ID OC3A\_HUMAN STANDARD; PRT; 360 AA.  
 AC Q01860; Q15167; Q15168; Q16422;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4).  
 GN POU5F1 OR OTF3 OR OCT3 OR OCT4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=93027160; PubMed=1408763;  
 RA Takeda J., Seino S., Bell G.I.;  
 RT "Human Oct3 gene family: cDNA sequences, alternative splicing, gene  
 RT organization, chromosomal location, and expression at low levels in  
 RT adult tissues.";  
 RL Nucleic Acids Res. 20:4613-4620(1992).  
 CC -1- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE OCTAMER MOTIF  
 CC ('ATTTCAT'). PRIME CANDIDATE FOR AN EARLY DEVELOPMENTAL CONTROL  
 CC GENE.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; OCT-3A (SHOWN HERE) AND OCT-3B  
 CC (AC P31359); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS  
 CC TO CLASS-5 POU.  
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CC EMBL; Z11898; CAA77951.1; -  
CC EMBL; Z21963; CAA79974.1; -  
CC EMBL; Z21964; CAA79975.1; -  
CC EMBL; S81255; AAB35990.1; -  
CC PIR; S25561; S25561.  
CC HSSP; P20263; 10CP.  
CC TRANSPAC; T00652; -  
CC MIM; 164177; -  
CC InterPro; IPR000327; -  
CC InterPro; IPR001356; -  
CC Pfam; PF00046; homeobox; 1.  
CC Pfam; PF00157; pou; 1.  
CC PRINTS; PR00028; POU DOMAIN.  
CC PROSITE; PS00027; HOMEBOX\_1; 1.  
CC PROSITE; PS00035; POU\_1; 1.  
CC PROSITE; PS00465; POU\_2; 1.  
CC PROSITE; PS50071; HOMEBOX\_2; 1.  
CC Homeobox; DNA-binding; Transcription regulation; Nuclear protein;  
KW Alternative splicing.  
FT DOMAIN 142 212 POU.  
FT DNA\_BIND 230 289  
FT CONFLICT 189 189 A -> G (IN REF. 2; Z21963).  
FT CONFLICT 220 220 I -> T (IN REF. 2; Z21963).  
FT CONFLICT 227 227 V -> L (IN REF. 2; Z21963).  
FT CONFLICT 230 230 R -> G (IN REF. 2; Z21964).  
FT CONFLICT 240 240 Q -> R (IN REF. 2; Z21964).  
FT CONFLICT 251 251 R -> Q (IN REF. 2; Z21964).  
FT CONFLICT 276 276 V -> VVRV (IN REF. 3).  
SQ SEQUENCE 360 AA; 38570 MW; 934C58DAEA0C535B CRC64;  
  
Query Match 45.6%; Score 41; DB 1; Length 360;  
Best Local Similarity 54.5%; Pred. No. 26;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 PPYGNPHYAM 12  
Db 323 PGYGSHPHTAL 333  
  
RESULT 9  
MURC\_MYCLE STANDARD; PRT; 407 AA.  
AC O69552;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE UDP-N-ACETYLGLUCOSAMINE--N-ACETYL-MURAMYL-(PENTAPEPTIDE)  
DE PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE  
DE (EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC  
DE TRANSFERASE).  
GN MURG OR MLCB268.02C.  
OS Mycobacterium leprae.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RL Brown D., Churcher C.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC  
SUBUNIT ON UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE (LIPID  
INTERMEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-  
(PENTAPEPTIDE)GLCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY).  
CC -!- PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.  
  
CC -!- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE MURG FAMILY.  
CC -----  
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DR PIR: A38175; A38175.  
 DR HSP: P00695; 2HEE.  
 DR InterPro: IPR002479; -.  
 DR Pfam: PF01473; CW\_binding\_1; 16.  
 KW Transferase; Glycosyltransferase; Signal; Repeat; Dental caries.  
 FT SIGNAL 1 38 POTENTIAL.  
 FT CHAIN 39 1592 GLUCOSYLTRANSFERASE-I.  
 FT DOMAIN 39 1044 CATALYTIC (APPROXIMATE).  
 FT DOMAIN 1093 1592 GLUCAN-BINDING (APPROXIMATE).  
 FT REPEAT 1093 1592 6.5 X TANDEM REPEATS.  
 FT REPEAT 1142 1207 1.  
 FT REPEAT 1158 1207 2.  
 FT REPEAT 1222 1272 3.  
 FT REPEAT 1287 1337 4.  
 FT REPEAT 1402 1451 5.  
 FT REPEAT 1514 1563 6.  
 FT REPEAT 1577 1592 7 (INCOMPLETE).  
 SQ SEQUENCE 1592 AA; 176167 MW; BC0A66D079351ECF CRC64;  
 Query Match 45.6%; Score 41; DB 1; Length 1592;  
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 5 GNPHYAMD 13  
 Db 1133 GNSHYAMD 1141  
 RESULT 11  
 ZAN\_PIG STANDARD; PRT; 2476 AA.  
 AC Q28983;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE ZONADHESIN PRECURSOR.  
 GN ZAN.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MEISHAN; TISSUE=Testis;  
 RX MEDLINE=96064658; PubMed=7592795;  
 RA Hardy D.M., Garbers D.L.;  
 RT "A sperm membrane protein that binds in a species-specific manner to  
 the egg extracellular matrix is homologous to von Willebrand  
 factor.";  
 RL J. Biol. Chem. 270:26025-26028(1995).  
 CC - FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA  
 CC OF THE EGG.  
 CC - SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.  
 CC -! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -! TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.  
 CC NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.  
 CC -! DOMAIN: THE UNIQUE N-TERMINAL DOMAIN AND THE MUCIN-LIKE DOMAINS  
 CC ARE MISSING FROM THE ZONADHESIN THAT BINDS TO THE EGG  
 CC EXTRACELLULAR MATRIX. PROCESSING MIGHT OCCUR DURING SPERM  
 CC MATURATION AND/OR CAPACITATION.  
 CC -! DOMAIN: THE UNIQUE N-TERMINAL DOMAIN PROBABLY MEDIATES SPERM  
 CC ADHESION TO THE ZONA PELLUCIDA.  
 CC -! DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,  
 CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF  
 CC SPERMATOZOON OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.  
 CC -! DOMAIN: THE VWF DOMAINS 1 AND 2 MAY MEDIATE COVALENT  
 CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).  
 CC -! SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 CC -! SIMILARITY: CONTAINS 4.5 VWF DOMAINS.  
 CC -! SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.  
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 CC -----  
 CC EMBL; U40024; AAC48486.1; -.  
 DR InterPro: IPR000561; -.  
 DR InterPro: IPR000998; -.  
 DR InterPro: IPR001846; -.  
 DR InterPro: IPR002919; -.  
 DR Pfam: PF00629; MAM; 2.  
 DR Pfam: PF01826; TIL; 5.  
 DR Pfam: PF00094; vwd; 4.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS00740; MAM\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 4.  
 DR PROSITE: PS00060; MAM\_2; 2.  
 KW Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;  
 KW Repeat.  
 FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 2476 ZONADHESIN.  
 FT DOMAIN 30 2418 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 2419 2439 POTENTIAL.  
 FT DOMAIN 2440 2476 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 144 312 MAM.  
 FT DOMAIN 319 687 53 X HEPTAPEPTIDE REPEATS (APPROXIMATE)  
 FT DOMAIN 688 799 (MUCIN-LIKE DOMAIN).  
 FT DOMAIN 800 1184 VWF 1 (PARTIAL).  
 FT DOMAIN 1185 1573 VWF 2.  
 FT DOMAIN 1574 1968 VWF 3.  
 FT DOMAIN 1969 2370 VWF 4.  
 FT DOMAIN 2366 2402 VWF 5.  
 FT DOMAIN 2370 2381 EGF-LIKE.  
 FT DISULFID 2370 2381 BY SIMILARITY.  
 FT DISULFID 2375 2390 BY SIMILARITY.  
 FT DISULFID 2392 2401 BY SIMILARITY.  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 735 735 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 758 758 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 833 833 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1154 1154 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1329 1329 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1448 1448 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1544 1544 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1596 1596 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1654 1654 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1843 1843 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1965 1965 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 2122 2122 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 2165 2165 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 2178 2178 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 2329 2329 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 2359 2359 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 2476 AA; 270364 MW; A13B890375A6548C CRC64;  
 Query Match 45.6%; Score 41; DB 1; Length 2476;  
 Best Local Similarity 60.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 4 YGNPHYAMD 13  
 Db 804 YGDPHYLTFD 813  
 RESULT 12  
 SFR9\_HUMAN STANDARD; PRT; 221 AA.  
 ID SFR9\_HUMAN  
 AC Q13242;  
 DT 15-DEC-1998 (Rel. 37, Created)



```

GN YGFU.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9279503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE XANTHINE/URACIL PERMEASES FAMILY.
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CC
DR EMBL: U28375; AAA83069.1; ALT_INIT.
DR EMBL: AE000372; AAC75926.1; ALT_INIT.
DR Ecogene: EGI3071; Y9fU.
DR InterPro: IPR000444; -.
DR Pfam: PF00860; xan_ur_permease; 1.
DR PROSITE: PS01116; XANTH_URACIL_PERMASE; 1.
KW Hypothetical protein; Transmembrane; Transport.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.
FT TRANSMEM 205 225 POTENTIAL.
FT TRANSMEM 262 282 POTENTIAL.
FT TRANSMEM 338 358 POTENTIAL.
FT TRANSMEM 360 380 POTENTIAL.
FT TRANSMEM 393 413 POTENTIAL.
FT TRANSMEM 422 442 POTENTIAL.
FT SEQUENCE 482 AA; 51758 MW; E08EF1D4CBD9D066 CRC64;
SQ
Query Match 44.4%; Score 40; DB 1; Length 482;
Best Local Similarity 42.9%; Pred. No. 51;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0
QY 1 DPQYGNPHYVYAMDY 14
: | | | | | :
DB 176 NPQYGNPVLGISF 189
RESULT 14
PPCK_NEOFR
ID PPCK_NEOFR STANDARD; PRT; 608 AA.
AC P22130;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
DE (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK).
OS Neocallimastix frontalis (Rumen fungus).
OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC Neocallimastacaceae; Neocallimastix.
OC NCBI_TaxID=4757;
OX [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92184115; PubMed=1339359;

```





